

New York University School of Medicine
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No Blast Hits ()

FEATURES

source Location/Qualifiers

1. .1037
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17X"
/sub_species="yoelii"
/db_xref="taxon:73239"
/dev_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million plasmidium yoelii 17X sporozoites were isolated from salivary glands of infected Anopheles stephensi mosquitoes and purified over a DE52 cellulose column. The sporozoites were cultured for 24h at 37C in the presence of 5% CO2 and 10% FBS as described in 'Transformation of sporozoites into early exoerythrocytic malaria parasites does not require host cells', (J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BD Biosciences SMART cDNA synthesis kit. Double stranded cDNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."

ORIGIN

Query Match 5.8%; Score 271.8; DB 14; Length 1037;
Best Local Similarity 91.9%; Pred. No. 1.4e-36;
Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
QY 571 GCTGACATTTATATCCCGAATCAGGTAAATGGCTTTTGTGTCATTTTCGG 630
Db 496 GCTGACATTTATATCCCGAATCAGGTAAATGGCTTTTGTGTCATTTTCGG 437
QY 631 GTGGCTGAGATCAGCATTTTCCCGATACCGGAGACCGGCACACTGGCCATATCGGT 690
Db 436 GTGGCTGAGATCAGCATTTTCCCGATACCGGAGACCGGCACACTGGCCATATCGGT 377
QY 691 GGTATATGCGCAGCTTTCATCCCGATATGACACCGGTAAGTTACGGGAGAC 750
Db 376 GGTATATGCGCAGCTTTCATCCCGATATGACACCGGTAAGTTACGGGAGAC 317
QY 751 TTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCGTCCCGGGGGTGTTC 810
Db 316 TTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCGTCCCGGGGGTGTTC 257
QY 811 AATAATATCCTCTGTAATCCACAAACAG--ACGATAACGGCTCTCTTTTATAGGTG 868
Db 256 AATAAGATCACTCTGTATCATCAGATACAGATAACCGNCTCTCTNTTTATAGGTC 197
QY 869 TAAACCTTAAACTGCATTC 888
Db 196 AAACCTTNAACCCGNTTC 177

RESULT 15

AG000791
LOCUS 724 bp DNA linear GSS 06-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000791
VERSION AG000791.1 GI:2579599
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)

AUTHORS

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1997)
2 (bases 1 to 724)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan [E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561]

FEATURES

source

Location/Qualifiers
1. .724

/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="64E11X4"

ORIGIN

Query Match 5.6%; Score 264.4; DB 23; Length 724;
Best Local Similarity 98.6%; Pred. No. 2.8e-35;
Matches 288; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
QY 847 ACGGCTCTCTCTTTTATAGGTGTAACCC-TTAAATGCAATTTACCAAGTCCCTGTTCG 905
Db 27 ACGGCTCTCTCTTTTATAGGTGTAACCC-TTAAATGCAATTTACCAAGTCCCTGTTCG 86
QY 906 TCAGCAAAAGAGCCGTTTCATTTCAATAAACCGGGGAGCTCAGCCATCCCTTCCTGATTT 965
Db 87 TCAGCAAAAGAGCCGTTTCATTTCAATAAACCGGGGAGCTCAGCCATCCCTTCCTGATTT 146
QY 966 TCCGCTTTCCAGCGTTCCGACGACGACGCGGCTTCATTTCTGATGTTGTGTTACC 1025
Db 147 TCCGCTTTCCAGCGTTCCGACGACGACGCGGCTTCATTTCTGATGTTGTGTTACC 206
QY 1026 AGACGGAGATTTGACATCATATATGCTTTGAGCACTGATAGCTGCTGTCAACTG 1085
Db 207 AGACGGAGATTTGACATC--ATATGCTTTGAGCACTGATAGCTGCTGTCAACTG 264
QY 1086 TCAGTGAATACGCTGCTTCATAGCAGACACCTCTTTTGACATACTTCGGGTA 1137
Db 265 TCAGTGAATACGCTGCTTCATAGCAGACACCTCTTTTGACATACTTCGGGTA 316

Search completed: May 9, 2004, 21:55:54
Job time : 7263.7 secs

COMMENT
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
1. 337
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-tokei standard"
/db_xref="taxon:35983"
/clone="jml8n08"
/tissue_type="mixture of flower and flower bud"
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Query Match 6.4%; Score 301.4; DB 12; Length 337;
Best Local Similarity 99.4%; Pred. No. 1.9e-41;
Matches 313; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 546 CTGCACAGTGGCTGTGTATAGAGGAGCCTCAGATTATATCCCGAGAACATCAGGTAA 605
DB 24 CTGCACAGTGGCTGTGTATAGAGGAGCCTGACATTATATCCCGAGAACATCAGGTAA 83
QY 606 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGG 665
DB 84 TGGC-TTTTTGTATGCCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGG 142
QY 666 AGACCGGCACATGCGCATATCGTGGTGCATATGCGCAGCTTTCATCCCGATATGCA 725
DB 143 AGACCGGCACATGCGCATATCGTGGTGCATATGCGCAGCTTTCATCCCGATATGCA 202
QY 726 CCACCGGGTAAAGTTTACCGGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGA 785
DB 203 CCACCGGGTAAAGTTTACCGGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGA 262
QY 786 TCACCATCGTCCCGGGGTGTCAATATATCATCTGTATATCATCCAAACAGCAGAT 845
DB 263 TCACCATCGTCCCGGGGTGTCAATATATCATCTGTATATCATCCAAACAGCAGAT 322
QY 845 AAGCGCTCTCTCTTT 860
DB 323 AAGCGCTCTCTCTTT 337

RESULT 13
CF469981/c
LOCUS
DEFINITION
P7-E11 Plasmodium yoelii 17X axenic hepatic stages Plasmodium
yeelii yoelii cDNA, mRNA sequence.

CF469981
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1068 bp mRNA linear EST 05-SEP-2003
1688 Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii
yeelii cDNA, mRNA sequence.

CF469981.1 GI:34487353
EST.
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1068)
Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nussenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
axenic culture
Unpublished (2003)
Contact: Bhanot P
Department of Pathology
New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop01@med.nyu.edu
similar to NR|GI-23483806 hypothetical protein [Plasmodium yoelii
yoelii] (e-108).

FEATURES
source
Location/Qualifiers
1. 1068
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17X"
/sub_species="yoelii"
/db_xref="taxon:73239"
/dev_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
exoerythrocytic malaria parasites does not require host
cells', (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN
Query Match 5.8%; Score 273.2; DB 14; Length 1068;
Best Local Similarity 90.0%; Pred. No. 7.7e-37;
Matches 278; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 571 GCGTCACATTTATATTTCCCGAACATCAGGTTAATGGGTTTGTATGTCATTTTCGGG 630
DB 562 GCGTGCATTTATATTTCCCGAACATCAGGTTAATGGGTTTGTATGTCATTTTCGGG 503
QY 631 GTGGCTGAGATCAGCCACTTCTTCCCGATTAACCGAGACCGGCACACTGGCCATATCGGT 690
DB 502 GTGGCTGAGATCAGCCACTTCTTCCCGATTAACCGAGACCGGCACACTGGCCATATCGGT 443
QY 691 GGTGATCATGCGCAGCTTTCATCCCGATTAACCGAGACCGGCACACTGGCCATATCGGT 750
DB 442 GGCATCATGCGCCAGCTTTCATCCCGATTAACCGAGACCGGCACACTGGCCATATCGGT 383
QY 751 TTTATCTGACAGCAGCTGCACTGGCAGGGGATCACTCCGTCGCGGGCGGTGTC 810
DB 382 TTTATCTGACAGCAGCAGCGGCACTGCGAGGNGATCACCNTCCGTCGCGGGCGGTGTC 323
QY 811 AATAATATCATCTGTATATCAACAAACAGACGATTAACGGCTCTCTCTTTTATAGTGA 870
DB 322 AANAATATCGCTCGGNNATCCACNANCNANANGANANGCGCTTNTNTTTTTCACAGTGNA 263
QY 871 AACCTTAA 879
DB 262 AACNTTGAA 254

RESULT 14
CF469119/c
LOCUS
DEFINITION
P1688 Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii
yeelii cDNA, mRNA sequence.

CF469119
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1037 bp mRNA linear EST 05-SEP-2003
Plasmodium yoelii 17X axenic hepatic stages Plasmodium yoelii
yeelii cDNA, mRNA sequence.

CF469119.1 GI:34486491
EST.
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1037)
Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nussenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
axenic culture
Unpublished (2003)
Contact: Bhanot P
Department of Pathology

philippe.vaglio@dfci.harvard.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

1..384
/organism="Caenorhabditis elegans"
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/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauvers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 7.3%; Score 340.2; DB 12; Length 384;
Best Local Similarity 97.7%; Pred. No. 4.2e-48;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 101 TAAAAACAGACTACATACTAGTAAACACACACATATCCAGTCACTATGATCAACTA 160
Db 32 TAATACACAGACTACATACTAGTAAACACACACATATCCAGTCACTATGATCAACTA 91
QY 161 CTTAGATGGTATTAGTACCTGAGCTGAGCGACGAGCTTCCAAATGTTCTTCGGGTGAT 220
Db 92 CTTAGATGGCTTTAGTGACCTGTAGTCGACCGACGAGCTTCCAAATGTTCTTCGGGTGAT 151
QY 221 GCTGCCAATCTAGTCAGCAGAGCCTTCCAAATGTTCTTCCAAACGGAATCGTGTAT 280
Db 152 GCTGCCAATCTAGTCAGCAGAGCCTTCCAAATGTTCTTCCAAACGGAATCGTGTAT 211
QY 281 CAGGCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAAGAAATAGAAAG 340
Db 212 CCACCTACTCGGTATTGTCTCAATGCGGTATTAAATCATATAAAGAAATAGAAAG 271
QY 341 AGTGGGAGCCTCTTTTGTGTGACAAATAAATAAATCTACTATTTCATATACGCTAG 400
Db 272 AGTGGGAGCCTCTTTTGTGTGACAAATAAATAAATCTACTATTTCATATACGCTAG 331
QY 401 TGTATAGTCTGAAATCATCTGATCAAGATCAAGAAACAATTCACAACTCTATAC 453
Db 332 TGTATAGTCTGAAATCATCTGATCAAGATCAAGAAACAATTCACAACTCTATAC 384

RESULT 11
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LOCUS OSTF043E11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
DEFINITION Fl1F1.5, mRNA sequence.
ACCESSION BI174407
VERSION BI174407.1 GI:14640210
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 384)

REFERENCE
AUTHORS Reboul, J., Vaglio, P., Tzallas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucet, R., Hartley, J. L., Temple, G. F., Brach, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.
TITLE Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
JOURNAL Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE 21135099
PUBMED 11242119
COMMENT Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome.Reboul@dfci.harvard.edu or philippe.vaglio@dfci.harvard.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

1..384
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauvers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 7.0%; Score 325.4; DB 12; Length 384;
Best Local Similarity 98.2%; Pred. No. 1.4e-45;
Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 306 TTTTATTTTGTACACAAAAAGAGCTCGACCTCTTTTCTTTATTTCTTTTATGATT 247
QY 3616 TAATACGGCATTTGAGCAATAGCGAGTAGGCTGGATACGAGATTCCGTTTGAGAAGAA 3675
Db 246 TAATACGGCATTTGAGCAATAGCGAGTAGGCTGGATACGAGATTCCGTTTGAGAAGAA 187
QY 3676 CATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAGAAACATTTGGAAGGC 3735
Db 186 CATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAGAAACATTTGGAAGGC 127
QY 3736 TGTGCGTGCAGCTACAGGTCACTAATACCATTAAGTAGTTGATTTCATAGTACGTGATAT 3795
Db 126 TGTGCGTGCAGCTACAGGTCACTAATACCATTAAGTAGTTGATTTCATAGTACGTGATAT 67
QY 3796 GTTGTGTTTACAGTATTATGTAGTCTGTTTTTA 3830
Db 66 GTTGTGTTTACAGTATTATGTAGTCTGTTATTA 32

RESULT 12

BI555980

LOCUS

BI555980

DEFINITION

CDNA clone jmln08 5', mRNA sequence.

ACCESSION

BI555980.1

VERSION

BI555980.1

KEYWORDS

EST.

SOURCE

Ipomoea nil (Japanese morning glory)

ORGANISM

Ipomoea nil

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Convolvulaceae; Ipomoea.

REFERENCE

1 (bases 1 to 337)

Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaoka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.

ESTs of Japanese morning glory

JOURNAL

Unpublished (2002)


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QY 786 TCACCATCGTCGCCGGCGGTGTCATTAATATCACTCTGTACATCCCAACAGACGAT 845
Db 263 TCACCATCGTCGCCGGCGGTGTCATTAATATCACTCTGTACATCCCAACAGACGAT 322
QY 846 AACGGCTCTCTTTATAGGTGTAACCTTAAACTGATTTACAGTCCCTGTTTCGG 905
Db 323 AACGGCTCTCTC-TTTATAGGTGTAACCTTAAACTGATTTACAGTCCCTGTTTCGG 381
QY 906 TCAGCAAAAGACCGGTTCATTTCAATAAACCGGGCGACTCAGCCATCC-ITTCCTGATT 964
Db 382 TCAGCAAAAGACCGGTTCATTTCAATAAACCGGGCGACTCAGCCATCCCTTTCCTGATT 441
QY 965 TTCGCTTTCCAGCGTTCGGCACGCGACGAC 996
Db 442 TTTGCTTTCCAGCGTTCGGCACGCGACGAC 473

RESULT 7
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ACCESSION AG000763
VERSION AG000763.1 GI:2579571
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE 2 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES
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    Best Local Similarity 92.2%; Pred. No. 3.8e-58;
    Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7;

QY 601 GTTAATGGGTTTTGATGTCATTTTCGGGTGGCTGAGATCAGCAGCTTCCTCCCGAT 660
Db 722 GTTAAGGCGCTTTTGGANGCAATTTTCGGGTGGC---GAGATCGCCAATTTTCCCGA 667
QY 661 AACGAGACCGGCACACCTGCCATATCGGTGTCATCGCGCAGCTTTCATCCCGGAT 720
Db 666 TAAGGACCGGCACAC-TGGCCATACGGTGGTCATCA-CGCGCAGCTTCA-CCCCGAT 610
QY 721 ATGCACACCGGGTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTCGACCTGGCCAG 780
Db 609 ATGCACACCGGNTAAAGTTTCAGGGAGACTTTAACNGACAGCAGACGTCGACCTGGCCAG 550
QY 781 GGGGATCAGATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCCAAAACAG 840
Db 549 GGGGATCAGATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCCAAAACAG 490
QY 841 ACGATAACGGCTCTCTCTTTATAGGTGTAACCTTAAACTGATTTACACGATCCCTGCT 900

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Db 489 ACGATAACGGCTCTCTCTTTATAGGTGTAACCTTAAACTGCAATTTACACGATCCCTGT 430
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Db 429 TCTGTCAGC-AAAGAGCGGTTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCT 371
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Db 370 GATTTTCGGCTTTCCAGGTTTCGGCACGACGACGAGCGGGTTCATCTGTCATGGTGTGTC 311
QY 1021 TTACGACCGGAGATATTCATATATGATATGCTTGGAGCACTGATAGCTGTGCTGTC 1080
Db 310 TTACGACCGGAGATATTCATATGATATGCTTGGAGCACTGATAGCTGTGCTGTC 254
QY 1081 AACTGTCACTGTATACGCTCTTCATAGCACACCTCTTTTGACATACCTTCGGGTA 1137
Db 253 AACTGTCACTGTATACGCTCTTCATAGCACACCTCTTTTGACATACCTTCGGGTA 197

RESULT 8
CB395230/c
LOCUS CB395230_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA linear EST 15-MAY-2003
DEFINITION OSUR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION CB395230.1 GI:30736941
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 487)
AUTHORS Reboul, J., Vaglio, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C. M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J. R., Hartley, J. L., Brasch, M. A., Vandenhaute, J., Boulton, S., Endress, G. A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P. P., Ptacek, J., Snyder, M., Huang, R., Chance, M. R., Lee, H., Doucette-Stamm, L., Hill, D. E. and Vidal, M.
TITLE C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
POLY(A)=No.
FEATURES
    Location/Qualifiers
    1..487
    /organism="Caenorhabditis elegans"
    /mol_type="mRNA"
    /strain="N2"
    /db_xref="taxon:6239"
    /sex="Hermaphrodite and male"
    /tissue_type="whole animal"
    /dev_stage="mixed stage"
    /clone_lib="AD-wrmcDNA"
    /note="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
ORIGIN
    Query Match 7.6%; Score 357; DB 14; Length 487;
    Best Local Similarity 93.6%; Pred. No. 5.2e-51;
    Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
JOURNAL Published Only in DataBase (1998)
TITLE Homo sapiens genomic DNA, chromosome 21q
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
JOURNAL Direct Submission
Submitted (07-SEP-1998) Mashira Hattori, Kitasato University,
Department of Science, JSR Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
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                     /clone="f32E9X13"

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Best Local Similarity 90.2%; Pred. No. 7.5e-60;
Matches 505; Conservative 0; Mismatches 47; Indels 8; Gaps 7;

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QY 640 ATCAGCAGCTTCTTCCCGGATACGAGACCGGACACTGGCCATATCGTGGTGCATCAT 699
Db 663 ATCAGCAGCTTCTTCCCGGATACGAGACCGGACACTGGCCATATCGTGGTGCATCAT 604
QY 700 GCGCCAGCTTTCATCCCGGATACGAGACCGGATACGAGACCGGATACGAGACCGGAT 758
Db 603 GCGCCAGCTTTCATCCCGGATACGAGACCGGATACGAGACCGGATACGAGACCGGAT 545
QY 759 ACAGCAGCTGCACTGGCC-AGGGGATCACCATCGTCCCGGCGGTGTCATTAATA 817
Db 544 ACAGCAGCTGCACTGGCCAGGGGATCACCATCGTCCCGGCGGTGTCATTAATA 486
QY 818 TCACTCTGTATCCACAAACAGACGTAACGGCTCTCTCTTTTATAGGTGTAACCTTA 877
Db 485 TCACTCTGTATCCACAAACAGACGTAACGGCTCTCTCTTTTATAGGTGTAACCTTA 427
QY 878 AACTGCAATTCACAGTCCCTGTTCGTGACGAAAGAGCGGTTCATTTCAATAAACCG 937
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QY 938 GCGGACCTGAGCATCCCTTCCTGATTTTCGGTTTCAGGTTCCGACGACGAGACG 997
Db 366 GCGGACCTGAGCATCCCTTCCTGATTTTCGGTTTCAGGTTCCGACGACGAGACG 307
QY 998 GGCTTTCATTCGTATGTTGTGCTTACGACACCGGAGATATGACATCATATATGCTTG 1057
Db 306 GGCTTTCATTCGTATGTTGTGCTTACGACACCGGAGATATGACATCATATATGCTTG 249
QY 1058 AGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAACTGCTTCATAGCACACCTC 1117
Db 248 AGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAACTGCTTCATAGCACACCTC 190
QY 1118 TTTTGTACATCTTCGGGTA 1137

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Db 189 TTTTGTACATCTTCGGGTA 170
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CB997937 522 bp mRNA linear EST 01-MAY-2003
AGENCOURT 13894516 NIH_MGC 148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
CB997937
CB997937.1 GI:30292457
EST.
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDM391 row: e column: 05
High quality sequence start: 68
High quality sequence stop: 256.
FEATURES             Location/Qualifiers
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directionally cloned using primer
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size 2.3 kb and normalized to 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI, in preparation).
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match      8.6%; Score 404; DB 14; Length 522;
Best Local Similarity 96.2%; Pred. No. 4.8e-59;
Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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QY 666 AGACCGGACACTGGCCATATCGTGGTTCATGCGCCAGCTTTCATCCCGATATGCA 725
Db 143 AGACCGGACACTGGCCATATCGTGGTTCATGCGCCAGCTTTCATCCCGATATGCA 202
QY 726 CCACCGGGTAAAGTTTCAACGGAGCTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGA 785
Db 203 CCACCGGGTAAAGTTTCAACGGAGCTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGA 262

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Email: cgapbs-remail.nih.gov
 Tissue procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 251.
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 /note="Organ: Placenta; Vector: pBluescriptR; Site: 1:
 all-XhoI; Site: 2: BamH; Oligo-dT primed using primer
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 insert size 2.3 kb and normalized to R0.5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NHGRI/NHGRI, National Institutes of Health). Note: This is
 a NIH MGC library."

FEATURES

source

ORIGIN

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Query Match      9.3%; Score 437.2; DB 14; Length 542;
Best Local Similarity 95.5%; Pred. No. 1e-64;
Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

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QY 606 TGGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 665
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Db 203 CCACCGGGTAAAGTTACGGGAGACTTTATCTGACAGAGAGCTGCACTGGCCAGGGGA 262

QY 786 TCACCATCCGTCCCGGGGCTGTCATATATATATATCTCTGTACATCCACAAACAGACGAT 845
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QY 846 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 905
Db 323 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 382

QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAACCGGGGACCTCAGCATCCCTTCTGATTT 965
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RESULT 4

AG000761/c

LOCUS

DEFINITION

AG000761

ACCESSION

AG000761

VERSION

AG000761.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 723)

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in Database (1997)

2 (bases 1 to 723)

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Direct Submission

Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:0427-78-9561)

Location/Qualifiers

1. .723

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Best Local Similarity 98.1%; Pred. No. 2e-60;
Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 606 TGGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 665
Db 390 TGGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGATAACGG 331

QY 666 AGACCGGCACACTGGCCATATCGTGGTGCATCATGCGCCAGCTTTTCATCCCGATATGCA 725
Db 330 AGACCGGCACACTGGCCATATCGTGGTGCATCATGCGCCAGCTTTTCATCCCGATATGCA 271

QY 726 CCACCGGGTAAAGTTACGGGAGACTTTATCTGACAGAGAGCTGCACTGGCCAGGGGA 785
Db 270 CCACCGGGTAAAGTTACGGGAGACTTTATCTGACAGAGAGCTGCACTGGCCAGGGGA 211

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QY 846 AACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 905
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QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAACCGGGGACCTCAGCATCCCTTCTGATTT 965
Db 90 TCAGCAAAAGAGCGGTTTCATTTCAATAACCGGGGACCTCAGCATCCCTTCTGATTT 31

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RESULT 5

AG013450/c

LOCUS

AG013450

725 bp

DNA

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GSS 14-APR-1999

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ORIGIN

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Best Local Similarity 98.9%; Pred. No. 1.3e-78;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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QY 639 GATCAGCACTTCTTCCCGGATAACGGAGACCGGACACTGGCCATATCGGTGGTCA 698
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QY 699 TGGCCAGGCTTTTATCCCGGATATGACACCGGGTAAAGTTTTCAGGGAGACTTTATCTG 758
Db 154 TGGCCA-NTTTCATCCCGGATATGACACCGGGTAAAGTTTTCAGGGAGACTTTATCTG 212
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Db 393 GCGACCTCAGCCATCCCTTCCGATTTTCGGTTTCCAGGTTTCGACGACGACGACG 452
QY 999 GCTTCATCTGATGTTGGTGTACAGACCGGAGATATGACATCATATATGTCCTTGA 1058
Db 453 GCTTCATCTGATGTTGGTGTACAGACCGGAGATATGACATCATATATGTCCTTGA 510
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Db 511 GCACTGATAGC-GTGGCTGTCACTGTCACTGTAAATGCTGCTGCTGCTGCTGCTGCT 569
QY 1119 TTTTGACATCTTCGGGTA 1137
Db 570 TTTTGACATCTTCGGGTA 588

RESULT 2
AG000762/c 713 bp DNA linear GSS 06-FEB-1999
LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.

ACCESSION AG000762

VERSION AG000762.1 GI:2579570

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Hattori.M., Ishii.K., Shiba.T. and Sakaki.Y.

JOURNAL Published Only in DataBase (1997)

REFERENCE Hattori.M., Ishii.K., Shiba.T. and Sakaki.Y.

TITLE Direct Submission

JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp).

Tel:0427-78-9732, Fax:0427-78-9561)

Location/Qualifiers

source
1. .713
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ORIGIN

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Best Local Similarity 94.2%; Pred. No. 6.7e-75;
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

QY 583 TATTCCCGAGAACATCAGGTTAAATGGCGTTTGTATGTCATTTTCGGCGTGGCTGAGATC 642
Db 599 TATATCCCGGAGNATCNGTTAATGCCGTTTGAAGNATTTTCGCCGTGGCTGAGAT 540
QY 643 AGCCATCTTCTTCCCGGATAACGGAGACCGGACACTGGCCATATCGGTGGTCACTGCG 702
Db 539 CACCAACTTTTCCCGATTACGAGACCGGACACTGNCATATCGGTGGTCACTGCG 480
QY 703 CAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTTCAGGGAGACTTTATCTGACAG 762
Db 479 CAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTTCAGGGAGACTTTATCTGACAG 420
QY 763 CAGAGCTGCTGCGCAGGGGATCACCATCCGTCGCCGGCGGTGTCAATAATATCACT 822
Db 419 CAGAGCTGCTGCGCAGGGGATCACCATCCGTCGCCGGCGGTGTCAATAATATCACT 360
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Db 359 CTGTGATCTCAAAACAGACGATACGGCTCTCTTTTATAGGTGTAAACCTTAACTG 300
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Db 299 CATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCAATAAACCAGGCGA 240
QY 943 COTCAGCCATCCCTTCTGATTTTCCGTTTCCAGGTTTCGACGACGACGACGCGCTT 1002
Db 239 COTCAGCCATCCCTTCTGATTTTCCGTTTCCAGGTTTCGACGACGACGACGCGCTT 180
QY 1003 CATTCGATGTTGTGCTTACAGACCGGAGATATGACATCATATATGCTTGGACAA 1062
Db 179 CATTCGATGTTGTGCTTACAGACCGGAGATATGACATC--ATATGCTTGGACAA 122
QY 1063 CTGATAGCTGCTGCTGCTCAACTGTCACTGTAATACTGCTTCAATAGCACCTCTTTT 1122
Db 121 CTGATANTGTGCTGCTCACTGTCACTGTAATACTGCTTCAATAGCACCTCTTTT 62
QY 1123 GACATACCTTCGGGTA 1137
Db 61 GACATACCTTCGGGTA 47

RESULT 3

CD109790

LOCUS

DEFINITION

AGENCOURT 13988518 NIH MGC 147 Homo sapiens cDNA clone

IMAGE:30346919 5', mRNA sequence.

CD109790

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)

NIH-MGC http://imgc.ncbi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 7262.5 Seconds

(without alignments)

19251.609 Million cell updates/sec

Title: US-10-055-001B-26_COPY_13000_17681

Perfect score: 4682

Sequence: 1 ttctatgttgagagacacg.....atagtgcacataatctgc 4682

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estom:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_pbg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	496.6	10.6	713	29	AG000762 Homo sapi
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C 4	411.8	8.8	723	29	AG000761 Homo sapi

C	5	408.4	8.7	725	29	AG013450	AG013450 Homo sapi
C	6	404	8.6	522	14	CB997937	CB997937 AGENCOURT
C	7	398.4	8.5	722	29	AG000763	AG000763 Homo sapi
C	8	357	7.6	487	14	CB395230	CB395230 OSTRL51B2
C	9	347.4	7.4	487	14	CB395230	CB395230 OSTRL51B2
C	10	340.2	7.3	384	12	BI174407	BI174407 OSTF043E1
C	11	325.4	7.0	384	12	BI174407	BI174407 OSTF043E1
C	12	301.4	6.4	337	12	BJ555980	BJ555980 BJ555980
C	13	273.2	5.8	1068	14	CF469981	CF469981 P7-E11 P1
C	14	271.8	5.8	1037	14	CF469119	CF469119 P16A8 P1a
C	15	264.4	5.6	724	29	AG000791	AG000791 Homo sapi
C	16	262.4	5.6	816	14	CF469496	CF469496 P22H07 P1
C	17	257.4	5.5	557	12	BG220129	BG220129 RST39901
C	18	255.8	5.5	656	14	CK291800	CK291800 RST754514
C	19	254	5.4	569	14	CF469084	CF469084 P1597 P1a
C	20	252.4	5.4	819	14	CF469247	CF469247 P18G02 P1
C	21	247.4	5.3	320	29	CG206516	CG206516 TOS0136 T
C	22	246	5.3	329	28	BH739300	BH739300 32283V63
C	23	245.4	5.2	1041	14	CF468941	CF468941 P13A3 P1a
C	24	243.6	5.2	1035	14	CF470036	CF470036 P8-B8 P1a
C	25	242.8	5.2	1017	14	CF470004	CF470004 P7-G5 P1a
C	26	239.2	5.1	659	14	CK287298	CK287298 EST750020
C	27	235.6	5.0	859	14	CF468865	CF468865 P11-E10 P1
C	28	234.8	5.0	506	14	CF468864	CF468864 P13E12 P1
C	29	234.8	5.0	657	14	CF468948	CF468948 P13B3 P1a
C	30	229	4.9	628	14	CF469215	CF469215 P17G11 P1
C	31	227.2	4.9	968	14	CF469474	CF469474 P21H01 P1
C	32	220	4.7	583	14	CB403882	CB403882 OSTRO13H1
C	33	220	4.7	583	14	CB403882	CB403882 OSTRO13H1
C	34	215.2	4.6	393	14	CB403984	CB403984 OSTRO15E7
C	35	215.2	4.6	393	14	CB403984	CB403984 OSTRO15E7
C	36	215.2	4.6	1020	14	CF469337	CF469337 P20A07 P1
C	37	214.6	4.6	1017	14	CF468787	CF468787 P10-C6 P1
C	38	214.2	4.6	1042	14	CF468958	CF468958 P13D10 P1
C	39	213.8	4.6	945	14	CF468807	CF468807 P10-E8 P1
C	40	213.2	4.6	509	14	CF468864	CF468864 P11-D8 P1
C	41	213.2	4.6	716	29	AG000792	AG000792 Homo sapi
C	42	204.6	4.4	398	14	CF974207	CF974207 PSU nep1
C	43	203.4	4.3	1013	14	CF469353	CF469353 P20C02 P1
C	44	203.2	4.3	973	14	CF469399	CF469399 P20H01 P1
C	45	200.4	4.3	586	14	CF470068	CF470068 P8-B8 P1a

ALIGNMENTS

RESULT 1	AG012840	Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.	698 bp	DNA linear	GSS 08-FEB-1999
LOCUS	AG012840				
DEFINITION	AG012840				
ACCESSION	AG012840				
VERSION	AG012840.1	GI:3435047			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 698)			
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.				
TITLE	Homo sapiens genomic DNA, chromosome 21q				
JOURNAL	Published Only in Database (1998)				
REFERENCE	2	(bases 1 to 698)			
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@jst.ac.jp, Tel:0427-78-9561)				
FEATURES	Location/Qualifiers				
source	1..698				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				

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Db 16404 TAAAAAGAAATAAGAAAAGAGGTGGAGCCTCTTTTGTGTGACAAAATAAAAAATC 16345
QY 381 TACCTATTTCATACGCTAGTGTCTAGTCTCTGAAATCATCTGCAATCAAGAACAAATTC 440
Db 16344 TACCTATTTCATACGCTAGTGTCTAGTCTCTGAAATCATCTGCAATCAAGAACAAAGT 16285
QY 441 ACAACTCTTATCTTTCTTTACAAAGTGGTGGGCTTCATCTGGATTTTCAGCCTCTAT 500
Db 16284 ATGTCAAAAGAGGTGTGCTATGAA---GCAGGTATTACAGTGACAGTGTGACGAGCA 16228
QY 501 ACTTACTAAACGCGTAAAGTTTCTGTAAATTTCTGTATCTGATCGACCTGCGAGCTGGCTGT 560
Db 16227 GCTATCAGTTGCTCAAGGCATATATGATGTCAATACTCCGGTCTGGTAAGCAACCAT 16168
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QY 975 CAGCGTTC---GGCAGCGACACGCGGCTTCATCTGCAATGGTTGTGCTTACCAACCG 1031
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QY 1328 AGTGACTGGATATTGTTGTGTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAA 1387
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Db 15405 AGTGACTGGATATTGTTGTTTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAA 15346
QY 1388 TTTAATATATTGATATTATATCATTTTACGTTTCTCGTTACGCTTTCTCTGACAAAGTG 1447
Db 15345 TTTAATATATTGATATTATATCATTTTACGTTTCTCGTTACGCTTTCTCTGACAAAGTG 15286
QY 1448 GTCTCAGGAATTCGGTACCOCAGCTGGTAAGGAAATAATTTATTTCTTTTCTCTTT 1507
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Db 15232 ---ATCCAAATGTAAGATCAATGATAACAATGATGATCTATCATGTTACCTTTGTT 15176
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QY 1808 ATAAATAAATTAATAATATTTTATGATTAATAGTTTATTAATAATAATCT 1867
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QY 1868 ATACATTTACTAAATTTTGTGTTTAAAGTTTAAATAATTTTGTGTAATAATCCAAATC 1927
Db 14983 -----ATTAATTTGTTTACTTTGTTTATTAATAATTTGTTTATGTAATAATACAG 14929
QY 1928 TCGTTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAAGTAAACAATAATATC 1987
Db 14928 CAGATTGGAATTTTCAACAAAATAATTTAATACTTTTAAACTAAAATAATTTAGTAATGT 14869
QY 1988 AAATTAATGAAACAGTAACTAAATGTAACAAAACATAATCTAATGCTAATAATAACAAG 2047
Db 14868 ATAGATAT----- 14861
QY 2048 CGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTTAATAATTTCTAAA 2107
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QY 2108 TAAATCTTGTAGTTTATTAATCTCTAAATGGAATGACTAATTAATAATTAATAATGATAGTCG 2167
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QY 2168 AACATGAATAACAAGGTAACATGATAGTATCATGTCATGCTGTTATCATTTGATCTTACAT 2227
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Db 14529 ACATCACTTAATTTTATCTAAAGAAAATAAATAATTTATTTCTTCTTCAACAGC 14470
|||||

APPLICANT: LI, XIAO
APPLICANT: ESPPOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
FILE REFERENCE: 0942 5120001
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 4627
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 23.5%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 6.7e-158;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 90 GCCAACTTTGTACAAAAAGCTGATATCGAAAGCTGTAATACTGTAATAACACATATCAATATAT 149

QY 86 AAATTAGATTTTGCATAAAAACAGACTACATACTGTAATAACACACATATCCAGTC 145
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QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGTAGTCGACCGAGAGCTTCCAAA 205
DB 210 ACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGTAGTCGACCGAGAGCTTCCAAA 269

QY 206 TGTCTTCGGGTGATGCTGCGAAGCTGATGTCGACCGAGAGCTTCCAAAAGTCTTCTCAA 265
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QY 506 CTAACAGTGAATAAGTTTCTGTAATTTCTATGTAATCTGTAATCTGTAATCTGTAATCTG 565
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QY 686 TCGGTGGTCAATGCGCCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTTCACGG 745
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QY 746 GAGACTTTATCTGACAGCAGAGCTGCTGCTGCGCAGGGGATCACCATCGTGGCCGGGC 805
DB 810 GAGACTTTATCTGACAGCAGAGCTGCTGCTGCGCAGGGGATCACCATCGTGGCCGGGC 869

QY 806 GTGTCAATAATATCATCTGTATCATCTCAAAACAGACGATACGGCTCTCTCTTTATAG 865
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QY 866 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTGTCAGCAAAAGACCGTTTCA 925
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QY 1106 ATAGCACACCTCTTTTGTGACATATCTTCGGGTA 1137
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RESULT 15
US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 23.0%; Score 1074.8; DB 15; Length 17476;
Best Local Similarity 59.9%; Pred. No. 1.7e-153;
Matches 2349; Conservative 0; Mismatches 1302; Indels 273; Gaps 22;

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QY 201 CCAATGTTCTTCGGGTGATGCTGCCAATCTTAGTCGACCGCAGCGCTTCCAAATGTTCTT 260
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1046 ATATATGCTTGAACCACTGATAGCTGTGCTGTCACTGTAATGACGCTGCTTC 1105
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1106 ATAGCACACCTCTTTTGTGACATACTTCGGGTA 1137
2019 ATAGCACACCTCTTTTGTGACATACTTCGGGTA 2050
RESULT 13
US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63
Query Match 23.5%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 6.7e-158;
Matches 1106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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210 ACTATGAATCAACTACTTGTAGATGTTATTAGTACCTGTGATGACGACGACGCTTCCAA 269

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266 ACGGAATCGTGGTATCCAGCCTTACTCGCTATTGTCCTCAATGCGGTATTAAATCATATAAA 325
330 ACGGAATCGTGGTATCCAGCCTTACTCGCTATTGTCCTCAATGCGGTATTAAATCATATAAA 389
326 AGAAATAGAAAAGAGGTCGAGCCTCTTTTGTGTGACAAAATAFAAAACATCTAATC 385
390 AGAAATAGAAAAGAGGTCGAGCCTCTTTTGTGTGACAAAATAFAAAACATCTAATC 449
386 ATTATATACGCTAGTGTGTCATAGTCTGAAATCATCTGCATCAAGAACAAATTTACACAC 445
450 ATTATATACGCTAGTGTGTCATAGTCTGAAATCATCTGCATCAAGAACAAATTTACACAC 509
446 TCTTATACCTTTTCTCTTACAGTCTGTCGGCTTCACTCTGATTTTTCAGCCTCTATACATTA 505
510 TCTTATACCTTTTCTCTTACAGTCTGTCGGCTTCACTCTGATTTTTCAGCCTCTATACATTA 569
506 CTAAGAGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGACTGGGTGTGATA 565
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626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGAGACCGGACACACTGGCCATA 685
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810 GAGACTTTATCTGACGACGACGCTGCACTGGCCAGGGGATCACCATCGTGGCCCGGGC 869
806 GTGTCAATATATCACTCTGTACATCCACAAAACAGACGATAACGGCTCTCTCTTTTATAG 865
870 GTGTCAATATATCACTCTGTACATCCACAAAACAGACGATAACGGCTCTCTCTTTTATAG 929
866 GTGTAAACCTTAACTGCACTTACAGGTCCTGTTCTGTCAGCAAAAAGAGCCGTTTCAAT 925
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926 TTCAATAAAGCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTTCGGC 985
990 TTCAATAAAGCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTTCGGC 1049
986 ACGGACGACGCGGCTTCAATCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1045
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1106 ATAGCACACCTCTTTTGTGACATACTTCGGGTA 1137
1170 ATAGCACACCTCTTTTGTGACATACTTCGGGTA 1201
RESULT 14
US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID

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Db 5363 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCAGCCGACAGCCTTCCAAA 5304
QY 206 TGTCTTCGGGTGATGTCGCCAACTTAGTCGACCGCAGAGCCTTCCAAATGTTCTTCTCAA 265
Db 5303 TGTCTTCGGGTGATGTCGCCAACTTAGTCGACCGCAGAGCCTTCCAAATGTTCTTCTCAA 5244
QY 266 ACCGAATCGTGTATCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAAATCAFAAAA 325
Db 5243 ACCGAATCGTGTATCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAAATCAFAAAA 5184
QY 326 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db 5183 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 5124
QY 386 ATTCATATACGTAGTGTATAGTCTCTGAAATFCATCTGCATCAAGAAACAATTTCAAC 445
Db 5123 ATTCATATACGTAGTGTATAGTCTCTGAAATFCATCTGCATCAAGAAACAATTTCAAC 5064
QY 446 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTCATCTGATTTTCAGGCTCTATACCTTA 505
Db 5063 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTCATCTGATTTTCAGGCTCTATACCTTA 5004
QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTGCAGCTGGCTGTGATA 565
Db 5003 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTGCAGCTGGCTGTGATA 4944
QY 566 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGTTTTTGTATGTCATTT 625
Db 4943 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGTTTTTGTATGTCATTT 4884
QY 626 TCGCGTGTGATGATCAGCCTCTCTCCCGATACCGGACCGGACCTGGCCATA 585
Db 4883 TCGCGTGTGATGATCAGCCTCTCTCCCGATACCGGACCGGACCTGGCCATA 4824
QY 686 TCGGTGGTTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTCACGG 745
Db 4823 TCGGTGGTTCATATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTCACGG 4764
QY 746 GAGACTTTATCGACGACGAGTGTCACCTGGCCAGGGGATCACCATTCGTCGCGCGGC 805
Db 4763 GAGACTTTATCGACGACGAGTGTCACCTGGCCAGGGGATCACCATTCGTCGCGCGGC 4704
QY 806 GTGTCAATTAATCACTCTGTATCATCCCAAACAGACGATACCGGCTCTCTTTTATAG 865
Db 4703 GTGTCAATTAATCACTCTGTATCATCCCAAACAGACGATACCGGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAAACATGCAATTCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 925
Db 4643 GTGTAAACCTTAAACATGCAATTCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 4584
QY 926 TTCAATACACCGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCAGGTTTCGGC 985
Db 4583 TTCAATACACCGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCAGGTTTCGGC 4524
QY 986 ACGCAGACGACGGCTTCATTTCTGATGTTGTGCTTACGACCGGAGATATGACATC 1045
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QY 1106 ATAGCACACCTCTTTTGGACATCTTCGGGTA 1137
Db 4403 ATAGCACACCTCTTTTGGACATCTTCGGGTA 4372
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RESULT 12

US-10-151-690-62

; Sequence 62, Application US/10151690

; Publication No. US2003012455A1

; GENERAL INFORMATION:

; APPLICANT: BRASCH, MICHAEL A.

```
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID M
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62
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Query Match 23.5%; Score 1102.4; DB 15; Length 4428;

Best Local Similarity 99.5%; Pred. No. 6.e-158;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 26 GACAAAGTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATAAATATCAATATATT 85
Db 939 GCCAATTTGTACAAAAAGCTGATATCGAAACGTAAATATGATATAAATATCAATATATT 998
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGTC 145
Db 999 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACATATCCAGTC 1058
QY 146 ACTATGATCACTACTTAGATGGTATTAGTGAACCTGTAGTCGACGAGAGCCTTCCAAA 205
Db 1059 ACTATGATCACTACTTAGATGGTATTAGTGAACCTGTAGTCGACGAGAGCCTTCCAAA 1118
QY 206 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 265
Db 1119 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 1178
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATCCGCTATTAAATCATATAAA 325
Db 1179 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCAATCCGCTATTAAATCATATAAA 1238
QY 326 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db 1239 AGAAATAAGAAAAAGAGTCCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 1298
QY 386 ATTCATATACGTAGTGTATAGTCTGAAAATCATCTGCATCAAGAAACAATTTCAAC 445
Db 1299 ATTCATATACGTAGTGTATAGTCTGAAAATCATCTGCATCAAGAAACAATTTCAAC 1358
QY 446 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTATCGGATTTTCAGGCTCTATACCTTA 505
Db 1359 TCTTATACCTTCTCTTACAAGTCGTTCCGCTTATCGGATTTTCAGGCTCTATACCTTA 1418
QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGATA 565
Db 1419 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGATA 1478
QY 566 AGGAGCCTGACATTTATTTCCCGAACAATCATAGGTTAATGCGCTTTTGTATGTCATTT 625
Db 1479 AGGAGCCTGACATTTATTTCCCGAACAATCATAGGTTAATGCGCTTTTGTATGTCATTT 1538
QY 626 TCGCGTGTGATGATCAGCCTTCCTTCCCGATACCGGACCGGACACCTGCCCAT 685
Db 1539 TCGCGTGTGATGATCAGCCTTCCTTCCCGATACCGGACCGGACACCTGCCCAT 1598
QY 686 TCGGTGGTTCATATGCGCCAGCTTTTCATCCCGATATGCAACCGGCTAAAGTTCACGG 745
Db 1599 TCGGTGGTTCATATGCGCCAGCTTTTCATCCCGATATGCAACCGGCTAAAGTTCACGG 1658
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OTHER INFORMATION: attP1 recombination site
FEATURE:
NAME/KEY: gene
LOCATION: (959)..(1264)
OTHER INFORMATION: ccdB gene
FEATURE:
NAME/KEY: gene
LOCATION: (1606)..(2265)
OTHER INFORMATION: Cam(r) gene
FEATURE:
NAME/KEY: misc feature
LOCATION: (2513)..(2744)
OTHER INFORMATION: attP2 recombination site
FEATURE:
NAME/KEY: gene
LOCATION: (2868)..(3677)
OTHER INFORMATION: Kan(r) gene
FEATURE:
NAME/KEY: misc feature
LOCATION: (3794)..(4537)
OTHER INFORMATION: pUC oriV / RK2 oriT
US-10-357-268-1

Query Match 23.7%; Score 1108.8; DB 16; Length 4892;
Best Local Similarity 99.8%; Pred. No. 7.3e-159; Mismatches 0; Indels 0; Gaps 0;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 161

QY 86 AAATAGATTTTCATATAAAGACAGACTACATATATCTGTAATAACACATATCCAGTC 145
DB 162 AAATAGATTTTCATATAAAGACAGACTACATATATCTGTAATAACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTATAGTGGTATTTAGTACCTGTAGTCAGCGACAGCCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTATAGTGGTATTTAGTACCTGTAGTCAGCGACAGCCCTTCCAAA 281

QY 206 TGTCTTCGGGTGATGTCGCACTAGTACGCGACAGCCCTTCCAAAATGTTCTTCTCAA 265
DB 282 TGTCTTCGGGTGATGTCGCACTAGTACGCGACAGCCCTTCCAAAATGTTCTTCTCAA 341

QY 266 ACGGAATCGTCGATCCAGCTACTCGCTATTCCTCTCAATGCGGTATTAATCATAAA 325
DB 342 ACGGAATCGTCGATCCAGCTACTCGCTATTCCTCTCAATGCGGTATTAATCATAAA 401

QY 326 AGAAATAAGAAAAAGAGGTGCGAGCCCTTTTGTGTGACAAATAAAAAACATCTACCT 385
DB 402 AGAAATAAGAAAAAGAGGTGCGAGCCCTTTTGTGTGACAAATAAAAAACATCTACCT 461

QY 386 ATTATATAGCTAGTGTCTATGCTCTGAAATCATCTGATCAAGAACAAATTTCAAC 445
DB 462 ATTATATAGCTAGTGTCTATGCTCTGAAATCATCTGATCAAGAACAAATTTCAAC 521

QY 446 TCTTATATCTTCTCTTACAAGTCGTTTCGGCTTCATCTGATTTTCAGCTCTTATCTTA 505
DB 522 TCTTATATCTTCTCTTACAAGTCGTTTCGGCTTCATCTGATTTTCAGCTCTTATCTTA 581

QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTATA 565
DB 582 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTATA 641

QY 566 AGGAGCCCTGACATTTATATTTCCCGAACATCAGGTTAATGCGGTTTGTATGTCATT 625
DB 642 AGGAGCCCTGACATTTATATTTCCCGAACATCAGGTTAATGCGGTTTGTATGTCATT 701

QY 626 TCGCGGTGGCTGAGATCAGCACTTCTTCCCGATAACGAGACCGGACACTGGCCATA 685
DB 702 TCGCGGTGGCTGAGATCAGCACTTCTTCCCGATAACGAGACCGGACACTGGCCATA 761

QY 686 TCGGTGTCTATGCGCCAGCTTTTCATCTCCCGATATGCAACCGGGTAAAGTTCAACGG 745

DB 762 TCGGTGTCTATCATCGCCAGCTTTTCATCCCCGATATGACACACCGGGTAAAGTTCAACGG 821
QY 746 GAGACTTTTATCTGACAGCAGCGTGCACCTGGCCAGGGGATCACCATCGTCGCCCGGCG 805
DB 822 GAGACTTTTATCTGACAGCAGCGTGCACCTGGCCAGGGGATCACCATCGTCGCCCGGCG 881
QY 806 GTGTCAATAATATCTCTGTACATCCACAAACAGACAGATACGGCTCTCTCTTTATAG 865
DB 882 GTGTCAATAATATCTCTGTACATCCACAAACAGACAGATACGGCTCTCTCTTTATAG 941
QY 866 GTGTAAACCTTAAACCTGCATTTTCCAGTTCCTGTCAGCAAAAGACGCGTTTCAAT 925
DB 942 GTGTAAACCTTAAACCTGCATTTTCCAGTTCCTGTCAGCAAAAGACGCGTTTCAAT 1001
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 1002 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 1061
QY 986 ACGCAGACGACGGGCTTCTTCTGATGTTGTGTGTACAGACCGGAGATATTGACATC 1045
DB 1062 ACGCAGACGACGGGCTTCTTCTGATGTTGTGTGTGTACAGACCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTGCAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTC 1105
DB 1122 ATATATGCTTGCAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTGGACATATCTCGGGA 1137
DB 1182 ATAGCACACCTCTTTTGGACATATCTCGGGA 1213

RESULT 11
US-10-151-690-61/c
; Sequence 61, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 23.7%; Score 1108.8; DB 15; Length 5584;
Best Local Similarity 99.8%; Pred. No. 7.7e-159; Mismatches 0; Indels 0; Gaps 0;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 85
DB 5483 GCAAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 5424

QY 86 AAATAGATTTTGCATATAAAGACAGACTACATTAATGTAATAACACACATATCCAGTC 145
DB 5423 AAATAGATTTTGCATATAAAGACAGACTACATTAATGTAATAACACACATATCCAGTC 5364

QY 146 ACTATGAATCAACTACTTATGATGGTATTAGTACCTGTAGTCAGCGGAGCTTCCAAA 205

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/
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (29)..(260)
/ OTHER INFORMATION: attP1
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/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (656)..(961)
/ OTHER INFORMATION: ccdB
/
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1099)..(1184)
/ OTHER INFORMATION: ccdA
/
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1303)..(1962)
/ OTHER INFORMATION: Cmr
/
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2210)..(2442)
/ OTHER INFORMATION: attP2
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/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (2565)..(3374)
/ OTHER INFORMATION: Kmr
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/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (3495)..(4134)
/ OTHER INFORMATION: ori
/
US-10-151-690-21

Query Match      23.7%; Score 1108.8; DB 15; Length 4470;
Best Local Similarity 99.8%; Pred. No. 7e-159;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTCAACGAGAAAGCTAAATATGATATAAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAAAGAGAAAGCTAAATATGATATAAATATCAATATATT 161

QY 86 AAATTAGATTTTGCATATAAAAAAGACTACATATAACTGTAAACACACATATCCAGTC 145
DB 162 AAATTAGATTTTGCATATAAAAAAGACTACATATAACTGTAAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCAGCAGAGCCCTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCAGCAGAGCCCTCCAAA 281

QY 206 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 265
DB 282 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 341

QY 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGTCGATTAATAATCATAAA 325
DB 342 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGTCGATTAATAATCATAAA 401

QY 326 AGAAATAAGAAAGAGAGGTGCGAGCCTCTTTTGTGTGACAAATAAAGACATCTACCT 385
DB 402 AGAAATAAGAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATAAAGACATCTACCT 461

QY 386 ATTATATATAGCTAGTGTATAGTCTGAAATCACTGATCAAGAAACAATTTCAAC 445
DB 462 ATTATATAGCTAGTGTATAGTCTGAAATCACTGATCAAGAAACAATTTCAAC 521

QY 446 TCTTATATCTTTCTCTTACAAGTCGTTGCGCTTCATCTGGATTTTCAAGCTCTATCTTA 505
DB 522 TCTTATATCTTTCTCTTACAAGTCGTTGCGCTTCATCTGGATTTTCAAGCTCTATCTTA 581

QY 506 CTAAGAGTGATAAGTTCTGTAATTTCTACTGATGACCTGCAGACTGCGTGTATA 565
DB 582 CTAAGAGTGATAAGTTCTGTAATTTCTACTGATGACCTGCAGACTGCGTGTATA 641

QY 566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTTTGTGTCATTT 625
DB 642 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTTTGTGTCATTT 701
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QY 626 TCGCGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACTGGCCATA 685
DB 702 TCGCGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACTGGCCATA 761

QY 686 TCGTGTGCTCATCATGCGCCAGCTTTCATCCCGATATGACCAACCGGGTAAAGTTACGG 745
DB 762 TCGTGTGCTCATCATGCGCCAGCTTTCATCCCGATATGACCAACCGGGTAAAGTTACGG 821

QY 746 GAGACTTTTATCTGACAGCAGAGTGCACTGGCCAGGGGATCACCATTCGTCGCCCGGC 805
DB 822 GAGACTTTTATCTGACAGCAGAGTGCACTGGCCAGGGGATCACCATTCGTCGCCCGGC 881

QY 806 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG 865
DB 882 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACGGCTCTCTTTTATAG 941

QY 866 GTGTAACCTTAAACTGCAATTTACAGTCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGC 925
DB 942 GTGTAACCTTAAACTGCAATTTACAGTCCCTTCTGATTTTCCGCTTTCCAGCGTTCCGC 1001

QY 926 TTCAATAAAACCGGGGAGCCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 1002 TTCAATAAAACCGGGGAGCCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCCGC 1061

QY 986 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTGCTTACACAGCCGAGATATGACATC 1045
DB 1062 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTGCTTACACAGCCGAGATATGACATC 1121

QY 1046 ATATATGCTTTCAGCAACTGATAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
DB 1122 ATATATGCTTTCAGCAACTGATAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181

QY 1106 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1213
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RESULT 10

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US-10-357-268-1
; Sequence 1, Application US/10357268
; Publication No. US20030219902A1
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael L
; APPLICANT: House, Brent L
; APPLICANT: Mortimer, Michael W
; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
; FILE REFERENCE: WSUB-1-20291
; CURRENT APPLICATION NUMBER: US/10/357,268
; PRIORITY FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/354,063
; PRIORITY FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4892
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (73)..(100)
; OTHER INFORMATION: T2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(563)
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Db 14856 ACTCTCAACTTTTATCTTCTTCTGCTTACACATCACTTGTGCATATTTTTTTTACATTA 14797
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Db 14796 TGTGCTTTTATGTAACAATATATTTTATAAATTTATTTTTCACAATATATAACATATAT 14737
Qy 2294 ATCATAGACACAGCAATTAAGTAATCAGATTATCAGTTAAAGCTATGTAATATTTGGC 2353
Db 14736 ATTATAATCACTAATTAACATCACTTAATTTTATCTAAATCTAAAGGAAAGAAAT 14677
Qy 2354 CATACCAATCAATTAATAAATAGATCAGTTTAAAGAAAGATCAAGCTCAAAAATAA 2413
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Qy 2414 AAAGAGAAAGGCTCTTAACCAAGAAATGAAGGAGAAACTAGAAATTTACCTGCACA 2473
Db 14620 GCAATAATGATTTTATTTTGACTGATAGTACCTGTTGCTGTTGCAACAAATTTGATAAGCA 14561
Qy 2474 AGCTTGGATCTCTAGACCACTTTTGTACAAGAAAGCTGAAACGAGAAAGCTAAATGATAT 2533
Db 14560 ATGCTTTCTTATAATGCTCACTTTGTACAAGAAAGCTGAAACGAGAAACGTAATAATGATAT 14501
Qy 2534 AATATCAATATTAATAATAGATTTTGCATAAAGAAACAGACTACATATCTGTAAGAAC 2593
Db 14500 AATATCAATATTAATAATAGATTTTGCATAAAGAAACAGACTACATATCTGTAAGAAC 14441
Qy 2594 ACAACATATCCAGTCACTATGATCACTTACATGATGATTTAGTACCTGCTAGTCGAC 2653
Db 14440 ACAACATATCCAGTCACTATGATCACTTACATGATGATTTAGTACCTGCTAGTCGAC 14381
Qy 2654 TAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGAATAAATCACTGTGACGGAAGATCA 2713
Db 14380 TAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGAATAAATCACTGTGACGGAAGATCA 14321
Qy 2714 CTTCCAGATTAATAATCTGGTGTCTCTGTTGATACCGGAGACCTGGCCCACTT 2773
Db 14320 CTTCCAGATTAATAATCTGGTGTCTCTGTTGATACCGGAGACCTGGCCCACTT 14261
Qy 2774 TTGGCGAAATGAGAGCTGATCGGATTTCACAACTCTTATATCTTCTTCTTACAAGTCG 2833
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Qy 2834 TTCGGCTTCATCTGGATTTTCAGCTCTATATCTTAACTGATGATAAGTTTCTGTAT 2893
Db 14204 CTATGAAGCAGCGTATTTACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCAT 14145
Qy 2894 TTCTACTGTATCGACTCGAGCTGG-----CTGTGTATAGGGAGCTGCATTT 2944
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Qy 2945 ATATTTCCAGAACATCAGGTTAAATGGCGTTTGTATGTCAATTTTCGGCTGGCTGAGAT 3004
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Qy 3005 CAGCCTCTCTTCCCGATTAACGAGACCGGACACTGGCCATATCGTGGTGTATCATC 3064
Db 14027 TATTGAATGAACGGCTCTTTTGTCTGACGAGAACAGGG-----ACTGTGGAATGCACT 13974
Qy 3065 GCAGCTTTTCATCCCGATATGACCAACCGGTTAAAGTTTCAGGGAGACTTTATCTGACA 3124
Db 13973 TTAAGGTTTACACTATAAAGAGAGAGCGCTTATCTGTGTTGTAATGACAGAGTG 13914
Qy 3125 GCAGAGTGCACCTGGCCAGGGGATCACCATCCGTCGCCCGGCGGTGTCAATAATATCAC 3184
Db 13913 ATATTATTGACACGCCCGGCGAGGATGTTGATCCCTGCGCAGTGCACGCTCTCTGT 13854
Qy 3185 TCTGTACATCCAAACAGAGATTAAGCTCTCTCTTTTATAGGTGTAAACCTTAACT 3244
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Qy 3245 GCATTTTCAAC-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAAC 3298

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Qy 3356 CGACGGCTTCATTCTCATGG---TTGTGCTTACAGACCGGAGATATTGACATCATAT 3412
Db 13673 TGTCAAGCTCCCTTATACACAGCCAGTCTGAGGTCGATACAGTAGAAAATTACAGAAAT 13614
Qy 3413 ATGCTTTGAGCACTGATAGTGTGCTGCTCACTGTGTCACTGTATACGCTGCTCATAG 3472
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Qy 3473 CACACCTCTTTTGCACATCTCTCTGTTCTTGATCGAGATGATTTTTCAGGACTATGACACT 3532
Db 13553 GAAAGATATAGAGTGTGTGAATTTGTTCTTGATCGAGATGATTTTTCAGGACTATGACACT 13494
Qy 3533 AGCTATATGATAGTAGTATGTTTATTTTGTTCACAAAAAGAGGCTCGCACCTCT 3592
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Qy 3593 TTTTCTTATTTCTTTTATGATTTAATACGCAATTGAGGCAATAGCGAGTAGGCTGGAT 3652
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Qy 3653 ACAGCAGTTCGCTTTGAGAGAACATTTGGAAGCTGTGCGTGCAGCTAAAGTTGGCAGCAT 3712
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Qy 3713 CACCGAAGAACATTTGGAAGCTGTGCGTGCAGCTACAGTCACTAATACCATCTAAGTA 3772
Db 13313 CACCGAAGAACATTTGGAAGCTGTGCGTGCAGCTACAGTCACTAATACCATCTAAGTA 13254
Qy 3773 GTTATTCTAGTCTGCTGATGTTGTTTACAGTATTATGATGCTGTTTATG 3832
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Qy 3833 CAAATCTAAATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3892
Db 13193 CAAATCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13134
Qy 3893 GTACAACTTGTCT 3905
Db 13133 GTACAACTTGTCT 13121

RESULT 9

US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR201

QY 26 GACAGTTTGTACAAAAAGCTGAACGAGAAAGCTAAATGATATATAATATCAATATAT 85
Db 16988 GCCAATCTTGTGTAACAAAAAGCTGAACGAGAAAGCTAAATGATATATAATATCAATATAT 16929
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Db 16511 CAGTTTCTCAAGGCATATATGATGTAATCTCTCGGTCTGGTAAACACAAACCATCGACA 16452
QY 566 AGGAGCCCTGACATTTATATCTCCAGACATCAGTTAATGCGGTTTGTGATGATTT 625
Db 16451 ATGAAGCCCGTCTGTCGCTGCGT---GAAAGCTGGAAGCGGAAATCAGGAAGGATGG 16395
QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCACACTGGCCATA 685
Db 16394 CTGAGTCCCGGTTTATGAAATGAACGGCTCTTTGCTGACGAGAACAGG----- 16341
QY 686 TCGGTGGTCAATGCGCCAGCTTTCAATCCCGATATGCACACCGGGTAAAGTTCAAGG 745
Db 16340 ACTGGTGAATGCAAGTTTAAGGTTTACACTATATAAAGAGAGAGCGGTTATCGTCTGTTT 16281
QY 746 GAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCCCGCGGC 805
Db 16280 GTGGATGTACAGATGATATTATGACACCGCCGCGCAGGATGGTGTATCCCGCTGGCC 16221
QY 806 GTGTCAATATATCACTCTGTATCATCCACAAACAGACAGATAACGGCTCTCTCTTTATAG 865
Db 16220 AGTGACGCTGCTGTGCATATAAGTCTCCCGTGAACCTTTACCGGTGGTGATATCGGG 16161
QY 866 GTGTAAACCTTAACTGATTTTCAAC-----AGTCCCTGTTCTGTGTACGAAAAAGAGCC 919
Db 16160 GATGAAGCTGGCGATGATGATGACACCGCATATGGCCAGTGTGCGGCTCTCCGTTATCGGG 16101
QY 920 GTTCTATTTCAATAAACCGGCGACCTCAGCCATCCCTCTGATTTTCGCTTCCAGCG 979
Db 16100 GAAGAAGCTGGCTATCTGACCAACCGGAAATGACATCAAAACGCCATTAACCTGATG 16041
QY 980 TTC---GGCAGCAGACGAGCGGCTTCAATCTGCATGGTGTGCTTACCGACCGGAGAT 1036
Db 16040 TTCGCGGAATATAATATGTCAGGCTCCCTTATACAGCCAGCTCTCGAGGTGATACAGT 15981
QY 1037 ATTGACATCATATATGCTTGGAGCAACTGATAGCTGTCTGCTGCACTGTCTATTA 1096
Db 15980 AGAATTTACAGAACTTTATCAGCTTTAGTAGATATAGAGGCTGAAAAATCCAGATGAAGC 15921

QY 1097 CGCT---GCTTCATAGCACACCTCTTTTGAACATACTTTCGGGTAGTCGCGATCAACGTCT 1153
Db 15920 CGAACGACTTGTAAAGAGAAAGTATAAGAGTTGTGAAATGGGTAGTCGCGATCAACGTCT 15861
QY 1154 CATTTTCGCCAAAAGTTGGCCCGCAGGCTTCCCGGTATCAACAGGGACACAGAGATTATT 1213
Db 15860 CATTTTCGCCAAAAGTTGGCCCGCAGGCTTCCCGGTATCAACAGGGACACAGAGATTATT 15801
QY 1214 TATTTCTCGGAAGTATCTTCCTGTCACAGGTATTTATTCGGCGCAAGTCGCTCGGTGAT 1273
Db 15800 TATTTCTCGGAAGTATCTTCCTGTCACAGGTATTTATTCGGCGCAAGTCGCTCGGTGAT 15741
QY 1274 GTGCGCAACTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGAC 1333
Db 15740 GCTGCGCAACTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGAC 15681
QY 1334 TCGATATGTTGTTTATACAGTATTTATGTCGTCTGTTTTATGCAAAATCTAAATTAAT 1393
Db 15680 TCGATATGTTGTTTATACAGTATTTATGTCGTCTGTTTTATGCAAAATCTAAATTAAT 15621
QY 1394 ATATTGATTTTATATATCAATTTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTGTCTCG 1453
Db 15620 ATATTGATTTTATATCAATTTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTGTCTCG 15561
QY 1454 AGAATTCGGTACCCGAGCTTGGTAAGGAAATPAATTTTCTTTTCTTTTCTTTTCTTTT 1513
Db 15560 ATAGAAGACATTTGCTTATCAATTTTGTGCAACGAACAGTCACTATCAGTCAAAATAA 15501
QY 1514 AATATGTTAAGTGAGTTAAATTTAGTATGATATATATATATAGTTGTTATATTTGTA 1573
Db 15500 ATCATTATTTGCCATCCAGCTCGAGCTCTTAGAGGATCCAAAGCTTATCGATTTCGAAC 15441
QY 1574 AATAATTTATAATATATTTTACATAAAACAAACATAGTATGTAATAAAATATACAA 1633
Db 15440 CAGCTTCCCACTGTAATCAATCCAAATGTAAGATCAATGAACACATGACATGATCT 15381
QY 1634 GTGATGTGACGAGGAGAGATAAAGTTGAGAGTAAATATTTATTTTATCAATAGTAAATTC 1693
Db 15380 ATCATGTTACCTTGTGTTTATTCATGTTTCGACTAATTCATTAAATTAATAGTCAATCCAT 15321
QY 1694 GATCGAACATGTAAGATGATATATCTAGCATTAATATTTGTTTTATCAATAGTAAATTC 1753
Db 15320 AGAAGTTAATAAACTCAAGTATTA---TTTGAATAATAAAGATGTTGATTTGAAAAATA 15262
QY 1754 TAGCTGGTTGATGAATTAATAATATCAATGATAAAAATCTATAGTAAAAATAAGATTAAT 1813
Db 15261 AACTATATAAATGATAGATCTTCGCTTGTATATTTAGCATTAGATTAATGTTGTT 15202
QY 1814 AATAATAATAATATTTTATGATTAATAGTTTATTTATATATATTAATAATATCTATACA 1873
Db 15201 ACATTAGATTACTGTTCT---ATTAGTTTGAATATTTATTTGTTACTTTAGCTTTGTTAT 15147
QY 1874 TTACTAATAATTTTATGTTTAAAGTTTAAATAATATTTGTTAGAAATTTCCCAATTCGCTG 1933
Db 15146 TTAAATTTTGTATTATGATAAATTTACAGCAGATTGGAATTTCTTACAAAATAATTTAT 15087
QY 1934 TAATTTTCAATAAACAATAATTAATAAACAAGCTAAAGTAAACAATAATATCAAACTA 1993
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QY 1994 ATAGAAACAGTAACTAATGTAACAAACATATCTAATGCTAATATATACAAAGCGCAG 2053
Db 15026 ATCATAAAAAATAATTTAATTTATTTATTTCTTTATTTTACTAT-----AGT 14977
QY 2054 ATCTATCATTTTATATAGTATTTTTCATCAACATTTCTTATTAATTTCTAAATAATAC 2113
Db 14976 ATTTTATCATGATATTTAATTCATCAACCGAGTAGAATTTACTATTTATGATTAATAA 14917
QY 2114 TTGTAGTTTATTAATCTTAAATGGATGACTATTAATTAATTAATGAATAGTTCGAACATG 2173
Db 14916 ATATTAAATGCTAGTATATCATCTTACATGTTTCGATCAAAATTCATTAATAATAATACT 14857
QY 2174 AATAACAGGTAAACATGATAGATCATGTCATGTTGTTATCATGTCATTTGATTTGGAT 2233

Db 16908 GGCTGAGATCAGCCACTTCTCCCGGATAAACGAGACCGGCACATCGGTGG 16967
Qy 3056 TCATCATCGCCAGCTTTTCATCCCGATATGACACCGGTAAGTTTACCGGGAGACTT 3115
Db 16968 TCATCATCGCCAGCTTTTCATCCCGATATGACACCGGTAAGTTTACCGGGAGACTT 17027
Qy 3116 TATCTGACAGCAGACGTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGCGGTGTCAA 3175
Db 17028 TATCTGACAGCAGACGTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGCGGTGTCOA 17087
Qy 3176 TAAATATCTCTGTATCATCAAAACAGACGATACCGGTCTCTCTTTTATAGGTGTAAA 3235
Db 17088 TAAATATCTCTGTATCATCAAAACAGACGATACCGGTCTCTCTTTTATAGGTGTAAA 17147
Qy 3236 CCTTAACTGCAATTCACACGTCCTCTCTCTGTCAGAAAAGAGCCGTTCAATCAATA 3295
Db 17148 CCTTAACTGCAATTCACACGTCCTCTCTCTGTCAGAAAAGAGCCGTTCAATCAATA 17207
Qy 3296 AACCGGGGACCTCAGCCATCCCTCTCTGATTTTCCGCTTTCAGCGTTTCGGCAGCAGA 3355
Db 17208 AACCGGGGACCTCAGCCATCCCTCTCTGATTTTCCGCTTTCAGCGTTTCGGCAGCAGA 17267
Qy 3356 CGACGGGCTTCATCTGCAATGTTGTGCTTACAGACCGGATATGACATCATATATG 3415
Db 17268 CGACGGGCTTCATCTGCAATGTTGTGCTTACAGACCGGATATGACATCATATATG 17327
Qy 3416 CTTTGAAGCAACTGATAGCTGCTGCTCAACTGCTCACTGATACGCTGCTCATAGACAC 3475
Db 17328 CTTTGAAGCAACTGATAGCTGCTGCTCAACTGCTCACTGATACGCTGCTCATAGACAC 17387
Qy 3476 ACCTCTTTTGAACATCTCTGTTCTGTGATGCGAGATGATTTTCAGGACTATGACATAGC 3535
Db 17388 ACCTCTTTTGAACATCTCTGTTCTGTGATGCGAGATGATTTTCAGGACTATGACATAGC 17447
Qy 3536 GTATATGATAGTATGATGTTTATTTTATTTGTCACACAAAAGAGGCTCGACCTCTTTT 3595
Db 17448 GTATATGATAGTATGATGTTTATTTTATTTGTCACACAAAAGAGGCTCGACCTCTTTT 17507
Qy 3596 TCTTATTTCTTTTATGATTAATAGGCAATGAGGACATAGGAGTGGCTGGATAGC 3655
Db 17508 TCTTATTTCTTTTATGATTAATAGGCAATGAGGACATAGGAGTGGCTGGATAGC 17567
Qy 3656 ACATTTCCGTTTGAGAGAAACATTTGGAAGCTGTCGGTCGACTAAGTTGGCGAGCATAC 3715
Db 17568 ACATTTCCGTTTGAGAGAAACATTTGGAAGCTGTCGGTCGACTAAGTTGGCGAGCATAC 17627
Qy 3716 CCGAAGAACATTTGGAAGCTGTCGGTCGACTACAGTCACTAATACCATCTAAGTAGTT 3775
Db 17628 CCGAAGAACATTTGGAAGCTGTCGGTCGACTACAGTCACTAATACCATCTAAGTAGTT 17687
Qy 3776 GATTCATAGTACTGGATATGTTGTGTTTACAGTATATGATAGTCTGTTTTTATGCAA 3835
Db 17688 GATTCATAGTACTGGATATGTTGTGTTTACAGTATATGATAGTCTGTTTTTATGCAA 17747
Qy 3836 AATCTAATTTAATATATGATATATATCAATTTACGTTTCCTGTTTCAGCTTTTGTGA 3895
Db 17748 AATCTAATTTAATATATGATATATATCAATTTACGTTTCCTGTTTCAGCTTTTGTGA 17807
Qy 3896 CAAACTTG----- 3903
Db 17808 CAAAGTGGCATTATAAAAGCATGCTCATCAATTTGTTGCAACGACAGTCACTAT 17867
Qy 3904 -----TCTAGAGTCTGCTT 3918
Db 17868 CAGTCAAAATAAATCATTTATTTGGGCGCCGAGATCCATGCTAGCTCTAGAGTCTGCTT 17927
Qy 3919 TAATGATATGCGAGACGCTATGATCGATGATATTTGCTTTCAATTTCTGTTGTCAC 3978
Db 17928 TAATGATATGCGAGACGCTATGATCGATGATATTTGCTTTCAATTTCTGTTGTCAC 17987
Qy 3979 GTTGTAAACACCTGAGCATGTTAGTCTAGATCTTTACCGCGGTTTTCGTTTCATCTTA 4038

Db 17988 GTTGTAAACACCTGAGCATGTTAGTCTAGATCCTTACCGCGGTTTCGTTTCATCTTA 18047
Qy 4039 ATGAATATATCACCGGTTACTATCGTATTTTATGAATAATATTTCCGTTCAATTTACT 4098
Db 18048 ATGAATATATCACCGGTTACTATCGTATTTTATGAATAATATTTCCGTTCAATTTACT 18107
Qy 4099 GATTGTACCCCTACTACTATATATGATACAAATATAAATGAAACAAATATATTGTGCTGAAT 4158
Db 18108 GATTGTACCCCTACTACTATATGATACAAATATAAATGAAACAAATATATTGTGCTGAAT 18167
Qy 4159 AGGTTTATAGCAGCATCTATGATAGAGCCGACAAATACAAATTCGTTTATTTATTT 4218
Db 18168 AGGTTTATAGCAGCATCTATGATAGAGCCGACAAATACAAATTCGTTTATTTATTT 18227
Qy 4219 ACAATCCAAATTTTAAATAAAGCGCAGAACCGGTCAAAACCTTAAAGACTGATTACATAA 4278
Db 18228 ACAATCCAAATTTTAAATAAAGCGCAGAACCGGTCAAAACCTTAAAGACTGATTACATAA 18287
Qy 4279 ATCTTATTCAAATTTTAAATAAAGCGCAGAACCGGTCAAAACCTTAAAGACTGATTACATAA 4338
Db 18288 ATCTTATTCAAATTTTAAATAAAGCGCAGAACCGGTCAAAACCTTAAAGACTGATTACATAA 18347
Qy 4339 CTAATAACGTTTACATGAAGGAACCTCCGTTTCCCGCGCGCGCATGGGTGAGATTCTT 4398
Db 18348 CTAATAACGTTTACATGAAGGAACCTCCGTTTCCCGCGCGCGCATGGGTGAGATTCTT 18407
Qy 4399 TGAAGTTGAGTATTTGGCGCTCCGCTCTACCGAAAGTTTACGGGACCAATTCACCCGGTCC 4458
Db 18408 TGAAGTTGAGTATTTGGCGCTCCGCTCTACCGAAAGTTTACGGGACCAATTCACCCGGTCC 18467
Qy 4459 AGCAGCGGCGCGGTTAAACGACTTGTCTGCCCGGAGAAATATGACGCAATTTTGTGTGT 4518
Db 18468 AGCAGCGGCGCGGTTAAACGACTTGTCTGCCCGGAGAAATATGACGCAATTTTGTGTGT 18527
Qy 4519 ATGTGCGGCGCCAAATGAAGTGCAGGTCAAACTTGCACAGTGCACAAATCGTTGGCGG 4578
Db 18528 ATGTGCGGCGCCAAATGAAGTGCAGGTCAAACTTGCACAGTGCACAAATCGTTGGCGG 18587
Qy 4579 GTCCAGGGCGAAATTTTGGACAAATGTCAGGCTCAGCAGACCTGCGAGGATGCAAGC 4638
Db 18588 GTCCAGGGCGAAATTTTGGACAAATGTCAGGCTCAGCAGACCTGCGAGGATGCAAGC 18647
Qy 4639 TAGCTTACTAGTATGATGATATTTCTATGTCACCTAAATCTGC 4682
Db 18648 TAGCTTACTAGTATGATGATATTTCTATGTCACCTAAATCTGC 18691

RESULT 7

US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 25.8%; Score 1208.4; DB 15; Length 17681;
Best Local Similarity 60.4%; Pred. No. 8.6e-174;
Matches 2374; Conservative 0; Mismatches 1476; Indels 80; Gaps 20;

1674 ATATTATTTTATGATGATCGAACATGTAAGATGATATAGCATTA 1726
14860 ATATTATTTTATGATGATCGAACATGTAAGATGATATAGCGCGGTTC 14919
1727 1726
14920 CAATTTTCACCAATGAATGAATAGATCACTACGCGCGTATTTT 14979
1727 1726
14980 TTCAGAGCTAAGGAAGCTAAAATGAGAAAAAATCCTGGATATAC 15039
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15040 ATCCCAATGGCATCGTAAGAACAATTTTGAGGCATTTTCAATGT 15099
1727 1726
15100 TAACCAAGCCGTTACGCTGGATATTACGGCTTTTAAAGACCGTA 15159
1727 1726
15160 CAAGTTTATCCGCCCTTTATTCACATTTCTTGCCCGCTGATGAT 15219
1727 1726
15220 CCGTATGGCAATGAAAGACGGTGAGCTGGTGATGGGATAGTGTTC 15279
1727 1726
15280 CGTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGA 15339
1727 1726
15340 CCGGCAGTTTTCACATATATTCGCAAGTGTGGCGTGTACGGTGAA 15399
1727 1726
15400 TTTCCCTAAAGGGTTTATGAGAATATGTTTTCGTCTCAGCCAAT 15459
1727 1726
15460 CACCAGTTTGAATTAACGTGGCCAAATATGGAACCTTCTCGCCCG 15519
1727 1726
15520 GGGCAAAATATTATACGAAGGACAAAGTGTGATGCCCTGGCGAT 15579
1727 1726
15580 TGCCGCTGTGATGGCTTCCATGTCCGCGAATGCTTAAATGAATT 15639
1727 1726
15640 TGAGTGGCAGGGCGGGCGTAATCGCGTGGATCCGGCTTACTAAAG 15699
1727 1726
15700 TGCGTATTTGCGGCTGATTTTTCGGGTATAGAAATATATAGTAT 1743
1744 ATAGTAATTTCTAGCTGTTTGTAGTAATTAATCAATGATAAATAC 1803
15760 ATAGTAATTTCTAGCTGTTTGTAGTAATTAATCAATGATAAAT 15819
1804 AAGATAAATAAATAAATAATTTTATGATTAATAGTTTATATATAAT 1863
15820 AAGATAAATAAATAAATAATTTTATGATTAATAGTTTATATATAAT 15879
1864 ATCTATACCAATTAATAATTTTATGTTTAAAGTTAATAAATTTTGT 1923
15880 ATCTATACCAATTAATAATTTTATGTTTAAAGTTAATAAATTTTGT 15939

1924 AATCTGCTTGTAAATTTATCAATAAACAATAATTAATAACAAGCTAA 1983
15940 AATCTGCTTGTAAATTTATCAATAAACAATAATTAATAACAAGCTAA 15999
1984 TATCAAACTAATAGAAAAAGTAATCTAATGTAAACAAAACATAATCT 2043
16000 TATCAAACTAATAGAAAAAGTAATCTAATGTAAACAAAACATAATCT 16059
2044 AAAGCGCAAGTCTATCAATTTTATATAGTATTTTCAATCAAACTT 2103
16060 AAAGCGCAAGTCTATCAATTTTATATAGTATTTTCAATCAAACTT 16119
2104 TAAATAATCTTGTAGTTTATTAATCTTCTAATAGGATGACTATTAA 2163
16120 TAAATAATCTTGTAGTTTATTAATCTTCTAATAGGATGACTATTAA 16179
2164 GTCCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTATT 2223
16180 GTCCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTATT 16239
2224 ACATTTGGATTCATTAACAGTTCGGGAAGCTGGGTTCGAAATCGATA 2283
16240 ACATTTGGATTCATTAACAGTTCGGGAAGTTCGGGTTCGAAATCGATA 16293
2284 TATCATCATCATATAGACACACGAAATAAAGTAATCAGATTTATCAG 2343
16294 CCTCTAGAGAGCTGCAGCTGGATGCAATAATGATTTTATTTGACT 16353
2344 ATATTTGGCCATTAACCAATCAATTAATAAATAAGATCAGTTTAA 2403
16354 TTTCTGTCACAAA 16367
2404 AAAAAAATAAAGAGAGAAAGGTCCTTAACCAAGAAAAATGAAGGAG 2463
16368 16367
2464 TACCTGCAACAGCTTGGATCTCTAGACCACTTTGTACAAGAAAGCT 2523
16368 TTGATAAGCAATGCTTCTTATAATGCCAACTTTGTACAAGAAAGCT 16427
2524 AAATGTATTAATATCAATATATTAATTAATAGATTTTGCATAAAA 2583
16428 AAATGTATTAATATCAATATATTAATTAATAGATTTTGCATAAAA 16487
2584 ACTGTAAAAACAACATATCCAGTCACTATGAATCAAACTACTAGAT 2643
16488 ACTGTAAAAACAACATATCCAGTCACTATGAATCAAACTACTAGAT 16547
2644 TGTAGTCGATTAAGTTGGCAGCATCACCGACGCTTTGCGCGGATTA 2703
16548 TGTAGTCGATTAAGTTGGCAGCATCACCGACGCTTTGCGCGGATTA 16607
2704 CGGAAGATCACTTCCAGAAATAAATAATCTGTTGCTTGTATCCGG 2763
16608 CGGAAGATCACTTCCAGAAATAAATAATCTGTTGCTTGTATCCGG 16667
2764 GGGCCAACTTTTGGGAAATGAGAGCTTGTATCGG 2815
16668 GGGCCAACTTTTGGGAAATGAGAGCTTGTATCGGCACTACCCATTT 16727
2816 CTTTCTCTTAAGAATCGTTTCGCTTCACTCGAATTTTCAGCTCTATA 2875
16728 CTTTCTCTTAAGAATCGTTTCGCTTCACTCGAATTTTCAGCTCTATA 16787
2876 TGATAAAGTTTCTGTAATTTTCTACTGTATCGACCTGCAGCTGGTGT 2935
16788 TGATAAAGTTTCTGTAATTTTCTACTGTATCGACCTGCAGCTGGTGT 16847
2936 CTGACATTTATATCCCGAGAACATCAGGTTAATGCGGTTTTTGTAT 2995
16848 CTGACATTTATATCCCGAGAACATCAGGTTAATGCGGTTTTTGTAT 16907
2996 GGCTGAGATCAGCAGCTTCTTCCCGATTAACGGAGACCGGCACACT 3055

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; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match      68.3%; Score 3199.6; DB 15; Length 18691;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 4460; Conservative 0; Mismatches 84; Indels 1140; Gaps 7;

QY 26 GACAGTTTGTACAAAAGAGCTGACGAGAAACGTAATAATGATATAATCAATATATT 85
DB 13121 GCCAACTTTGTACAAAAGAGCTGACGAGAAACGTAATAATGATATAATCAATATATT 13180

QY 86 AAATTAGATTTCGATATAAAACAGACTACATATACTGTAAACACAAATATCCAGTC 145
DB 13181 AAATTAGATTTCGATATAAAACAGACTACATATACTGTAAACACAAATATCCAGTC 13240

QY 146 ACTATGAATCAACTACTAGATTAGTATAGTATAGTACCTGTAGCTGACCGACAGCCCTCCAAA 205
DB 13241 ACTATGAATCAACTACTAGATTAGTATAGTATAGTACCTGTAGCTGACCGACAGCCCTCCAAA 13300

QY 206 TGTTCTTCGGGTGATGTCGCAACTAGTACGAGCAGCGACGCTTCCAAATGTTCTCTCAA 265
DB 13301 TGTTCTTCGGGTGATGTCGCAACTAGTACGAGCAGCGACGCTTCCAAATGTTCTCTCAA 13360

QY 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAA 325
DB 13361 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAA 13420

QY 326 AGAATAAGAAAAAGAGGTGCGAGCCCTCTTTTGTGTGCAAAAATAAAAAACATCTACCT 385
DB 13421 AGAATAAGAAAAAGAGGTGCGAGCCCTCTTTTGTGTGCAAAAATAAAAAACATCTACCT 13480

QY 386 ATTCAATAGCTAGTGTCTAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 445
DB 13481 ATTCAATAGCTAGTGTCTAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 13540

QY 446 TCTTATACCTTTCTTCTTACAGTGTGTCGGCTTCATCTGATTTTCAGCCCTCTATACCTTA 505
DB 13541 TCTTATACCTTTCTTCTTACAGTGTGTCGGCTTCATCTGATTTTCAGCCCTCTATACCTTA 13600

QY 506 CTAACGTGATAAAGTTTCTGTAATTTCTACTGATACGACTGCGACTGCGTGTGATA 565
DB 13601 CTAACGTGATAAAGTTTCTGTAATTTCTACTGATACGACTGCGACTGCGTGTGATA 13660

QY 566 AGGAGAGCTGACATTTATATTTCCCGAGACATCAGGTTAATGGGTTTTTTCATGTCATTT 625
DB 13661 AGGAGAGCTGACATTTATATTTCCCGAGACATCAGGTTAATGGGTTTTTTCATGTCATTT 13720

QY 626 TCGCGGTGGGTGAGATCAGCCACTTCTTCCCGGATAACGGACCGGCACACTGGCCATA 685
DB 13721 TCGCGGTGGGTGAGATCAGCCACTTCTTCCCGGATAACGGACCGGCACACTGGCCATA 13780

686 TCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTCAACGG 745
13781 TCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTCAACGG 13840

746 GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGCG 805
13841 GAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGCG 13900

806 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATACGGCTCTCTCTTTATAG 865
13901 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATACGGCTCTCTCTTTATAG 13960

866 GTGTAAACCTTAAACTGCAATTTACCAAGTCCCTGTTCTCGTCAGCAAAAAGACCGCTTCAT 925
13961 GTGTAAACCTTAAACTGCAATTTACCAAGTCCCTGTTCTCGTCAGCAAAAAGACCGCTTCAT 14020

926 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCGATTTTCGGTTTCCAGCGTTCCGC 985
14021 TTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCGATTTTCGGTTTCCAGCGTTCCGC 14080

986 AGCAGACAGCGGCTTCAATCTGCGATGTTGCTTACGACGCGAGATATTGACATC 1045
14081 AGCAGACAGCGGCTTCAATCTGCGATGTTGCTTACGACGCGAGATATTGACATC 14140

1046 ATATATGCTCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAATACGCTCTTC 1105
14141 ATATATGCTCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAATACGCTCTTC 14200

1106 ATAGCACACCTCTTTTGACATACCTTCGGGTAGTGCAGTCAACGCTCTCATTTTCGCCAA 1165
14201 ATAGCACACCTCTTTTGACATACCTTCGGGTAGTGCAGTCAACGCTCTCATTTTCGCCAA 14260

1166 AAGTTCCGCCAGCGCTTCCCGGTATCAACAGGACACACAGGATTTATTTATTTCTCGGAAG 1225
14261 AAGTTCCGCCAGCGCTTCCCGGTATCAACAGGACACACAGGATTTATTTATTTCTCGGAAG 14320

1226 TGATCTTCGCTCACAGGTATTTATTTCGGCGCAAAAGTCGCGGTGATCTGCAACTTGA 1285
14321 TGATCTTCGCTCACAGGTATTTATTTCGGCGCAAAAGTCGCGGTGATCTGCAACTTGA 14380

1286 GTCGACTCAGGTCATTAATCACTAAGTAGTGTGATTCATAGTACGACTGGATATGTTGT 1345
14381 GTCGACTCAGGTCATTAATCACTAAGTAGTGTGATTCATAGTACGACTGGATATGTTGT 14440

1346 GTTTTACAGTATTATAGTCTGTTTATGCAAAATCTAATTTAATATATATTGATATT 1405
14441 GTTTTACAGTATTATAGTCTGTTTATGCAAAATCTAATTTAATATATATTGATATT 14500

1406 ATATCAATTTTACGTTTCTCGTTCAGCTTTCTTTGTACAAAAGTGG- 1448
14501 ATATCAATTTTACGTTTCTCGTTCAGCTTTCTTTGTACAAAAGTGGCATTATAAGAAAGCAT 14560

1449 ----- 1448
14561 TGCTTATCAATTTGTTGCAACGAAACAGGTCATATCAGTCAAAATAAATATCATTTTGC 14620

1449 -----TCTCGAGGAATTCGGTACCCCGAGCTTGGTAAGGAAATAATTTATT 1493
14621 CATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAAATAATTTATT 14679

1494 TCTTTTTCCTTTTAGTATAAAATAGTTAAGTAGTGTAAATTAATAGTATGATTAATAATAA 1553
14680 TCTTTTTCCTTTTAGTATAAAATAGTTAAGTAGTGTAAATTAATAGTATGATTAATAATAA 14739

1554 TAGTCTGTATAATGTGAAAAAATAATTTATATAATATTTGTTTACATAAAACAAATAGT 1613
14740 TAGTCTGTATAATGTGAAAAAATAATTTATATAATATTTGTTTACATAAAACAAATAGT 14799

1614 AATGTAAAAAATAATGACAAAGTAGTGTAAAGCAAGAAAGATAAAGTTGAGAGTAAGT 1673
14800 AATGTAAAAAATAATGACAAAGTAGTGTAAAGCAAGAAAGATAAAGTTGAGAGTAAGT 14859
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QY	3526	TGACACTAGCGTATATGAATAGCTAGATGTTTATTTATTTTGTGCACAAAAAGAGCTCG	3585
Db	16609	TGACACTAGCGTATATGAATAGCTAGATGTTTATTTTGTGCACAAAAAGAGCGTCTG	16668
QY	3586	CACCTCTTTTCTTATTTCTTTTATGATTAATACGCCATTCAGGACAATAGCAGTAG	3645
Db	16669	CACCTCTTTTCTTATTTCTTTTATGATTAATACGCCATTCAGGACAATAGCAGTAG	16728
QY	3646	GCTGGATACACAGATTCGGTTTGAGAAGAACATTTGGAAAGGCTGTGCTGCAGTAAGTTG	3705
Db	16729	GCTGGATACACAGATTCGGTTTGAGAAGAACATTTGGAAAGGCTGTGCTGCAGTAAGTTG	16788
QY	3706	GCAGCATCACCCGAAGAACATTTTGGAAAGGCTGCGCTGCAGTACAGTCACTAAATACCAT	3765
Db	16789	GCAGCATCACCCGAAGAACATTTTGGAAAGGCTGCTCGCTGCAGTACAGTCACTAAATACCAT	16848
QY	3766	CTAAGTAGTTGATTCATPAGTACCTGGATATGTTGTCTTTTACAGATTAATGTAGTCTGTT	3825
Db	16849	CTAAGTAGTTGATTCATPAGTACCTGGATATGTTGTCTTTTACAGATTAATGTAGTCTGTT	16908
QY	3826	TTTTTATGCCAAAACTAAATTTTAATATATCGATTTTATATCATTTTACGGTTCTTCGTTCCAG	3885
Db	16909	TTTTTATGCCAAAACTAAATTTTAATATATCGATTTTATATCATTTTACGGTTCTTCGTTCCAG	16968
QY	3886	CTTTTTTGTACAAACTTG-----	3903
Db	16969	CTTTTTTGTACAAAGTTGGCATTTATAAAAGCAATGCTCATCAATTTGTTGCAACGAAC	17028
QY	3904	-----	3908
Db	17029	AGGTCACATTCAGTCAAAATAAAATCATTTATTGGGGCCCGAGATCCCATGTAGTCTCTAG	17088
QY	3909	AGTCCCTGCTTTAATGAGATATCGAGACGCCCTATGATCGCATGATATTGCTTTCAATTC	3968
Db	17089	AGTCCCTGCTTTAATGAGATATCGAGACGCCCTATGATCGCATGATATTGCTTTCAATTC	17148
QY	3969	TGTTGTGCGAGTTGTAAAAAACTGAGAGATGTGTAGTCCAGATCCCTTACCGCGGTTTTCG	4028
Db	17149	TGTTGTGCGAGTTGTAAAAAACTGAGAGATGTGTAGTCCAGATCCCTTACCGCGGTTTTCG	17208
QY	4029	GTTTCATTCTAAUGAATATATCACCCGTTACTACTCGTATTTTTTATCGAATAATTTCTCCGT	4088
Db	17209	GTTTCATTCTAAUGAATATATCACCCGTTACTACTCGTATTTTTTATCGAATAATTTCTCCGT	17268
QY	4089	TCAATTTACTGATGTACCCCTACTCTTATATGTACAATPATTPATAAATGAAACCAATATAT	4148
Db	17269	TCAATTTACTGATGTACCCCTACTCTTATATGTACAATPATTPATAAATGAAACCAATATAT	17328
QY	4149	TGTGCTGGAATAGTTTATAGCGACATCTATGATAGAGCGCCACATATACCAACANTTCGG	4208
Db	17329	TGTGCTGGAATAGTTTATAGCGACATCTATGATAGAGCGCCACATATACCAACANTTCGG	17388
QY	4209	TTTTTATTTACAAATCCAAATTTTTAAAAAGCGGCAGAACCCGGTCAAAACCTTAAAGACT	4268
Db	17389	TTTTTATTTACAAATCCAAATTTTTAAAAAGCGGCAGAACCCGGTCAAAACCTTAAAGACT	17448
QY	4269	GATTACATAAATCTTATTCAAATTTCAAAGGCCCGGAGGTAGTATCTTAGCACACACC	4328
Db	17449	GATTACATAAATCTTATTCAAATTTCAAAGGCCCGGAGGTAGTATCTTAGCACACACC	17508
QY	4329	GAGCGCGGAACCTAAATAACCGTTCACTGAAGGGAACCTCCGGTCCCGCGCGCGCATGGG	4388
Db	17509	GAGCGCGGAACCTAAATAACCGTTCACTGAAGGGAACCTCCGGTCCCGCGCGCGCATGGG	17568
QY	4389	TGAGATTCCTTGAAGTTGAGTATTGCCCGTCCGCTCTACGGAAGTTTACGGGCACCAATTC	4448
Db	17569	TGAGATTCCTTGAAGTTGAGTATTGCCCGTCCGCTCTACGGAAGTTTACGGGCACCAATTC	17628
QY	4449	AAACCCGGTCCAGCACCGCGCGCGGGTAAACCGACTTGCTGCCCGGAGAAATTTATGACGANTT	4508
Db	17629	AAACCCGGTCCAGCACCGCGCGCGGGTAAACCGACTTGCTGCCCGGAGAAATTTATGACGANTT	17688

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Qy 4509 TTTTGGTGATGTGGGCCCCAAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAAT 4568
Db 17689 TTTTGGTGATGTGGGCCCCAAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAAT 17748
Qy 4569 CGTTGGGCGGCTCCAGGSCGAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTGCAG 4628
Db 17749 CGTTGGGCGGCTCCAGGSCGAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTGCAG 17808
Qy 4629 GCATGCAAGCTAGCTTACTACTAGTATGCATATTTCTATAGTGTCACTAAATCTGC 4682
Db 17809 GCATGCAAGCTAGCTTACTACTAGTATGCATATTTCTATAGTGTCACTAAATCTGC 17862

RESULT 6
US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17830)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14650)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)

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QY 4381 CGCATGGGTGAGATTCCTGAAAGTTGAGTATTGGCCGTCGCTCTACCGAAAGTTACGGG 4440
Db 17157 CGCATGGGTGAGATTCCTGAAAGTTGAGTATTGGCCGTCGCTCTACCGAAAGTTACGGG 17216
QY 4441 CACCATTCAACCCGGTCCAGACGGCGCGGGTAACCGACTTGTGCCCCCGAGAAATTAT 4500
Db 17217 CACCATTCAACCCGGTCCAGACGGCGCGGGTAACCGACTTGTGCCCCCGAGAAATTAT 17276
QY 4501 GCAGCAATTTTTTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACTTCGACAGTGA 4560
Db 17277 GCAGCAATTTTTTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACTTCGACAGTGA 17336
QY 4561 CGACAAATCGTTGGCGGGTCCAGGGCGAAATTTTGGCGAACAATGTCGAGGCTCAGCAGG 4620
Db 17337 CGACAAATCGTTGGCGGGTCCAGGGCGAAATTTTGGCGAACAATGTCGAGGCTCAGCAGG 17396
QY 4621 ACCTGCAGGCGATCGAAGCTAGCTTACTAGTGTGATGATGATATCTATAGTGTGTCACCTAAATCT 4680
Db 17397 ACCTGCAGGCGATCGAAGCTAGCTTACTAGTGTGATGATGATATCTATAGTGTGTCACCTAAATCT 17456
QY 4681 GC 4682
Db 17457 GC 17458

RESULT 5

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match 87.1%; Score 4077.2; DB 15; Length 17862;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 447; Conservative 0; Mismatches 68; Indels 309; Gaps 5;

QY 26 GACAAGTTTGTACAAAAAGCTGAACGAGAAAGCTAAATGATATAAATATCAATATAT 85
Db 13121 GCCAATTTGTACAAAAAGCTGAACGAGAAAGCTAAATGATATAAATATCAATATAT 13180
QY 86 AAATTAGATTTTGCATAAAAAAGCTGACATAAATCTGTAAACACAAATATCCAGTC 145
Db 13181 AAATTAGATTTTGCATAAAAAAGCTGACATAAATCTGTAAACACAAATATCCAGTC 13240
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCCGACGAGCCCTTCCAAAGCTTCCAA 205
Db 13241 ACTATGAATCAACTACTTAGATGGTATTAGTACCCGACGAGCCCTTCCAAAGCTTCCAA 13300
QY 206 TGTCTTCGGGTGATGCTGCCAATCTAGTCGACGAGCCCTTCCAAAGCTTCTCTCAA 265
Db 13301 TGTCTTCGGGTGATGCTGCCAATCTAGTCGACGAGCCCTTCCAAAGCTTCTCTCAA 13360
QY 266 ACGGAATCGTGTATCCAGGCTACTCGCTATTGTCTCAATGCGGATTAAATCATATAA 325
Db 13361 ACGGAATCGTGTATCCAGGCTACTCGCTATTGTCTCAATGCGGATTAAATCATATAA 13420

QY 326 AGAAATAAGAAAAAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
Db 13421 AGAAATAAGAAAAAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 13480
QY 386 ATTCAATATACGCTAGTGTCTAGTCTGAAATATCATCTGCATCAAGAAACAATTTCAAC 445
Db 13481 ATTCAATATACGCTAGTGTCTAGTCTGAAATATCATCTGCATCAAGAAACAATTTCAAC 13540
QY 446 TCTTATACCTTTCTCTTACAGTCTGTTCCGCTTCATCTGGAATTTTTCAGCTCTATCTATA 505
Db 13541 TCTTATACCTTTCTCTTACAGTCTGTTCCGCTTCATCTGGAATTTTTCAGCTCTATCTATA 13600
QY 506 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGACACTGGCTGTGTATA 565
Db 13601 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGACACTGGCTGTGTATA 13660
QY 566 AGGAGCCTGACATTTATATTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCAAT 625
Db 13661 AGGAGCCTGACATTTATATTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCAAT 13720
QY 626 TCGCGGTGCTGAGATCAGCAGCCACTTCTCCCGATAACGAGACCGGCACACTGGCCATA 685
Db 13721 TCGCGGTGCTGAGATCAGCAGCCACTTCTCCCGATAACGAGACCGGCACACTGGCCATA 13780
QY 686 TCGGTGCTCATATGCGCCAGCTTTTATCCCGATATGACCAACCGGGTAAAGTTCAACG 745
Db 13781 TCGGTGCTCATATGCGCCAGCTTTTATCCCGATATGACCAACCGGGTAAAGTTCAACG 13840
QY 746 GAGACTTTATCTGACGACGAGCTGCTGCGCCAGGGGATCAGATCCGTCGCGCGGC 805
Db 13841 GAGACTTTATCTGACGACGAGCTGCTGCGCCAGGGGATCAGATCCGTCGCGCGGC 13900
QY 806 GTGTCAATATATCACTCTGTATATCCACAAACAGACGATTAACGGCTCTCTCTTTATAG 865
Db 13901 GTGTCAATATATCACTCTGTATATCCACAAACAGACGATTAACGGCTCTCTCTTTATAG 13960
QY 866 GTGTAAACCTTAAACTGCAATTTTCAAGTCCCTGTTCTGTCAGCAAAAAGAGCGGTTCA 925
Db 13961 GTGTAAACCTTAAACTGCAATTTTCAAGTCCCTGTTCTGTCAGCAAAAAGAGCGGTTCA 14020
QY 926 TTCAATTAACCGGGCGACTGACGCTCCCTCTCCGATTTTCCGCTTTCCAGGTTCCGC 985
Db 14021 TTCAATTAACCGGGCGACTGACGCTCCCTCTCCGATTTTCCGCTTTCCAGGTTCCGC 14080
QY 986 ACGCAGACGACGGGCTTCAATCTGCTATGTTGTTTACAGACCGGAGATTTGACATC 1045
Db 14081 ACGCAGACGACGGGCTTCAATCTGCTATGTTGTTTACAGACCGGAGATTTGACATC 14140
QY 1046 ATATATGCTTGAAGCACTGATAGTGTGCTGCTCAACTGTCACTGTATACGCTGCTTC 1105
Db 14141 ATATATGCTTGAAGCACTGATAGTGTGCTGCTCAACTGTCACTGTATACGCTGCTTC 14200
QY 1106 ATAGCACACCTCTTTTTCACATACCTTCCGGTAGTCCGATCAACGCTCTCATTTTCGCA 1165
Db 14201 ATAGCACACCTCTTTTTCACATACCTTCCGGTAGTCCGATCAACGCTCTCATTTTCGCA 14260
QY 1166 AAGTTGGCCCGGCTTCCCGGTATCAACAGAGGACACAGAGATTTATTTATCTCGAAG 1225
Db 14261 AAGTTGGCCCGGCTTCCCGGTATCAACAGAGGACACAGAGATTTATTTATCTCGAAG 14320
QY 1226 TGATCTTCGGTCAAGGTATTTTTCGGGCAAGTGGTGGGTGATGCTGCCAATTA 1285
Db 14321 TGATCTTCGGTCAAGGTATTTTTCGGGCAAGTGGTGGGTGATGCTGCCAATTA 14380
QY 1286 GTCGACTACGCTACTAATACCTAAGTAGTTGATTCATAGTACGTGATATGTTGT 1345
Db 14381 GTCGACTACGCTACTAATACCTAAGTAGTTGATTCATAGTACGTGATATGTTGT 14440
QY 1346 GTTTTACAGTATATAGTACTGTGTTTTTATGCAAAAATCTAATTTAATATATGATATTT 1405
Db 14441 GTTTTACAGTATATAGTACTGTGTTTTTATGCAAAAATCTAATTTAATATATGATATTT 14500
QY 1406 ATATCAATTTTACGTTTCTGCTTACGCTTCTTTGTACAAAGTGG----- 1448

Db	15156	TTAGTCGAACATCAATAAACAAAGGTAAACATGATAGATCATGTGTTATCATTTGAT	15215
Qy	2221	CTTACATTTTGGATTGATTACAGTTGGGAAGCTTGGGTTTCGAAATCGATAAGCTTGGCGTGC	2280
Db	15216	CTTACATTTTGGATTGATTACAGTTACTTACCT	15247
Qy	2281	AGTTATCATCATCATCATAGACACACGAATAAAGTAATCAGATTATCAGTTAAAGCTTAT	2340
Db	15248	-----	15247
Qy	2341	GTAATATTTGCGCCATAACCAATCAATTAAATAATAGATCAGTTTAAAGAAGATCAAG	2400
Db	15248	-----	15247
Qy	2401	CTCAAAAAATAAAGAGAGAAAAAGGTCCTAAACCAAGAAAAATGAAGGAGAAAAACTAGAA	2460
Db	15248	-----	15247
Qy	2461	ATTTACCTGCACAAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAAGCTGAAACGAGAAA	2520
Db	15248	-----TAAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAAGCTGAAACGAGAAA	15296
Qy	2521	CGTAAATGATATAAATATCAATATATTAATTAATTTAGATTTTGCATAAAAAACAGACTACAT	2580
Db	15297	CGTAAATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAACAGACTACAT	15356
Qy	2581	AATACTGTAAAAACAACATATCCAGTCACTATGATCAACTACCTTGTAGATGGTATTAGTG	2640
Db	15357	AATACTGTAAAAACAACATATCCAGTCACTATGATCAACTACCTTGTAGATGGTATTAGTG	15416
Qy	2641	ACCTGTAGTCGACTAAGTTGGCAGCATACCCGACGCACCTTTGCGCCGAATAAATACCTGT	2700
Db	15417	ACCTGTAGTCGACTAAGTTGGCAGCATACCCGACGCACCTTTGCGCCGAATAAATACCTGT	15476
Qy	2701	TGACGGAAGATCACTTCGCAGAAATAAATAAATCCTGGTGTCCCTGTTTCATACCCGGGAAC	2760
Db	15477	TGACGGAAGATCACTTCGCAGAAATAAATAAATCCTGGTGTCCCTGTTTCATACCCGGGAAC	15536
Qy	2761	CTTGGGCCAACTTTTGGCGAAAAATGAGACGTTTGAATCGGATTTTCACAACTCTTATACCTTT	2820
Db	15537	CTTGGGCCAACTTTTGGCGAAAAATGAGACGTTTGAATCGGATTTTCACAACTCTTATACCTTT	15596
Qy	2821	CTCTTACAAGTCGTTCCGCTTCACTCTGGATTTTCAGCCTCTATACCTTACTAAACGTGATA	2880
Db	15597	CTCTTACAAGTCGTTCCGCTTCACTCTGGATTTTTCAGCCTCTATACCTTACTAAACGTGATA	15656
Qy	2881	AGTTTTCTGTAAATTTCTACTGTATCGACTGCAGACTGGCTGTGTATTAAGGAGCCCTGAC	2940
Db	15657	AGTTTTCTGTAAATTTCTACTGTATCGACTGCAGACTGGCTGTGTATTAAGGAGCCCTGAC	15716
Qy	2941	ATTATATATTTCCCGAGAACATCAGGTTAATGGCGTTTGTATGTCTATTTTCGCGTGGCTG	3000
Db	15717	ATTATATATTTCCCGAGAACATCAGGTTAATGGCGTTTGTATGTCTATTTTCGCGTGGCTG	15776
Qy	3001	AGATCAGCAGCTTTCTCCCGATACCGGAGACCGGCAACACTGGGCGATATCGGTGGTCAATC	3060
Db	15777	AGATCAGCAGCTTTCTCCCGATACCGGAGACCGGCAACACTGGGCGATATCGGTGGTCAATC	15836
Qy	3061	ATNGCGCAGCTTTTCATCCCGGATATGCACCAACCGGTTAAAGTTTACCGGAGACTTTTATCT	3120
Db	15837	ATNGCGCAGCTTTTCATCCCGGATATGCACCAACCGGTTAAAGTTTACCGGAGACTTTTATCT	15896
Qy	3121	GACAGCAGAGCTGCACTGGCCAGGGGGATCACCATCCGTCGCGCGGGCGTGTCAATTAATA	3180
Db	15897	GACAGCAGAGCTGCACTGGCCAGGGGGATCACCATCCGTCGCGCGGGCGTGTCAATTAATA	15956
Qy	3181	TCACTCTGTACATCCCAACACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTTA	3240
Db	15957	TCACTCTGTACATCCCAACACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTTA	16016
Qy	3241	AACTGCATTTTCAACGTCCTGTTCTCGTCAGCAAAAGAGCGGTTTCATTTCAATAAACCG	3300

Db	16017	AAC	TGCATTTCCACGAGTCCTCGTCTCGTAGCAAAAGAGCCGTTCATTTCATTAATAAACGG	1607
Qy	3301	GGC	GACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCAGCGTTTCGGCACGACGACGACG	3360
Db	16077	GGC	GACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCAGCGTTTCGGCACGACGACGACG	16136
Qy	3361	GGC	TCATTCGATGGTTGTGCTTACCAGACGGGAGATATTGACATCATATATGCCTTTG	3420
Db	16137	GGC	TCATTCGATGGTTGTGCTTACCAGACGGGAGATATTGACATCATATATGCCTTTG	16196
Qy	3421	AGC	ACTGATAGCTGTCGCTGTCACATGTCATCTGTHAATACGCTGCTTCATACACACCTC	3480
Db	16197	AGC	ACTGATAGCTGTCGCTGTCACATGTCATCTGTHAATACGCTGCTTCATACACACCTC	16256
Qy	3481	TTTT	TGACATACTCTCTGTTCTTGATCGAGATGAATTTTCAGGACTATGACACTAGCGGTATA	3540
Db	16257	TTTT	TGACATACTCTCTGTTCTTGATCGAGATGAATTTTCAGGACTATGACACTAGCGGTATA	16316
Qy	3541	TGA	ATAGGTAGATGTTTTTATTTTTGTCA CAAAAAGAGGCTCGCACCTCTTTTCTTTA	3600
Db	16317	TGA	ATAGGTAGATGTTTTTATTTTTGTCA CAAAAAGAGGCTCGCACCTCTTTTCTTTA	16376
Qy	3601	TTT	CTTTTTATGATTAATAACGCGATTGAGGACAATAGCGAGTAGGCTGGATACGACGAT	3660
Db	16377	TTT	CTTTTTATGATTAATAACGCGATTGAGGACAATAGCGAGTAGGCTGGATACGACGAT	16436
Qy	3661	TCG	TTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAACTTCGCGAGCATCACCCGAA	3720
Db	16437	TCG	TTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAACTTCGCGAGCATCACCCGAA	16496
Qy	3721	GAA	CATTTGGAAGGCTGTCGGTCGACTACAGSTCACTAATACCATCTAAGTAGTTGATTC	3780
Db	16497	GAA	CATTTGGAAGGCTGTCGGTCGACTACAGSTCACTAATACCATCTAAGTAGTTGATTC	16556
Qy	3781	ATA	GACTCGGATATGTTGTGTTTTACAGTATATGTAGTCGTGTTTTTATGCAAAAATCT	3840
Db	16557	ATA	GACTCGGATATGTTGTGTTTTACAGTATATGTAGTCGTGTTTTTATGCAAAAATCT	16616
Qy	3841	AA	TTAATATATGATATATTTATATCATNTTTACGTTTTCTCGTTCCAGCTTTTTTGTAACAAC	3900
Db	16617	AA	TTAATATATGATATATTTATATCATNTTTACGTTTTCTCGTTCCAGCTTTTTTGTAACAAC	16676
Qy	3901	TTG	CTAGAGTCCTGCTTTAATGAGATATCGAGACGGCTATGATCGCATGATATTGCT	3960
Db	16677	TTG	CTAGAGTCCTGCTTTAATGAGATATCGAGACGGCTATGATCGCATGATATTGCT	16736
Qy	3961	TT	CAATCTGTTGTCGACGTTGTAAAAACCTTGAGCATGTGTAGCTCAGATCCTTACCGC	4020
Db	16737	TT	CAATCTGTTGTCGACGTTGTAAAAACCTTGAGCATGTGTAGCTCAGATCCTTACCGC	16796
Qy	4021	CGG	TTCCGTTCAATTCATTAATGAATATATCACCCGTTTACTATCGTATTTTTATGAATAATA	4080
Db	16797	CGG	TTCCGTTCAATTCATTAATGAATATATUACCCGTTTACTATCGTATTTTTATGAATAATA	16856
Qy	4081	TT	CTCGGTCOAATTTACTGATGTACCCCTPACTTTATATGTACAATATTAATAATGAAAA	4140
Db	16857	TT	CTCGGTCOAATTTACTGATGTACCCCTPACTTTATATGTACAATATTAATAATGAAAA	16916
Qy	4141	CA	ATATATTTGTGCTGAATAGGTTTTATAGCGACATCTATGATAGCGGCCACATACAAA	4200
Db	16917	CA	ATATATTTGTGCTGAATAGGTTTTATAGCGACATCTATGATAGCGGCCACATACAAA	16976
Qy	4201	CA	ATTCGGTTTTATTTATACAATCCAATTTTAAAAAAGCGGACAGCCGTCCAAACCT	4260
Db	16977	CA	ATTCGGTTTTATTTATACAATCCAATTTTAAAAAAGCGGACAGCCGTCCAAACCT	17036
Qy	4261	AAA	AGACTGATTTACATFAAACTCTTATTCAAATTTCAAAAAGCCCCAGGCGCTAGTATCTAC	4320
Db	17037	AAA	AGACTGATTTACATFAATCTTATTCAAATTTCAAAAAGCCCCAGGCGCTAGTATCTAC	17096
Qy	4321	GAC	ACACCGGAGCGGAACTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCGCGCG	4380
Db	17097	GAC	ACACCGGAGCGGCAACTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCGCGCG	17156

QY	1	TTTCAATTTGGAGAGGACACGCTCGAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGT	60
Db		TTTCAATTTGGAGAGGACACGCTCGAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGT	13059
QY	61	AAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	120
Db		AAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	13119
QY	121	ACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTTAGATGGTATTAGTACC	180
Db		ACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTTAGATGGTATTAGTACC	13179
QY	181	TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCG	240
Db		TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCG	13239
QY	241	ACAGCCTTCCAAATGTTCTTCGAAAGGAAATCGTATCCAGCCTACTCGCTATTGTC	300
Db		ACAGCCTTCCAAATGTTCTTCGAAAGGAAATCGTATCCAGCCTACTCGCTATTGTC	13299
QY	301	CTCAATGCCGTATTAATCATAAAAAAGAAATAGAAAGAGGTGGAGCCTCTTTTTCG	360
Db		CTCAATGCCGTATTAATCATAAAAAAGAAATAGAAAGAGGTGGAGCCTCTTTTTCG	13359
QY	361	TGTGACAAATTAACACATCTACTATCATATACGCTAGTGTCAATAGTCTCTGAAATCA	420
Db		TGTGACAAATTAACACATCTACTATCATATACGCTAGTGTCAATAGTCTCTGAAATCA	13419
QY	421	TCTGCATCAAGAACATTTTCAACATCTTATCTTTCTTTTCTTTTCTTTTCTTTTCT	480
Db		TCTGCATCAAGAACATTTTCAACATCTTATCTTTCTTTTCTTTTCTTTTCTTTTCT	13479
QY	481	TCTGGATTTTACGCTCTTACTTACTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTA	540
Db		TCTGGATTTTACGCTCTTACTTACTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTA	13539
QY	541	TGACCTGACAGTGGCTGTATATAGGAGGCTGACATTTATTTCCCGAACAATCAG	600
Db		TGACCTGACAGTGGCTGTATATAGGAGGCTGACATTTATTTCCCGAACAATCAG	13599
QY	601	GTTAATGGCGTTTTCATCTGATTTTCGGGTGGCTGAGATCAGCCACTCTTCCCGAT	660
Db		GTTAATGGCGTTTTCATCTGATTTTCGGGTGGCTGAGATCAGCCACTCTTCCCGAT	13659
QY	661	AACGAGACCGGCACACTGGCCATATCGGTGTCTATCATGCGCCAGCTTTTATCCCGAT	720
Db		AACGAGACCGGCACACTGGCCATATCGGTGTCTATCATGCGCCAGCTTTTATCCCGAT	13719
QY	721	ATGACCCACCGGTAAAGTTTCAGGAGACTTTATCTGACAGACGTCGACTGGCCAG	780
Db		ATGACCCACCGGTAAAGTTTCAGGAGACTTTATCTGACAGACGTCGACTGGCCAG	13779
QY	781	GGGGATCACCATCCGTCGGCGGGGTGTCATATATCATCTGTCATATCCACAAACAG	840
Db		GGGGATCACCATCCGTCGGCGGGGTGTCATATATCATCTGTCATATCCACAAACAG	13839
QY	841	ACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGATTTTACCAAGTCCCTGT	900
Db		ACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGATTTTACCAAGTCCCTGT	13899
QY	901	TCTCGTCAGCAAAAGCGGTTTCAATTAACAAACGGGGGACCTCAGCCATCCCTTCT	960
Db		TCTCGTCAGCAAAAGCGGTTTCAATTAACAAACGGGGGACCTCAGCCATCCCTTCT	13959
QY	961	GATTTTCCGCTTTCAGCGTTCGGACGACAGCGGCTTCAATCTGATGGTGTGTC	1020
Db		GATTTTCCGCTTTCAGCGTTCGGACGACAGCGGCTTCAATCTGATGGTGTGTC	14019
QY	1021	TTACGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGCTGTC	1080
Db		TTACGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGCTGTC	14079

QY	1081	AACTGTCACTTAATAACGCTGCTTCATAGCACACCTCTTTTTCACATCTCTGGGTAGTG	1140
Db		AACTGTCACTTAATAACGCTGCTTCATAGCACACCTCTTTTTCACATCTCTGGGTAGTG	14139
QY	1141	CGATCAACGCTCTCAATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGAC	1200
Db		CGATCAACGCTCTCAATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGAC	14199
QY	1201	ACCAGATTTATTTTCTTCGCAAGTGATCTTCCGTCACAGGTATTTTTCGGCGCAAG	1260
Db		ACCAGATTTATTTTCTTCGCAAGTGATCTTCCGTCACAGGTATTTTTCGGCGCAAG	14259
QY	1261	TGCGTGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAAATACCATCTAAAGTAGTT	1320
Db		TGCGTGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAAATACCATCTAAAGTAGTT	14319
QY	1321	GATTCATAGTGAATGATGTTGTTTCAAGTATTAAGTATTAAGTATTAAGTATTAAGT	1380
Db		GATTCATAGTGAATGATGTTGTTTCAAGTATTAAGTATTAAGTATTAAGTATTAAGT	14379
QY	1381	AATCTAAATTTAATATATGATATTTTATATCACTTTTACGTTTCTCGTTCAGCTTCTTGT	1440
Db		AATCTAAATTTAATATATGATATTTTATATCACTTTTACGTTTCTCGTTCAGCTTCTTGT	14439
QY	1441	CAAAGTGGTCTCGAGGAATTCGGTACCCCGAGCTTGGTAAGGAAATAATATTTTCTTTT	1500
Db		CAAAGTGGTCTCGAGGAATTCGGTACCCCGAGCTTGGTAAGGAAATAATATTTTCTTTT	14495
QY	1501	TGCTTTTATGATAAATAGTTAAGTGAATTAATTAAGTATTAAGTATTAAGTATTAAGT	1560
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QY	1561	TATAATTTGAAAAAATAATTTTATATAATTTTATATAATTTTATATAATTTTATATA	1620
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QY	1621	AAAAATATGACAAAGTGTGTGAAGCAAGAAAGATAAAGTTGAGAGTAAGTATTAAT	1680
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QY	1741	ATAATAGTAAATTTCTAGCTGTTTGAATTAATTAATTAATTAATTAATTAATTAAT	1800
Db		ATAATAGTAAATTTCTAGCTGTTTGAATTAATTAATTAATTAATTAATTAATTAAT	14795
QY	1801	AATAAGATAAATAAATTTAAATAATTTTATGATTAATAGTATTAATTAATTAATTA	1860
Db		AATAAGATAAATAAATTTAAATAATTTTATGATTAATAGTATTAATTAATTAATTA	14855
QY	1861	AATATCTATACCATTTTAAATAATTTTAAAGTATTAATTAATTAATTAATTAATTA	1920
Db		AATATCTATACCATTTTAAATAATTTTAAAGTATTAATTAATTAATTAATTAATTA	14915
QY	1921	TCCAAATCTGTTGTAATTTTATCAATAAATAAATAAATAAATAAATAAATAAATAA	1980
Db		TCCAAATCTGTTGTAATTTTATCAATAAATAAATAAATAAATAAATAAATAAATAA	14975
QY	1981	TAATATCAAACTAATAGAAACAGTAATCTAATGTAACAAAACTAATCTAATGCTAAT	2040
Db		TAATATCAAACTAATAGAAACAGTAATCTAATGTAACAAAACTAATCTAATGCTAAT	15035
QY	2041	AACAAAGCGAGATCTATCAATTTTATAGTATTTTCAATCAACATCTTAATTAAT	2100
Db		AACAAAGCGAGATCTATCAATTTTATAGTATTTTCAATCAACATCTTAATTAAT	15095
QY	2101	TTCTAAATTAATTTGATGTTTATTAATTTTAAAGTATTAATTTTAAATTAATTA	2160
Db		TTCTAAATTAATTTGATGTTTATTAATTTTAAAGTATTAATTTTAAATTAATTA	15155
QY	2161	TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATCTGTTGTTTATCAT	2220

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Db 15735 ATTTATTTCCCGAAGCATCAGTTAATGCGCTTTTGGGTCATTTTCGCGGTGGCTG 15794
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Db 15795 AGATCAGCACCTTTCTCCCGGATAACGAGACCGGACACCTGCGCATATCGGTGGTCATC 15854
QY 3061 ATGCGGACGCTTTCATCCCGGATATGACACCGGGTAAAGTTTCAGCGGAGACTTTATCT 3120
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QY 3121 GACAGCAGACGCTGCTGCGGAGGATCACCATCCGTCGCGCGGCGTGTCAATAATA 3180
Db 15915 GACAGCAGACGCTGCTGCGGAGGATCACCATCCGTCGCGCGGCGTGTCAATAATA 15974
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Db 17475 GC 17476
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RESULT 4
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 89.7%; Score 4200; DB 15; Length 17458;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 4449; Conservative 0; Mismatches 10; Indels 223; Gaps 2;

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QY 3001 AGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATATCGGTGTCAATC 3060
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Db 15855 ATGCGCCAGCTTTCACTCCCGGATATGACACACCGGGTAAAGTTTCAAGGAGACTTTATCT 15914
QY 3121 GACAGCAGACGTGCTACTGGCCAGGGGATCAACATCCGTGCGCCGGCGGTGCAATAATA 3180
Db 15915 GACAGCAGACGTGCTACTGGCCAGGGGATCAACATCCGTGCGCCGGCGGTGCAATAATA 15974
QY 3181 TCACCTGTACATCCACAAACAGACGATTAACCGCTCTCTTTTATAGGTAAACCTTA 3240
Db 15975 TCACCTGTACATCCACAAACAGACGATTAACCGCTCTCTTTTATAGGTAAACCTTA 16034
QY 3241 AACTGCATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCG 3300
Db 16035 AACTGCATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCG 16094
QY 3301 GCGACCTCAGCAATCCCTTCCCTGATTTTCCGCTTTCAGCGTTCGCGACAGCAGACG 3360
Db 16095 GCGACCTCAGCAATCCCTTCCCTGATTTTCCGCTTTCAGCGTTCGCGACAGCAGACG 16154
QY 3361 GCTTTCATTTCTGCATGTTGCTTACAGACCGGAGATATTGACATCATATATGCTTTG 3420
Db 16155 GCTTTCATTTCTGCATGTTGCTTACAGACCGGAGATATTGACATCATATATGCTTTG 16214
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QY 3601 TTTCTTTTATGATTTAATACCGCATTTGAGGACAATAGCGAGTGGATCGGATACGACGAT 3660
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QY 4681 GC 4682
Db 17680 GC 17681

RESULT 2
US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 91.08; Score 4262; DB 15; Length 17476;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 205; Gaps 1;

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QY 181 TGTAGTCGACGACGAGCGCTTCCAAATGTCTTCGGGTGATGTCTGCCAACTTAGTCGACCG 240
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QY 301 CTCAATGCGGTATTAATATCAATAAAGAAATAAGAAAGAGGTGCGAGCGCTCTTTTGTG 360
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QY 361 TGTGACAAAATAAATACTACCTATTTCATATACGTAGTGTGATAGTCTCTGAAATCA 420
Db 13360 TGTGACAAAATAAATACTACCTATTTCATATACGTAGTGTGATAGTCTCTGAAATCA 13419
QY 421 TCTGCATCAAGAACAAATTTCAACTCTTATACCTTTCTCTTCAAGTCGTTGGCTTCA 480
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Db 13480 TCTGGATTTTCAGCCTCTATACTTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTA 13539
QY 541 TCGACCTGAGACTGGCTGTGTATAGGAGAGCTGACATTTATATTTCCCGAACAATCA 600
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QY 1021 TTACACAGCGGAGATATTGACATCATATATGCTTGAACAACTGATAGTCTGCTGTGTC 1080
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Db 14440 CAAAGTGGTCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATAAATTTCTTTTTT 14499
QY 1501 TCCCTTTTAGTATATAAATAGTGTAAAGTGTAAATAGTATGATTAATAAATAATAGTTGT 1560
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QY 2641 ACCTGTAGTCGATAAGTTGGCAGCATACCCGACGCACTTTGCGCCGCAATAAATAACCTG 2700
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DB 15700 TGACGGAAGATCACTTCGCGAGATTAATAATCCCTGGTCTCCCTGTTGATACGGGAAGC 15759
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QY 2161 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCAATGTCATTTGTGTTATCATTTAT 2220
Db 15160 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCAATGTCATTTGTGTTATCATTTAT 15219
QY 2221 CTTTACATTTGGATTTGATTTACAGTTCGGAGCTGGGTTCCGAATCGATAGCTTGGCTGC 2280
Db 15220 CTTTACATTTGGATTTGATTTACAGTTCGGAGCTGGGTTCCGAATCGATAGCTTGGCTGC 15279
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Db 15280 AGTTATCATCATCATCATAGACACACGAATAAAGTAATTAATCAGATTTACGTTTAAAGCTAT 15339

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 1248.43 Seconds
(without alignments)

16988.923 Million cell updates/sec

Title: US-10-055-001b-26_COPY_13000_17681

Perfect score: 4682

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 588172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4262	91.0	17476	15	US-10-385-546-7
4	4200	89.7	17458	15	US-10-055-001A-25
5	4077.2	87.1	17862	15	US-10-055-001A-23
6	3199.6	68.3	18691	15	US-10-055-001A-13
C 7	1208.4	25.8	17681	15	US-10-055-001A-26
C 8	1174.2	25.1	17862	15	US-10-055-001A-23
9	1108.8	23.7	4470	15	US-10-151-690-21
10	1108.8	23.7	4892	16	US-10-357-268-1
C 11	1108.8	23.7	5584	15	US-10-151-690-61
12	1102.4	23.5	4428	15	US-10-151-690-62
C 13	1102.4	23.5	4627	15	US-10-151-690-63
14	1102.4	23.5	4627	15	US-10-151-690-64

C 15	1074.8	23.0	17476	15	US-10-055-001A-24	Sequence 24, Appl
C 16	1074.8	23.0	17476	15	US-10-385-546-7	Sequence 7, Appl
C 17	1072.8	22.9	17458	15	US-10-055-001A-25	Sequence 25, Appl
C 18	780	16.7	786	15	US-10-385-521-9	Sequence 9, Appl
C 19	737	15.7	3002	15	US-10-353-454-57	Sequence 57, Appl
C 20	736	15.7	2116	12	US-10-644-335-3	Sequence 3, Appl
C 21	735.6	15.7	2873	15	US-10-356-088-55	Sequence 55, Appl
C 22	735.6	15.7	2873	15	US-10-353-454-38	Sequence 38, Appl
C 23	735	15.7	3034	15	US-10-356-088-48	Sequence 48, Appl
C 24	735	15.7	3034	15	US-10-353-454-31	Sequence 31, Appl
C 25	713	15.2	4847	9	US-09-118-276-21	Sequence 21, Appl
C 26	710.2	15.2	7599	15	US-10-027-880-5	Sequence 5, Appl
C 27	703	15.0	2867	15	US-10-176-884-9	Sequence 9, Appl
C 28	703	15.0	2867	15	US-10-177-478-20	Sequence 20, Appl
C 29	617.6	13.2	18691	15	US-10-055-001A-13	Sequence 13, Appl
C 30	597	12.8	1846	15	US-10-023-208-63	Sequence 63, Appl
C 31	597	12.8	5558	15	US-10-241-596-137	Sequence 137, Appl
C 32	597	12.8	6464	15	US-10-151-690-20	Sequence 20, Appl
C 33	597	12.8	7278	17	US-10-097-034A-37	Sequence 37, Appl
C 34	597	12.8	9249	16	US-10-389-120-2	Sequence 2, Appl
C 35	597	12.8	10463	16	US-10-389-120-1	Sequence 1, Appl
C 36	597	12.8	12789	13	US-10-666-778-9	Sequence 9, Appl
C 37	593.8	12.7	11180	9	US-09-887-576-581	Sequence 581, Appl
C 38	478.8	10.2	528	15	US-10-162-214-4	Sequence 4, Appl
C 39	406.8	8.7	4470	15	US-10-151-690-21	Sequence 21, Appl
C 40	406.8	8.7	4892	16	US-10-357-268-1	Sequence 1, Appl
C 41	406.8	8.7	5584	15	US-10-151-690-61	Sequence 61, Appl
C 42	400.4	8.6	4428	15	US-10-151-690-62	Sequence 62, Appl
C 43	400.4	8.6	4627	15	US-10-151-690-63	Sequence 63, Appl
C 44	400.4	8.6	4627	15	US-10-151-690-64	Sequence 64, Appl
C 45	323.4	6.9	2877	13	US-09-861-925-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Weslev, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

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Best Local Similarity	100.0%	Pred. No.	0				
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Gaps	0						
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Db	13060	AAATGATATAAATATCAATATATTAATAGATTTTGCATAAAAAAGCTACATAT	13119				
QY	121	ACTGTAAACACCAATATCCAGTCACTATGATCACTACTAGATGGTATTAGTACC	180				

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ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pKIL 19
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..378
OTHER INFORMATION:
US-08-379-614-3

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Best Local Similarity 99.1%; Pred. No. 4.5e-60;
Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 799 CCGGGCGGTGTCAATAATATCACTCTGTATCCCAAAACAGACGATACGGCTCTCTCT 858
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
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; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANNA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
; US-08-379-614-2

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Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTCGA 617
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QY 618 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 677
Db 343 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 284
QY 678 TGGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 737
Db 283 TGGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGATATGCCACCGGGTAAA 224
QY 738 GTTCACGGGAGACTTTATCTGACAGCAGACAGTGCATCGCCAGGGGGATCACCATCCGTC 797
Db 223 GTTCACGGGAGACTTTATCTGACAGCAGCTGCTGCTGATATCCCAAAACAGACGATAACGGCTCTCTC 857
QY 798 GCCCGGGCGTGTCAATAATATCCTCTGATATCCCAAAACAGACGATAACGGCTCTCTC 857
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QY 858 TTTTATAGGTGTAAACCTTAAACTGCA 884
Db 103 TTTTATAGGTGTAAACCTTAAACTGCA 77

RESULT 15
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; Sequence 3, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE93/00051
; FILING DATE: 02-AUG-1993

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANNA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
; US-08-379-614-2

Query Match
Best Local Similarity 7.0%; Score 325.4; DB 2; Length 420;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTCGA 617
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QY 618 TGTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGCACAC 677
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QY 858 TTTTATAGGTGTAAACCTTAAACTGCA 884
Db 103 TTTTATAGGTGTAAACCTTAAACTGCA 77

RESULT 14
US-09-225-152A-2/c
; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANNA10.001CPI

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QY 4452 CCGGTCACGACGCGCGCGGTTACCG 4479
Db 7650 CCGGTCACGACGCGCGCGGTTACCG 7677

RESULT 12

US-08-673-768-1/c
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 12.1%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.8e-111;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4092 ATTTACTGATGTACCTACTACTTATATGTACAAATATTAATAAGAAACAAATATTTGT 4151
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Db 13854 CCGGTCACGACGCGCGCGGTTACCG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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RESULT 10
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;PATENT NO. 5428147
;APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
;TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
;NUMBER OF SEQUENCES: 17
;CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/91,538
;  FILING DATE: 13-JUL-1993
;PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 869,216
;  FILING DATE: 13-APR-1992
;  APPLICATION NUMBER: 869,216
;  FILING DATE: 13-APR-1992
;  APPLICATION NUMBER: 440,432
;  FILING DATE: 21-NOV-1989
;  APPLICATION NUMBER: 553,786
;  FILING DATE: 19-NOV-1983
;  APPLICATION NUMBER: 741,034
;  FILING DATE: 06-AUG-1991
;  APPLICATION NUMBER: 144,775
;  FILING DATE: 20-JAN-1988
;  APPLICATION NUMBER: 485,614
;  FILING DATE: 15-APR-1983
;  APPLICATION NUMBER: 713,624
;  FILING DATE: 10-JUN-1991
;  APPLICATION NUMBER: 260,574
;  FILING DATE: 21-OCT-1988
;  APPLICATION NUMBER: 848,733
;  FILING DATE: 01-APR-1986
;  APPLICATION NUMBER: 535,354
;  FILING DATE: 26-SEP-1983
;SEQ ID NO:1:
;  LENGTH: 24595
5428147-1
Query Match 15.1%; Score 707; DB 6; Length 24595;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3913 CTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCCTTTCAATTCGT 3972
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QY 3973 GTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTTC 4032
DB 12481 GTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTTC 12422
QY 4033 ATTCTAATGAATATATACCCGTTACTATCGTATTTTATGATATATTCCTCGTTCAA 4092
DB 12421 ATTCTAATGAATATATACCCGTTACTATCGTATTTTATGATATATTCCTCGTTCAA 12362
QY 4093 TTTACTGATTGTACCTTACTTATATGATATATTAATAAATGAAAAAATAATATTTGTG 4152
DB 12361 TTTACTGATTGTACCTTACTTATATGATATATTAATAAATGAAAAAATAATATTTGTG 12302
QY 4153 CTGAATAGTTTATAGGACATCTATGATAGCGGCAATAAACAACAAATTCGTTT 4212
DB 12301 CTGAATAGTTTATAGGACATCTATGATAGCGGCAATAAACAACAAATTCGTTT 12242
QY 4213 ATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAGACGTATT 4272
DB 12241 ATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAGACGTATT 12182
QY 4273 ACATAAATCTTATTCAAAATTTCAAAAGGCCCGGAGGCTAGTATCTACGACACACCGAGC 4332
DB 12181 ACATAAATCTTATTCAAAATTTCAAAAGGCCCGGAGGCTAGTATCTACGACACACCGAGC 12122
QY 4333 GCGGAACATAATACGTTTCACTGAAGGAACTCCGGTTCCCGGCGCGGCGCATGGGTGAG 4392
DB 12121 GCGGAACATAATACGTTTCACTGAAGGAACTCCGGTTCCCGGCGCGGCGCATGGGTGAG 12062
QY 4393 ATTCTTTGAAGTTGAGTATTGGCCGCTCTTACCAGAAAGTTACGGGACCAATTCACCC 4452
Db 12061 ATTCTTTGAAGTTGAGTATTGGCCGCTCTTACCAGAAAGTTACGGGACCAATTCACCC 12002
QY 4453 CGGTCCAGCAGCGGCGCGGTAAACCGACTTGCTGCCCGGAGAAATTATGACGACATTTT 4512
DB 12001 CGGTCCAGCAGCGGCGCGGTAAACCGACTTGCTGCCCGGAGAAATTATGACGACATTTT 11942
QY 4513 TGGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACTTGACAGTGCAGCAAAATCGTT 4572
DB 11941 TGGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACTTGACAGTGCAGCAAAATCGTT 11882
QY 4573 GGGCGGTCAGGCGCAATTTTGCAGCAACATGTCAGGCTCAGCAG 4619
DB 11881 GGGCGGTCAGGCGCAATTTTGCAGCAACATGTCAGGCTCAGCAG 11835
RESULT 11
US-08-673-768-1
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1
Query Match 12.1%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.8e-111;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3912 CTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCCTTTCAATTCGT 3971
DB 7110 CTGCTTTAATGAGATATGCGAGCGCTATGATCGCATGATATTCCTTTCAATTCGT 7169
QY 3972 TGTGACGCTGTGAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4031
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OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-J1"

FEATURE:

NAME/KEY: -
LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
NAME/KEY: -
LOCATION: 3257..4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-025-583-2

Query Match 15.2%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3912 CTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTCAATTCTGT 3971
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QY 3972 TGTGACGTTGTAAAAAACCCTGAGCATGTAGCTCAGATCTCTACCGCGGTTTCGGTT 4031
Db 3489 TGTGACGTTGTAAAAAACCCTGAGCATGTAGCTCAGATCTCTACCGCGGTTTCGGTT 3548
QY 4032 CATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATATATCTCCGTTCA 4091
Db 3549 CATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATATATCTCCGTTCA 3608
QY 4092 ATTACTGATGTAACCTACTACTATATGTAATATTAATAATGAAAAACAATATATGT 4151
Db 3609 ATTACTGATGTAACCTACTACTATATGTAATATTAATAATGAAAAACAATATATGT 3668
QY 4152 GCTGATAGTTTATAGCAGCATCTATGATAGCGCCCAATAACAACAATTCGGTTT 4211
Db 3669 GCTGATAGTTTATAGCAGCATCTATGATAGCGCCCAATAACAACAATTCGGTTT 3728
QY 4212 TATTATTACAAATCCAAATTTAAAAAAGCGGAGAACCGGTCAAAACCTAAAGACTGTAT 4271
Db 3729 TATTATTACAAATCCAAATTTAAAAAAGCGGAGAACCGGTCAAAACCTAAAGACTGTAT 3788
QY 4272 TACATAAATCTTATTCAAAATTTCAAAAGCCCGAGGGGTAGTATCTAGACACCCGAG 4331
Db 3789 TACATAAATCTTATTCAAAATTTCAAAAGCCCGAGGGGTAGTATCTAGACACCCGAG 3848
QY 4332 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCGCCCGCGCGCATGGTGA 4391
Db 3849 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCGCCCGCGCGCATGGTGA 3908
QY 4392 GATTCCTTGAAGTTGAGTATGTCGCGTCTTACCGAAAGTTACGGGCAACCATTCAC 4451
Db 3909 GATTCCTTGAAGTTGAGTATGTCGCGTCTTACCGAAAGTTACGGGCAACCATTCAC 3968
QY 4452 CCGGTCCAGCACCGCGCGGGTAAACGACTTCTGCTCCCGGAGAAATATGACGATTTTT 4511
Db 3969 CCGGTCCAGCACCGCGCGGGTAAACGACTTCTGCTCCCGGAGAAATATGACGATTTTT 4028
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Db 4029 TTGGTGTATGTGGGCCCCCAAAATGAAGTGAAGTCAAAACCTTGACAGTACGACAAATCGT 4088
QY 4572 TGGCGGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGGACCT 4624
Db 4089 TGGCGGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGGACCT 4141

RESULT 9

US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION: David M
; APPLICANT: Rhoads,
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 15.2%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 3.9e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3912 CTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTCAATTCTGT 3971
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QY 3972 TGTGACGTTGTAAAAAACCCTGAGCATGTAGCTCAGATCTCTACCGCGGTTTCGGTT 4031
Db 9890 TGTGACGTTGTAAAAAACCCTGAGCATGTAGCTCAGATCTCTACCGCGGTTTCGGTT 9949
QY 4032 CATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATATATCTCCGTTCA 4091
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QY 4152 GCTGATAGTTTATAGCAGCATCTATGATAGCGCCCAATAACAACAATTCGGTTT 4211
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QY 4332 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCGCCCGCGCGCATGGTGA 4391
Db 10250 CGGCGAACTAATAACGTTCACTGAAGGAACTCCGGTTCGCCCGCGCGCATGGTGA 10309
QY 4392 GATTCCTTGAAGTTGAGTATGTCGCGTCTTACCGAAAGTTACGGGCAACCATTCAC 4451
Db 10310 GATTCCTTGAAGTTGAGTATGTCGCGTCTTACCGAAAGTTACGGGCAACCATTCAC 10369
QY 4452 CCGGTCCAGCACCGCGCGGGTAAACGACTTCTGCTCCCGGAGAAATATGACGATTTTT 4511
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QY 4572 TGGCGGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGGACCT 4624
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/ LOCATION: 3257..4315
/ OTHER INFORMATION: /label= 3'ocs
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA octopine synthase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 4316..6555
/ OTHER INFORMATION: /label= pUC18
/ OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-351-413-2
Query Match 15.2%; Score 709.8; DB 1; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3912 CCGCTCTTATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTCAATTCGT 3971
Db 3429 CCGCTTATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTCAATTCGT 3488
QY 3972 TGTGACGTTGTAATAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTGGTT 4031
Db 3489 TGTGACGTTGTAATAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTGGTT 3548
QY 4032 CATTCTAATGAATATATCACCGGTACTACTGATTTTATGAAATATTTCTCGTTCA 4091
Db 3549 CATTCTAATGAATATATCACCGGTACTACTGATTTTATGAAATATTTCTCGTTCA 3608
QY 4092 ATTACTGATTTGACCTTACTTATATGTATGATTAATTAATTAATTAATTAATTTCT 4151
Db 3609 ATTACTGATTTGACCTTACTTATATGTATGATTAATTAATTAATTAATTTCT 3668
QY 4152 GCTGAATAGTTTATAGCAGATCTATGATAGAGCGCCCAATTAACAAATTTGGTTT 4211
Db 3669 GCTGAATAGTTTATAGCAGATCTATGATAGAGCGCCCAATTAACAAATTTGGTTT 3728
QY 4212 TATTATTAATATCCATTTTAAATAAGGCGAGACCGGTCAAACTTAAAGCTGAT 4271
Db 3729 TATTATTAATATCCATTTTAAATAAGGCGAGACCGGTCAAACTTAAAGCTGAT 3788
QY 4272 TACATAAATCTTATCAAAATTTCAAAGGCGCCGAGGCTAGTATCTACGACACCGAG 4331
Db 3789 TACATAAATCTTATCAAAATTTCAAAGGCGCCGAGGCTAGTATCTACGACACCGAG 3848
QY 4332 CGCGCACTAATTAAGCTTACTGAAGGAACTCCGGTCCCGCGCGGCGATGGGTGA 4391
Db 3849 CGCGCACTAATTAAGCTTACTGAAGGAACTCCGGTCCCGCGCGGCGATGGGTGA 3908
QY 4392 GATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACGAAAGTTACGGGCAACCATTCAC 4451
Db 3909 GATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACGAAAGTTACGGGCAACCATTCAC 3968
QY 4452 CCGGTCACGACGCGCGCGGTAACCGACTTGTGCGCGGAGAAATATGACGATTTT 4511
Db 3969 CCGGTCACGACGCGCGCGGTAACCGACTTGTGCGCGGAGAAATATGACGATTTT 4028
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Db 4029 TTGGTGTATGGGCGGCGGCAATGAAGTGAGGTCGAGTCAAACTTGACAGTACGACAAATCGT 4088
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RESULT 8

US-09-025-583-2

; Sequence 2, Application US/09025583

; Patent No. 5977433

; GENERAL INFORMATION:

; APPLICANT: Williams, Mark

; APPLICANT: Leemans, Jan

; TITLE OF INVENTION: Maintenance of male-sterile plants

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/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
/ STREET: 8110 Gatehouse Road, Suite 500 East
/ CITY: Falls Church
/ STATE: Virginia
/ COUNTRY: U.S.A.
/ ZIP: 2046
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,583
/ FILING DATE:
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/351,413
/ FILING DATE:
/ APPLICATION NUMBER: US 07/899,072
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/970,849
/ FILING DATE: 03-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Svensson, Leonard R.
/ REGISTRATION NUMBER: 30,330
/ REFERENCE/DOCKET NUMBER: 2121-102PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ TELEX: 248345
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6555 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: plasmid pVE144 (replicable in E.coli)
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..396
/ OTHER INFORMATION: /label= pUC18
/ OTHER INFORMATION: /note= "pUC18 derived sequence"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (397..751)
/ OTHER INFORMATION: /label= 3'nos
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA napaline synthase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (752..1024)
/ OTHER INFORMATION: /label= barstar
/ OTHER INFORMATION: /note= "coding region of the barstar gene of
/ OTHER INFORMATION: Bacillus amyloliquefaciens"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (1025..1607)
/ OTHER INFORMATION: /label= TA29
/ OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
/ OTHER INFORMATION: Nicotiana tabacum"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1608..2440
/ OTHER INFORMATION: /label= 35S3
/ OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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; LOCATION: 3161..5399
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-084-889-1

Query Match      15.2%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3912 CCTGCTTTTATGATGATGGAGACGCTATGATCGCATGATTTTGGCTTTCAATTCCTG 3971
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Db |||
QY 3972 TGTGACGTTGTAATAAATCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTGGTT 4031
Db |||
QY 2333 TGTGACGTTGTAATAAATCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTGGTT 2392
QY 4032 CATCTCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATTTCCGTTCA 4091
Db |||
QY 2393 CATCTCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATTTCCGTTCA 2452
QY 4092 ATTACTGATTTGACCTACTACTTATATGTACAAATATTAATAATGAATAATATTTCT 4151
Db |||
QY 2453 ATTACTGATTTGACCTACTACTTATATGTACAAATATTAATAATGAATAATATTTCT 2512
QY 4152 GCTGAATAGGTTTATAGGACATCTATGATAGAGCGCCCAATAAACAATATGCGTTT 4211
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QY 2513 GCTGAATAGGTTTATAGGACATCTATGATAGAGCGCCCAATAAACAATATGCGTTT 2572
QY 4212 TATTATTAACAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 4271
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QY 2573 TATTATTAACAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 2632
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Db |||
QY 2633 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGAGGCTAGTATCTAGCACACCCGAG 2692
QY 4332 CGGCGAATTAATAGCTTACTGAGAGGAATCTCGGTTCGCCCGCGCGGCGGATGGTGA 4391
Db |||
QY 2693 CGGCGAATTAATAGCTTACTGAGAGGAATCTCGGTTCGCCCGCGCGGCGGATGGTGA 2752
QY 4392 GATTCCTTGAAGTTGAGTATGCGCTCGCTCTACGAAAGTTACGGGACCAATCAAC 4451
Db |||
QY 2753 GATTCCTTGAAGTTGAGTATGCGCTCGCTCTACGAAAGTTACGGGACCAATCAAC 2812
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QY 2873 TTGGTGTATGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2932
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RESULT 7

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; US-08-351-413-2
; Sequence 2, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
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; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pVE144 (replicable in E.coli)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..396
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (397..751)
; OTHER INFORMATION: /label= 3' nos
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; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (752..1024)
; OTHER INFORMATION: /label= barstar
; OTHER INFORMATION: /note= "coding region of the barstar gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (1025..1607)
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; OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
; OTHER INFORMATION: Nicotiana tabacum"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1608..2440
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
; OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"
; FEATURE:
; NAME/KEY: -
; LOCATION: 2441..3256
; OTHER INFORMATION: /label= neo
; OTHER INFORMATION: /note= "coding region of the neomycine
; OTHER INFORMATION: phosphotransferase gene of Tn5"
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; NAME/KEY: -
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; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; NAME/KEY: -
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; OTHER INFORMATION: /label= pUC18
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; Best Local Similarity 15.2%; Score 709.8; DB 3; Length 5399;
; Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; DB 2273 CTTGCTTTTATGATGATGCGAGACGCTATGATCGCATGATTTTCTTCAATTCTGT 2332
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; QY 3972 TGTGACGTTGTAATAAACTGAGCAATGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 4031
; DB 2333 TGTGACGTTGTAATAAACTGAGCAATGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 2392
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; QY 4032 CATCTTAATGAATATATCAACCGTACTATCGTATTTTATGATTAATATTCCTCGTTCA 4091
; DB 2393 CATCTTAATGAATATATCAACCGTACTATCGTATTTTATGATTAATATTCCTCGTTCA 2452
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; QY 4092 ATTTACTGATTTGACCTACTACTATATGATGATCAATATTAATAATGAAACAATATTTGT 4151
; DB 2453 ATTTACTGATTTGACCTACTACTATATGATGATCAATATTAATAATGAAACAATATTTGT 2512
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; QY 4152 GCTGAATAGTTTATAGCGATCTATGATAGAGCGGCACATATAACAACAATTCGGTT 4211
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; QY 4212 TATTATTACAAATCCCAATTTTAAAAAGGCGGAGAACCGGTCAAAACCTAAAGACTGAT 4271
; DB 2573 TATTATTACAAATCCCAATTTTAAAAAGGCGGAGAACCGGTCAAAACCTAAAGACTGAT 2632
;
; QY 4272 TACATAAATCTTATCAAAATTTCAAAAGCCCGGAGGCTAGTATCTAGACACACCGAG 4331
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; QY 4392 GATTCTCTTGAAGTTGAGTATGCGGCTCCGCTCTACCGAAGTTACGGGCAACCAATCAAC 4451
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; QY 4512 TTGTGTATGTGGGCCCCCAATTAAGTGCAGGTCAAACTTGCAGTGACGACAAATCGT 4571
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; QY 4572 TGGCGGGGTTCAGGCGGAAATTTTGCAGCAACATGTTCAGGCTCAGCAGGACCT 4624
; DB 2933 TGGCGGGGTTCAGGCGGAAATTTTGCAGCAACATGTTCAGGCTCAGCAGGACCT 2985
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; RESULT 6
; US-09-084-889-1
; Sequence 1, Application US/09084889
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; Patent No. 6074877
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; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Burns, Doane, Swecker & Mathis
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
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; FEATURE:
; NAME/KEY: -
; LOCATION: 452..1284
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
; OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-J1"
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; FEATURE:
; NAME/KEY: -
; LOCATION: 1285..2100
; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
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; FEATURE:
; NAME/KEY: -
; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
;
; NAME/KEY: -
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FEATURE:						
NAME/KEY: -						
LOCATION: 2101..3160	/label= 3'ocs					
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NAME/KEY: -						
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US-08-478-015-1						
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3972	TGTGCACGTTGTAAAAAACCTGAGCATGCTAGCTCAGATCCTTACCGCGGTTTCGGTT	4031				
2333	TGTGCACGTTGTAAAAAACCTGAGCATGCTAGCTCAGATCCTTACCGCGGTTTCGGTT	2392				
4032	CATTCTAATGAATATATCACCGTTACTATCGTATTTTATGAATATATTCCTCCGTTCA	4091				
2393	CATTCTAATGAATATATCACCGTTACTATCGTATTTTATGAATATATTCCTCCGTTCA	2452				
4092	ATTTACTGATTGTACCGTACTACTTATATGTAACAATTTAAATGAAAAACAATATATGT	4151				
2453	ATTTACTGATTGTACCGTACTACTTATATGTAACAATTTAAATGAAAAACAATATATGT	2512				
4152	GCTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAATGCGGTTT	4211				
2513	GCTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAATGCGGTTT	2572				
4212	TATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAAAGACTGAT	4271				
2573	TATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAAAGACTGAT	2632				
4272	TACATAAATCTTATTCAAATTTTCAAAGGCGCCAGGGCTAGTATCTACGACACCGGAG	4331				
2633	TACATAAATCTTATTCAAATTTTCAAAGGCGCCAGGGCTAGTATCTACGACACCGGAG	2692				
4332	CGGCGAACTAATAACGTTTCACTGAAGGGAACCTCGGTTCCCGCGCGCGCATGGGTGA	4391				
2693	CGGCGAACTAATAACGTTTCACTGAAGGGAACCTCGGTTCCCGCGCGCGCATGGGTGA	2752				
4392	GATTTCCTGAAGTTGAGTATTTGGCCGTCCTGCTATACGAAAGTTTACGGGCAACAATCAAC	4451				
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2813	CCGGTCAGACACGCGCGCCGGTAAACGACTTGTGTCGCCGAGAAATTTATCGACATTTT	2872				
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 ; Sequence 1, Application US/08478015
 ; Patent No. 5712135
 ; GENERAL INFORMATION:
 ; APPLICANT: D'HALLUIN, Kathleen
 ; APPLICANT: GOBEL, Elke
 ; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
 ; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,015
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90403332.1
 ; FILING DATE: 23-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 91401888.2
 ; FILING DATE: 08-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,121
 ; FILING DATE: 23-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm K.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 010830-088
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5399 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: Double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: plasmid pDE108
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..451

TOPOLOGY: circular					
MOLECULE TYPE: DNA (genomic)					
HYPOTHETICAL: NO					
ANTI-SENSE: NO					
ORIGINAL SOURCE:					
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NAME/KEY: -					
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OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosaic virus isolate CabBB-JI"					
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OTHER INFORMATION:					
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NAME/KEY: -					
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OTHER INFORMATION:					
FEATURE:					
NAME/KEY: -					
LOCATION: 3161..5399 /label= pUC18					
OTHER INFORMATION: /note= "pUC18 derived sequence"					
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Best Local Similarity 99.7%; Pred. No. 2.7e-142;					
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	3912	CCTGCTTTAATGAGATATGCAGACGCCCTATGATCATCGATTAATTGGTTCCAATTCGT	3971		
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QY	3972	TGTGCAGTTTGTA AAAAACCTGAGCAGTGTAGCTCAGATCCCTTACGCCGGGTTTCGGTT	4031		
Db	2333	TGTGCAGTTTGTA AAAAACCTGAGCAGTGTAGCTCAGATCCCTTACGCCGGGTTTCGGTT	2392		
QY	4032	CAITCTAATGAATATATCACCCGTTACTATCGTATTTTATGAATTAATATTCCTCGTTCA	4091		
Db	2393	CAITCTAATGAATATATCACCCGTTACTATCGTATTTTATGAATTAATATTCCTCGTTCA	2452		
QY	4092	ATTTACTGATGTGACCTCTACTTNTATGTACAATATTAATAATGAAAACAATATATCTG	4151		
Db	2453	ATTTACTGATGTGACCTCTACTTNTATGTACAATATTAATAATGAAAACAATATATCTG	2512		
QY	4152	GCTGAATAGTTTTATPAGGCACATCTATGATAGCGGCCCAATAACAAATATGCGTTT	4211		
Db	2513	GCTGAATAGTTTTATPAGGCACATCTATGATAGCGGCCCAATAACAAATATGCGTTT	2572		
QY	4212	TATTTATCAAATCCAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAAGACTGAT	4271		
Db	2573	TATTTATCAAATCCAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAAGACTGAT	2632		
QY	4272	TACATAAATCTTTATTCAAATTTCAAAAGCCCCCGAGGGCTAGTAGTCTACGACACACCGAG	4331		
Db	2633	TACATAAATCTTTATTCAAATTTCAAAAGSCCCGAGGGCTAGTAGTCTACGACACACCGAG	2692		
QY	4332	CGCGCAACTAATAAAGCTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCATGGTGA	4391		
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; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
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; ORGANISM: plasmid DNA designated as pJD884
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; LOCATION: 1..1869
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; LOCATION: 1877..2110
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; OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
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; OTHER INFORMATION: derived from Cauliflower mosaic virus."
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; OTHER INFORMATION: /note= "Coding sequence of
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; OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
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; US-08-232-016-22
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; Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; QY 4083 CTCGGTTCATTTACTGATTTGACCCCTACTATATGATGATACATATTAATGAATAACA 4142
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; QY 4143 ATATATTGTCGTAATAGTTTATAGCATATCTATGATGAGCGCCACATAACAACA 4202
; DB 4016 ATATATTGTCGTAATAGTTTATAGCATATCTATGATGAGCGCCACATAACAACA 4075
; QY 4203 ATTTCGGTTTTATTATCAATCCAAATTTTAAAAAGCGCGAGAACCGGTCAAAACCTAA 4262
; DB 4076 ATTTCGGTTTTATTATCAATCCAAATTTTAAAAAGCGCGAGAACCGGTCAAAACCTAA 4135

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; QY 4263 AAGACTGATTACATAAATCTTATTCAAATTTCAAAGGCCCCCAGGGGCTAGTATCTACGA 4322
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; QY 4383 CATGGGTGAGATTCCTTTGAAAGTTGAGTATTGGCCGCTCTTACCGAAAGTTACGGGCA 4442
; DB 4256 CATGGGTGAGATTCCTTTGAAAGTTGAGTATTGGCCGCTCTTACCGAAAGTTACGGGCA 4315
; QY 4443 CCAATTCACCCCGTCCAGCACGGCGCGGTAACCGACTTGTCTCCCGCGAGAAATATGC 4502
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; QY 4503 AGCATTTTGTGCTGTATGTGGGCCCCCAAAATGAAGTGAGGTCAAACTTGACAGTGAGC 4562
; DB 4376 AGCATTTTGTGCTGTATGTGGGCCCCCAAAATGAAGTGAGGTCAAACTTGACAGTGAGC 4435
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RESULT 3

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; US-08-064-121-1
; Sequence 1, Application US/08064121
; Patent No. 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,121
; FILING DATE: 24-MAY-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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ORGANISM: plasmid DNA designated as pPS0212
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LOCATION: 1..1785
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OTHER INFORMATION: truncated modified bt2 (cryIAb) gene, also designated as the
OTHER INFORMATION: cryIAb6 gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA gene 7."
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NAME/KEY: misc feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
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OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
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NAME/KEY: misc feature
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OTHER INFORMATION: T-DNA octopine synthase gene."
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NAME/KEY: misc feature
LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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NAME/KEY: misc feature
LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
US-08-232-016-23
Query Match 15.6%; Score 728.8; DB 2; Length 7566;
Best Local Similarity 99.7%; Pred. No. 2.7e-146;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
3903 GTCTAGAGTCTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTGCTTT 3962
3692 GTCTAGAGTCTGCTTTAATGAGATATGCGAGAGCGCTATGATCGCATGATATTGCTTT 3751
3963 CAATTCGTGTGTCACGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCG 4022
3752 CAATTCGTGTGTCACGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCG 3811
4023 GTTTCGGTCAATTAATGATATATACCGTTACTATCGTATTTTATGATAATATT 4082
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4083 CTCGTTCAATTTACTGATGTACCTTACTTATATGATGATATTAATAAGAAACA 4142
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3992 ATTTCGTTTATTTATTAATCAATCAATTTTAAAAAGCGCGACACCGGTCAACCTAA 4051
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Db 4052 AAGACTGATTACATAATCTTATTCAAAATTTCAAAAGCGCGGTAGTATCTACGA 4111
QY 4323 CACACCGAGCGCGAAGCTTAATTAACGTTTCACTGAAGGGAATCCCGTTCCCGCGCGCG 4382
Db 4112 CACACCGAGCGCGAAGCTTAATTAACGTTTCACTGAAGGGAATCCCGTTCCCGCGCGCG 4171
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RESULT 2
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; Sequence 22, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETABERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN RARSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7639 base pairs
; TYPE: nucleic acid

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 202.187 Seconds
(without alignments)
12850.857 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 582709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/pdata/2/ina/6D_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	709.8	15.2	5399	3	US-08-475-975-1
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8	709.8	15.2	6555	2	US-09-025-583-2
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19	289.2	6.2	13188	4	US-08-961-527-70
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31 148.4 3.2 4411 2 US-08-929-967-5 Sequence 5, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 23, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN RAARSSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
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; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

Job time : 1122.53 secs

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QY 1106 ATAGCACACCTTTTGTGACATCTTCGGGTA 1137
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RESULT 14

ABZ58770

ID ABZ58770 standard; DNA; 4627 BP.

XX AC ABZ58770;
XX ACDT 01-MAY-2003 (first entry)
XX ACDE Destination plasmid pDONR212(R) nucleotide sequence.
XX ACKW Nucleic acid insertion; recombination; nucleic acid selection;
XX AC
KW Nucleic acid isolation; ds.
XX ACOS Synthetic.
XX ACPN WO200295055-A2.
XX ACPD 28-NOV-2002.
XX ACPF 21-MAY-2002; 2002WO-US015947.
XX ACPR 21-MAY-2001; 2001US-0291973P.
XX ACPA (INVI-) INVITROGEN CORP.
XX AC

PI Brach MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.
DR
XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 29B-C; 27pp; English.
XX

CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(R) nucleotide sequence
XX

SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 23.5%; Score 1102.4; DB 7; Length 4627;
Best Local Similarity 99.5%; Pred. No. 2.2e-147;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 446 TCTTATACCTTTTCTTACAGTCTGTCGGCTTCTCATCTGGATTTTTCAGCCTCTATACCTA 505
Db 510 TCTTATACCTTTTCTTACAGTCTGTCGGCTTCTCATCTGGATTTTTCAGCCTCTATACCTA 569
QY 506 CTAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCGACTGGCTGTGTATA 565
Db 570 CTAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCGACTGGCTGTGTATA 629
QY 566 AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
Db 630 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGTCATTT 689
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGACACTGGCCATA 685
Db 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGACACTGGCCATA 749

1119 TGTTCCTGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 1178
266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAMAA 325
1179 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAMAA 1238
326 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAAATCATACCT 385
1239 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAAATCATACCT 1298
386 ATTATATACGCTAGTGTCTGAAATCATCTGCATCAAGAAATTTTTCAGCCTCTATACCTA 445
1299 ATTATATACGCTAGTGTCTGAAATCATCTGCATCAAGAAATTTTTCAGCCTCTATACCTA 1358
446 TCTTATACCTTTCTCTTACAAGTCGTTGGCTTCTATCTGGAATTTTTCAGCCTCTATACCTA 505
1359 TCTTATACCTTTCTCTTACAAGTCGTTGGCTTCTATCTGGAATTTTTCAGCCTCTATACCTA 1418
506 CTAAAGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGTGTATATA 565
1419 CTAAAGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGTGTATATA 1478
566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGCTTTTGTGTGATTCATTT 625
1479 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGCTTTTGTGTGATTCATTT 1538
626 TCGCGTGGCTGAGATCAGCCATCTTCTCCCGATAAAGAGACCGGCACACTGCGCCATA 685
1539 TCGCGTGGCTGAGATCAGCCATCTTCTCCCGATAAAGAGACCGGCACACTGCGCCATA 1598
686 TCGGTGGTATCATCGCGCAGCTTTCATCCCGATATGACACACCGGTAAAGTTTCAGG 745
1599 TCGGTGGTATCATCGCGCAGCTTTCATCCCGATATGACACACCGGTAAAGTTTCAGG 1658
746 GAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGATCACCATCGTCCGCGCGGC 805
1659 GAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGATCACCATCGTCCGCGCGGC 1718
806 GTGTCAATAATATCACTGTATCATCCAAACAGACGATACCGCTCTCTTTTATAG 865
1719 GTGTCAATAATATCACTGTATCATCCAAACAGACGATACCGCTCTCTTTTATAG 1778
866 GTGTAACCTTAACTGATTTTCAACAGTCCCTGTCTCTGTCAGAAAAGACCGCTTAT 925
1779 GTGTAACCTTAACTGATTTTCAACAGTCCCTGTCTCTGTCAGAAAAGACCGCTTAT 1838
926 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
1839 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 1898
986 ACGCAGACGCGGCTTCTATCTGATGTTGTGCTTACCGAGACCGGAGATTTGACATC 1045
1899 ACGCAGACGCGGCTTCTATCTGATGTTGTGCTTACCGAGACCGGAGATTTGACATC 1958
1046 ATATATGCTTGTGACAACTGATGTCTGCTGTCAACTGTCACTGTATACGCTGCTTC 1105
1959 ATATATGCTTGTGACAACTGATGTCTGCTGTCAACTGTCACTGTATACGCTGCTTC 2018
1106 ATAGCACACCTCTTTTGTGACATACCTTCGGGTA 1137
2019 ATAGCACACCTCTTTTGTGACATACCTTCGGGTA 2050

RESULT 13

ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.
XX
AC ABZ58769;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212(F) nucleotide sequence.
XX

KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
OS Synthetic.
XX

PN WO200295055-A2.
XX

PD 28-NOV-2002.
XX

PF 21-MAY-2002; 2002WO-US015947.
XX

PR 21-MAY-2001; 2001US-0291973P.
XX

PA (INVI-) INVITROGEN CORP.
XX

PI Braesch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX

XX WPI; 2003-129436/12.
XX

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

Disclosure; Fig 28B-C; 273pp; English.

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212(F) nucleotide sequence

Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 23.5%; Score 1102.4; DB 7; Length 4627;

Best Local Similarity 99.5%; Pred. No. 2.2e-147;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGCTAAATGATATAAATCAATATATT 85

DB 90 GCCAATTTGTACAAAAAAGCTGATTCGAAACGTAATGATATAAATCAATATATT 149

QY 86 AAATTAGATTTTGATAAAAACAGACTACATAATCTGTAAAAACAACATATCCAGTC 145

DB 150 AAATTAGATTTTGATAAAAACAGACTACATAATCTGTAAAAACAACATATCCAGTC 209

QY 146 ACTATGATCAACTACTTAGTATGATAGCTAGCTAGTCGACGAGCCTTCCAAATTTCTTCAA 205

DB 210 ACTATGATCAACTACTTAGTATGATAGCTAGCTAGTCGACGAGCCTTCCAAATTTCTTCAA 269

QY 206 TGTTCCTTCGGGTGATGCTGCCAATCTAGTCGACGAGCCTTCCAAATTTCTTCAA 265

DB 270 TGTTCCTTCGGGTGATGCTGCCAATCTAGTCGACGAGCCTTCCAAATTTCTTCAA 329

QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATAAA 325

DB 330 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAAATCATAAA 389

QY 326 AGAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAAATAAAAAATCATCTACCT 385

DB 390 AGAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAAATAAAAAATCATCTACCT 449

QY 386 ATTATATACGCTAGTGTCTAGTCCTGAAAATCATCTGATCAAGAAACAAATTTTCAAC 445

DB 450 ATTATATACGCTAGTGTCTAGTCCTGAAAATCATCTGATCAAGAAACAAATTTTCAAC 509

QY 446 TCTTATACCTTTCTCTTACAAAGTCGTTCCGCTTCACTGGATTTTCAGCCTCTATACCTA 505

QY 26 GACAAGTTTGTACAAAGAACTGACGAGAAACGTAATAATGATATAATATCAATATAT 85
Db |||||
5483 GCCAACTTTGTACAAAAGAACTGACGAGAAACGTAATAATGATATAATATCAATATAT 5424
QY 86 AATATAGATTTGCAATAAAGAAAGAGTACATATATCTGTAATAACACATATATCCAGTC 145
Db |||||
5423 AATATAGATTTGCAATAAAGAAAGAGTACATATATCTGTAATAACACATATATCCAGTC 5364
QY 146 ACTATGAATCAACTACTTATAGATGATATAGTACCTGTAGTACGACGAGAGCCCTCCAAA 205
Db |||||
5363 ACTATGAATCAACTACTTATAGATGATATAGTACCTGTAGTACGACGAGAGCCCTCCAAA 5304
QY 206 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACGAGAGCCCTCCAAAAGTTCTCTCAA 265
Db |||||
5303 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACGAGAGCCCTCCAAAAGTTCTCTCAA 5244
QY 266 ACGGAATCGTGTATCGAGGCTACTCGCTATTGCTCAATGCGTATTAAATCATATAAA 325
Db |||||
5243 ACGGAATCGTGTATCGAGGCTACTCGCTATTGCTCAATGCGTATTAAATCATATAAA 5184
QY 326 AGAATAAGAAAGAGGTGCGAGCCCTTTTTTGTGTGACAAAAATAAAACATCTACCT 385
Db |||||
5183 AGAATAAGAAAGAGGTGCGAGCCCTTTTTTGTGTGACAAAAATAAAACATCTACCT 5124
QY 386 ATTATATAGCTAGTGTATAGTACCTGAAATCATCTGATCAAGCAATATTTCAAC 445
Db |||||
5123 ATTATATAGCTAGTGTATAGTACCTGAAATCATCTGATCAAGCAATATTTCAAC 5064
QY 446 TCTTATATCTTCTCTTACAAAGTCGTTGGGCTTCATCTGGATTTTCAGGCTCTATATCTTA 505
Db |||||
5063 TCTTATATCTTCTCTTACAAAGTCGTTGGGCTTCATCTGGATTTTCAGGCTCTATATCTTA 5004
QY 506 CTRAAAGTGAATAAGTTTCTGTAATTTCTACTGTATCGACCTGCAAGTGGTGTGTATA 565
Db |||||
5003 CTRAAAGTGAATAAGTTTCTGTAATTTCTACTGTATCGACCTGCAAGTGGTGTGTATA 4944
QY 566 AGGAGCCCTGACATTTATATCCCGAGAACATCAGGTTAATGCGCTTTTGTATGTCATTT 625
Db |||||
4943 AGGAGCCCTGACATTTATATCCCGAGAACATCAGGTTAATGCGCTTTTGTATGTCATTT 4884
QY 626 TCGCGTGGTGTAGATCAGCACTTCTTCCCGATACGAGACCGGACACTGGGCATA 685
Db |||||
4883 TCGCGTGGTGTAGATCAGCACTTCTTCCCGATACGAGACCGGACACTGGGCATA 4824
QY 686 TCGGTGGTGTATGCGCCAGCTTTTATCCCGATATGACACCGGTAAGTTTCAAGG 745
Db |||||
4823 TCGGTGGTGTATGCGCCAGCTTTTATCCCGATATGACACCGGTAAGTTTCAAGG 4764
QY 746 GAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCCGTGCGCCGGC 805
Db |||||
4763 GAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCCGTGCGCCGGC 4704
QY 806 GTGTCAATATATCACTCTGTATCAATCAAAACAGACGATACCGGCTCTCTTTTATAG 865
Db |||||
4703 GTGTCAATATATCACTCTGTATCAATCAAAACAGACGATACCGGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCT 925
Db |||||
4643 GTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCT 4584
QY 926 TTCAATAAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCCAGGTTTCGGC 985
Db |||||
4583 TTCAATAAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCCAGGTTTCGGC 4524
QY 986 ACGCAGACGAGCGGCTTCAATCTGCAATGTTGTGCTTACAGACCGAGATATGACATC 1045
Db |||||
4523 ACGCAGACGAGCGGCTTCAATCTGCAATGTTGTGCTTACAGACCGAGATATGACATC 4464
QY 1046 ATATATGCTTGCAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db |||||
4463 ATATATGCTTGCAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4404

QY 1106 ATAGCACACCTCTCTTTTGACATACCTCTCGGTA 1137
Db |||||
4403 ATAGCACACCTCTCTTTTGACATACCTCTCGGTA 4372

RESULT 12
ABZ58768
ID ABZ58768 standard; DNA; 4428 BP.
XX
AC ABZ58768;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brach MA, Cheo D, Li X, Eposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 27B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212 nucleotide sequence
XX
SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 23.5%; Score 1102.4; DB 7; Length 4428;
Best Local Similarity 99.5%; Pred. No. 2.2e-147;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAGCTGTAACGAGAAACGTAATAATGATATAATATCAATATAT 85
Db |||||
939 GCCAACTTTGTACAAAAGCTGTAACGAGAAACGTAATAATGATATAATATCAATATAT 998
QY 86 AATATAGATTTGCAATAAAGAAAGAGTACATATATCTGTAATAACACATATATCCAGTC 145
Db |||||
999 AATATAGATTTGCAATAAAGAAAGAGTACATATATCTGTAATAACACATATATCCAGTC 1058
QY 146 ACTATGAATCAACTACTTATAGATGATATAGTACCTGTAGTCGACGAGCCCTCCAAA 205
Db |||||
1059 ACTATGAATCAACTACTTATAGATGATATAGTACCTGTAGTCGACGAGCCCTCCAAA 1118
QY 206 TGTCTTCGCGGTGATGCTGCCAACTTAGTCGACGAGCCCTCCAAATGTTCTCTCAA 265
Db |||||

CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (i), (ii), (iii), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;
Query Match 23.7%; Score 1108.8; DB 3; Length 5584;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAAAGTTTGTACAAAAGCTGACGAGAAAGCTGAAATGATATATATATCAATATATT 85
DB 5483 GCAACTTTTGTACAAAAGCTGACGAGAAAGCTGAAATGATATATATATCAATATATT 5424
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATATATCTGTAAACACACATATCCAGTC 145
DB 5423 AAATTAGATTTTGCATAAAAAACAGACTACATATATCTGTAAACACACATATCCAGTC 5364
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGACGAGCTTCCAAA 205
DB 5363 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGACGAGCTTCCAAA 5304
QY 206 TGTTCCTCGGGTGATGTCGCCAACTAGTCGACGACGAGCTTCCAAATGTTCTCTCAA 265
DB 5303 TGTTCCTCGGGTGATGTCGCCAACTAGTCGACGACGAGCTTCCAAATGTTCTCTCAA 5244
QY 266 ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
DB 5243 ACGGAATCGTGTATCCAGCCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 5184
QY 326 AGAAATAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAACATCTACT 385
DB 5183 AGAAATAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAACATCTACT 5124
QY 386 ATTCATATACGCTAGTGTATAGTCTGAAATATCATCTGCATCAAGAAACATTTTCAACAC 445
DB 5123 ATTCATATACGCTAGTGTATAGTCTGAAATATCATCTGCATCAAGAAACATTTTCAACAC 5064
QY 446 TCTTATATCTTTCTTACAGCTGTCGGCTTCACTGGATTTTTCAGCCCTCTAFACTTA 505
DB 5063 TCTTATATCTTTCTTACAGCTGTCGGCTTCACTGGATTTTTCAGCCCTCTAFACTTA 5004
QY 506 CTAAACGCTGATAAGCTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGTGTATA 565
DB 5003 CTAAACGCTGATAAGCTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGTGTATA 4944
QY 566 AGGAGGCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTTCGATGTCATTT 625
DB 4943 AGGAGGCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTTCGATGTCATTT 4884
QY 626 TCGCGGTGGCTGAGATACGACCTTTCTTCCCGATAACGAGAACCGGACACTGGCCCATTA 685
DB 4883 TCGCGGTGGCTGAGATACGACCTTTCTTCCCGATAACGAGAACCGGACACTGGCCCATTA 4824
QY 686 TCGGTGGCTCATCGCCGAGCTTTTCATCCCGATATGCACCCAGCGGTAAAGTTTCAGG 745
DB 4823 TCGGTGGCTCATCGCCGAGCTTTTCATCCCGATATGCACCCAGCGGTAAAGTTTCAGG 4764
QY 746 GAGACTTTATCTGACAGCAGAGCTGCTGGCCAGGGGATCACCATCCGTCGCGCCGGGC 805
DB 4763 GAGACTTTATCTGACAGCAGAGCTGCTGGCCAGGGGATCACCATCCGTCGCGCCGGGC 4704
QY 806 GTGTCAATAATATATCTCTGTATCATCCAAACAGACGATACAGGCTCTCTCTTTTATAG 865
DB 4703 GTGTCAATAATATATCTCTGTATCATCCAAACAGACGATACAGGCTCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 925

DB 4643 GTGTAAACCTTAAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 4584
QY 926 TTCAATAAACCGGGGACCTCAGCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 985
DB 4583 TTCAATAAACCGGGGACCTCAGCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCCGC 4524
QY 986 ACGCAGACGACGGGCTTTCATTTCTGATGGTGTGCTTACCAAGACCGGAGATATTGACATC 1045
DB 4523 ACGCAGACGACGGGCTTTCATTTCTGATGGTGTGCTTACCAAGACCGGAGATATTGACATC 4464
QY 1046 ATATATGCTTGTAGCAACTGATAGCTGTGCTGCTCAACTGTCACTGTATACGCTGCTTC 1105
DB 4463 ATATATGCTTGTAGCAACTGATAGCTGTGCTGCTCAACTGTCACTGTATACGCTGCTTC 4404
QY 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
DB 4403 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 4372
RESULT 11
ABZ58766/c
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
XX
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX
KW Nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
PS WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 18B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence
XX
SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;
Query Match 23.7%; Score 1108.8; DB 7; Length 5584;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Query Match 23.7%; Score 1108.8; DB 7; Length 5584;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.

Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;

Query Match 23.7%; Score 1108.8; DB 3; Length 4939;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAGTTTGTACAAAAGAGCTGACGAGAAAGCTAAATGATATATATCAATATATT 85
DB 3636 GCNACTTTGTACAAAAGAGCTGACGAGAAAGCTAAATGATATATATCAATATATT 3695

QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAACTGTAAACACACATATCCAGTC 145
DB 3696 AAATTAGATTTTGCATAAAAAACAGACTACATAACTGTAAACACACATATCCAGTC 3755

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGAGCTTCCAAA 205
DB 3756 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGAGCTTCCAAA 3815

QY 206 TGTCTTCGGGTGATGCTCCCACTTAGTCGACGAGAGCTTCCAAAAGTCTCTCAA 265
DB 3816 TGTCTTCGGGTGATGCTCCCACTTAGTCGACGAGAGCTTCCAAAAGTCTCTCAA 3875

QY 266 ACGGAATCGCTGATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAATCATATAAA 325
DB 3876 ACGGAATCGCTGATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAATCATATAAA 3935

QY 326 AGAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATAAATAAATCATCTACCT 385
DB 3936 AGAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATAAATAAATCATCTACCT 3995

QY 386 ATTATATATAGCTAGTGTCTAGTCTGAAATCATCTGATCAAGAAACAATTTTCAACAC 445
DB 3996 ATTATATATAGCTAGTGTCTAGTCTGAAATCATCTGATCAAGAAACAATTTTCAACAC 4055

QY 446 TCTTATATCTTTCTCTACAAGTCGTTCGGCTTCATCTGATTTTCAGGCTCTATATCTTA 505
DB 4056 TCTTATATCTTTCTCTACAAGTCGTTCGGCTTCATCTGATTTTCAGGCTCTATATCTTA 4115

QY 506 CTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565
DB 4116 CTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 4175

QY 566 AGGAGCGCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTGTGATGTCAATT 625
DB 4176 AGGAGCGCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTGTGATGTCAATT 4235

QY 626 TCGCGTGGCTGAGTACAGCACTTCTTCCCGATAAACGAGACCCGCGACACTGGCCATA 685
DB 4236 TCGCGTGGCTGAGTACAGCACTTCTTCCCGATAAACGAGACCCGCGACACTGGCCATA 4295

QY 686 TCGGTGGTATCATGCGCAGCTTCTATCCCGATATGACACCCGCGTAAAGTTCAAGG 745
DB 4296 TCGGTGGTATCATGCGCAGCTTCTATCCCGATATGACACCCGCGTAAAGTTCAAGG 4355

QY 746 GAGACTTTATCTGACAGACAGCTGACCTGGCCAGAGGGGATCACCATCGCTCGCCGGGC 805
DB 4356 GAGACTTTATCTGACAGACAGCTGACCTGGCCAGAGGGGATCACCATCGCTCGCCGGGC 4415

QY 806 GTGTCAATAATATCACTCTGTATATCCAAAACAGACGATPACGGCTCTCTCTTTATAG 865
DB 4416 GTGTCAATAATATCACTCTGTATATCCAAAACAGACGATPACGGCTCTCTCTTTATAG 4475

QY 866 GTGTAACCTTAAACTGCAATTTACAGTCCCTCTCTCGTCAGAAAAAGAGCCGTTTCA 925
DB 4476 GTGTAACCTTAAACTGCAATTTACAGTCCCTCTCTCGTCAGAAAAAGAGCCGTTTCA 4535

QY 926 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGGC 985
DB 4536 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCCGGC 4595

QY 986 ACGCAGACGAGCGGCTTCATTTCTGATGTTGTGCTTACACGACCGGAGATATTGACATC 1045
DB 4596 ACGCAGACGAGCGGCTTCATTTCTGATGTTGTGCTTACACGACCGGAGATATTGACATC 4655

QY 1046 ATATATGCTTGAACAATGATAGTGTGCTGTCACACTGTCATGTAATACGCTGCTTC 1105
DB 4656 ATATATGCTTGAACAATGATAGTGTGCTGTCACACTGTCATGTAATACGCTGCTTC 4715

QY 1106 ATAGCACACCTCTTTTGTGACATATCTCGGTA 1137
DB 4716 ATAGCACACCTCTTTTGTGACATATCTCGGTA 4747

RESULT 10
AAC55632/c
ID AAC55632 standard; DNA; 5584 BP.
XX AAC55632;
AC AAC55632;
DT 11-JAN-2001 (first entry)
XX Donor plasmid pDONR207 nucleotide sequence.
DE Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
KW Bacteriophage lambda.
XX Bacteriophage lambda.
OS Synthetic.
OS
XX WO200052027-A1.
PN 08-SEP-2000.
XX 02-MAR-2000; 2000WO-US005432.
XX 02-MAR-1999; 99US-0122389P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI WPI; 2000-543948/49.
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 recombination sequence useful for the recombination cloning of polypeptides.
PT
XX Disclosure; Fig 97; 459pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods

PT protein production.

PS Claim 41; Page 47-51; 52pp; English.

XX The invention comprises a method for moving an insert nucleic acid molecule between vectors, the method involves moving an insert nucleic acid from one vector to another using site-specific recombination. The method of the invention is useful for studying the biology of an organism, including array construction, reporter gene fusions, CC mutagenesis, protein production and characterisation. The present DNA CC sequence represents the plasmid vector pMK2010 of the invention.

XX SQ Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;

Query Match 23.7%; Score 1108.8; DB 8; Length 4892;

Best Local Similarity 99.8%; Pred. No. 2.7e-148;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTGTACAAAAAGCTGAACGAGAAACGTAAGATATATAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAGATATATAATATCAATATATT 161

QY 86 AATATAGATTTGCATATAAACAAGACTACATATATCTTAAACAACATATCCAGTC 145
DB 162 AATATAGATTTGCATATAAACAAGACTACATATATCTTAAACAACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCAGCGACAGCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCAGCGACAGCCTTCCAAA 281

QY 206 TGTTCCTCGGTGATGTCGCAACTTAGTCAGCGACAGCCTTCCAAAATGTTCTTCTCAA 265
DB 282 TGTTCCTCGGTGATGTCGCAACTTAGTCAGCGACAGCCTTCCAAAATGTTCTTCTCAA 341

QY 266 ACGGAATCGTGTATCGAGCTACTCGTATTCTCTCAATCGCGTATTAATCATATAAA 325
DB 342 ACGGAATCGTGTATCGAGCTACTCGTATTCTCTCAATCGCGTATTAATCATATAAA 401

QY 326 AGAATAAGAAAAAGAGTTCGAGCCTCTTTTGTGTGACAAAAATAAACAATCTACCT 385
DB 402 AGAATAAGAAAAAGAGTTCGAGCCTCTTTTGTGTGACAAAAATAAACAATCTACCT 461

QY 386 ATTATATAGCGTAGTGTATAGTCTGAAATCATCTGCATCAAGAAACATTTTCAAC 445
DB 462 ATTATATAGCGTAGTGTATAGTCTGAAATCATCTGCATCAAGAAACATTTTCAAC 521

QY 446 TCTATATCTTTCTCTTACAAAGTCGTTCGCGCTTCATCTGGATTTTCAGCCTCTATACTTA 505
DB 522 TCTATATCTTTCTCTTACAAAGTCGTTCGCGCTTCATCTGGATTTTCAGCCTCTATACTTA 581

QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTATTA 565
DB 582 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTATTA 641

QY 566 AGGAGCGCTGACATTTATATATCCCGACAAATCAGTGTATGCGTTTTCATGTCATTT 625
DB 642 AGGAGCGCTGACATTTATATATCCCGACAAATCAGTGTATGCGTTTTCATGTCATTT 701

QY 626 TCGCGTGGCTGAGATCAGACCACTTCTTCCCGATACCGAGACCGGCACACTGGCCATA 685
DB 702 TCGCGTGGCTGAGATCAGACCACTTCTTCCCGATACCGAGACCGGCACACTGGCCATA 761

QY 686 TCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGGTAAAGTTACGG 745
DB 762 TCGGTGTGATCATGCGCCAGCTTTTCATCCCGATATGCAACACCGGGTAAAGTTACGG 821

QY 746 GAGACTTTATCTGACAGCAGCTGCATCGGCCAGGGGATCACCATCCGTCGCCCGGC 805
DB 822 GAGACTTTATCTGACAGCAGCTGCATCGGCCAGGGGATCACCATCCGTCGCCCGGC 881

QY 806 GTGTCAATATATACCTCTGTACATCCACAAAGAGAGATAACGGCTCTCTCTTTTATAG 865
DB 882 GTGTCAATATATACCTCTGTACATCCACAAAGAGAGATAACGGCTCTCTCTTTTATAG 941

QY 866 GTGTAAACCTTAAACTGCATTTACAGTCCCTGTCTGTAGCAAAAGAGCCGTTTCAT 925
DB 942 GTGTAAACCTTAAACTGCATTTACAGTCCCTGTCTGTAGCAAAAGAGCCGTTTCAT 1001
QY 926 TTCAATAAACCGGGGAGCTCAGCCATCCCTTCCCTGTATTTCCGCTTCCAGCGTTCGGC 985
DB 1002 TTCAATAAACCGGGGAGCTCAGCCATCCCTTCCCTGTATTTCCGCTTCCAGCGTTCGGC 1061
QY 986 ACGCAGACGAGCGGCTTCATTTCTGCATGTTGTCTTACACGACGAGATATTGACATC 1045
DB 1062 ACGCAGACGAGCGGCTTCATTTCTGCATGTTGTCTTACACGACGAGATATTGACATC 1121
QY 1046 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATAGCTGCTTC 1105
DB 1122 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATATAGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTTCACATATCTTCGGTA 1137
DB 1182 ATAGCACACCTCTTTTTCACATATCTTCGGTA 1213

RESULT 9

AAC55525

ID AAC55525 standard; DNA; 4939 BP.

XX AC AAC55525;

XX DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR205 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX PD 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US005432.

XX PR 02-MAR-1999; 99US-0122389P.

XX PR 23-MAR-1999; 99US-0126049P.

XX PR 28-MAY-1999; 99US-0136744P.

XX PA (LIFE-) LIFE TECHNOLOGIES INC.

XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;

XX DR WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.

XX Example 10; Fig 53; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attR1, attR2, attL1, and attL2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated

XX 21-MAY-2002; 2002WO-US015947.
PF
XX
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
XX Disclosure; Fig 26B-C; 273pp; English.
XX
XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR201 nucleotide sequence
XX
XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
SQ
Query Match 23.7%; Score 1108.8; DB 7; Length 4470;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACACCTTTGTACAAAAGCTGAACGAGAAAGTAAATGATATATAATCAATATATT 85
DB 102 GCCAATTTGTACAAAAGCTGAACGAGAAAGTAAATGATATATAATCAATATATT 161
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACAAATATCCAGTC 145
DB 162 AAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACAAATATCCAGTC 221
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCAGCAGAGCCCTTCCAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCAGCAGAGCCCTTCCAA 281
QY 206 TGTCTTCGGGTGATGCTGCAACTTAGTCAGCCGAGCCTTCCAAATGTTCTTCTCAA 265
DB 282 TGTCTTCGGGTGATGCTGCAACTTAGTCAGCCGAGCCTTCCAAATGTTCTTCTCAA 341
QY 266 ACGGAATCGTCGTATCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAAATCATAAAA 325
DB 342 ACGGAATCGTCGTATCAGCCTACTCGCTATTGTCCTCAATGCGGTATTAAATCATAAAA 401
QY 326 AGAAATAGAAAAGAGGTCGGAGCCTCTTTTGTGTGACAAAATAAACAATCTACCT 385
DB 402 AGAAATAGAAAAGAGGTCGGAGCCTCTTTTGTGTGACAAAATAAACAATCTACCT 461
QY 386 ATTCAATAGCTAGTGTCTATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCCAAAC 445
DB 462 ATTCAATAGCTAGTGTCTATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCCAAAC 521
QY 446 TCTTATATCTTCTCTTACAGTCGTTCCGCTTCATCTGGAATTTTCAAGCTCTATATCTTA 505
DB 522 TCTTATATCTTCTCTTACAGTCGTTCCGCTTCATCTGGAATTTTCAAGCTCTATATCTTA 581
QY 506 CTAAACCTGTAAAGTTTCTGTAAATTTCTATCTGATCGACTCGAGACTGCTGTGTATA 565
DB 582 CTAAACCTGTAAAGTTTCTGTAAATTTCTATCTGATCGACTCGAGACTGCTGTGTATA 641
QY 566 AGGAGGCTGACATTTTATATTTCCCGAGAACATCAGGTTAATGGGTTTGTGATGTCATTT 625

DB 642 AGGAGGCTGACATTTATATTTCCCGAACAATCAGGTTATATGGGTTTTCATGTCATTT 701
QY 626 TCGCGTGGCTGAGATCAGCCACTTTTCCCGAATAACGAGACCGGACACATCGGCCATA 685
DB 702 TCGCGTGGCTGAGATCAGCCACTTTTCCCGAATAACGAGACCGGACACATCGGCCATA 761
QY 686 TCGGTGTGTCATGCGCCAGCTTTTCATCCCGATATGCACCCGCGGTAAAGTTTCAGG 745
DB 762 TCGGTGTGTCATGCGCCAGCTTTTCATCCCGATATGCACCCGCGGTAAAGTTTCAGG 821
QY 746 GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGC 805
DB 822 GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGC 881
QY 806 GTGTCAATATATCACTCTGTATATCCCAAAACAGAGATTAACGGCTCTCTCTTTTATAG 865
DB 882 GTGTCAATATATCACTCTGTATATCCCAAAACAGAGATTAACGGCTCTCTCTTTTATAG 941
QY 866 GTGTAAACCTTAAATGCAATTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCAT 925
DB 942 GTGTAAACCTTAAATGCAATTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCAT 1001
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCGGC 985
DB 1002 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTTCCAGCGTTCGGC 1061
QY 986 AGCAGACGACGGGCTTCATTTCTGATGGTGTGCTTACAGAGCGGAGATATTGACATC 1045
DB 1062 ACGCAGACGACGGGCTTCATTTCTGATGGTGTGCTTACAGAGCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTGGACCACTGATAGTGTGCTGTCAACTGTCACTGTATATACGCTGCTTC 1105
DB 1122 ATATATGCTTGGACCACTGATAGTGTGCTGTCAACTGTCACTGTATATACGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTTCACATCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTTCACATCTTCGGGTA 1213
RESULT 8
ADA50329
ID ADA50329 standard; DNA; 4892 BP.
XX
AC ADA50329;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid vector pMK2010 DNA sequence.
XX
DE site-specific recombination; array construction; reporter gene fusion;
KW mutagenesis; protein production; protein characterisation;
KW plasmid pMK2010; ds.
XX
OS Synthetic.
XX
XX WO2003064623-A2.
XX
XX 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003176.
XX
PR 31-JAN-2002; 2002US-0354063P.
XX
XX (UNIV) UNIV WASHINGTON STATE RES FOUND.
PA Kahn ML, House BL, Mortimer MW;
PI WPI; 2003-679497/64.
XX
XX Moving an insert nucleic acid between vectors using sire-specific
PT recombination in vivo, useful for studying the biology of the organism,
PT including array construction, reporter gene fusions, mutagenesis and

PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
PF
XX 02-MAR-1999; 99US-0122389P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
PI WPI; 2000-543948/49.
XX
DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX Example 9; Fig 49; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 23.7%; Score 1108.8; DB 3; Length 4470;
Best Local Similarity 99.8%; Pred. No. 2.7e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAGAGCTGAACGAGAAAGCTAAATATGATATAAATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAGAGCTGAACGAGAAAGCTAAATATGATATAAATCAATATATT 161
QY 86 AAATAGATTTTGCATATAAAGACAGCTACATAATCTGTAAACACACATATCCAGTC 145
DB 162 AAATAGATTTTGCATATAAAGACAGCTACATAATCTGTAAACACACATATCCAGTC 221
QY 146 ACTATCAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACCGACAGCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACCGACAGCCTTCCAAA 281
QY 206 TGTCTCTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 265
DB 282 TGTCTCTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 341
QY 266 ACGGAATGCGTATACGAGCTACTCGCTATTGCTCAATGCGGTATTAAATCATAAA 325
DB 342 ACGGAATGCGTATACGAGCTACTCGCTATTGCTCAATGCGGTATTAAATCATAAA 401
QY 326 AGAAATAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAATAAACAATCTACCT 385

DB 402 AGAAATAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAATAAACAATCTACCT 461
QY 386 ATTCATATACGCTAGTGTATAGTCCCTGAAATCATCTGCAATCAAGAAACAATTTCAAC 445
DB 462 ATTCATATACGCTAGTGTATAGTCCCTGAAATCATCTGCAATCAAGAAACAATTTCAAC 521
QY 446 TCTTATACCTTTCTCTTCAAGTGTGGCTTCAATCTGGATTTTTCAGCCCTCTATACCTA 505
DB 522 TCTTATACCTTTCTCTTCAAGTGTGGCTTCAATCTGGATTTTTCAGCCCTCTATACCTA 581
QY 506 CTAAACGTGATAAAGTCTCTGTAATTTCTATGATATGACCTGAGACCTGGCTGTGTATA 565
DB 582 CTAAACGTGATAAAGTCTCTGTAATTTCTATGATATGACCTGAGACCTGGCTGTGTATA 641
QY 566 AGGAGCCTGACATTTATTTATTTCCCGACAAATCATAGTTTAAATGGCTTTTTCATGTCATTT 625
DB 642 AGGAGCCTGACATTTATTTATTTCCCGACAAATCATAGTTTAAATGGCTTTTTCATGTCATTT 701
QY 626 TCGCGGTGGCTGAGATCAGCCACTTTCTTCCCGATACGAGACCGGACACACTGGCCATA 685
DB 702 TCGCGGTGGCTGAGATCAGCCACTTTCTTCCCGATACGAGACCGGACACACTGGCCATA 761
QY 686 TCGGTGGTCAATCATGCGCCAGCTTTTCTATCCCGATATGACACCGGGTAAAGTTCAAGG 745
DB 762 TCGGTGGTCAATCATGCGCCAGCTTTTCTATCCCGATATGACACCGGGTAAAGTTCAAGG 821
QY 746 GAGACTTTTATCTGACGACGACGTGCTACTGGCCAGGGGGATCAACCATCCGTGCGCCGGGC 805
DB 822 GAGACTTTTATCTGACGACGACGTGCTACTGGCCAGGGGGATCAACCATCCGTGCGCCGGGC 881
QY 806 GTGTCAATTAATATCACTGTGTACATCCCAACACAGACGATTAACGGCTCTCTCTTTATAG 865
DB 882 GTGTCAATTAATATCACTGTGTACATCCCAACACAGACGATTAACGGCTCTCTCTTTATAG 941
QY 866 GTGTAAACCTTAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 925
DB 942 GTGTAAACCTTAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
QY 926 TTCATTAACACCGGGGCGACCTCAGCCATCCCTTCTGATTTTCCGTTTCCAGCGTTCCGC 985
DB 1002 TTCATTAACACCGGGGCGACCTCAGCCATCCCTTCTGATTTTCCGTTTCCAGCGTTCCGC 1061
QY 986 ACGGACGACGCGGCTTCAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
DB 1062 ACGGACGACGCGGCTTCAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
QY 1046 ATATATGCTTGCAGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
DB 1122 ATATATGCTTGCAGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
QY 1106 ATAGCACACCTCTTTTTCACATATCTCGGTA 1137
DB 1182 ATAGCACACCTCTTTTTCACATATCTCGGTA 1213

RESULT 7
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
AC ABZ58767;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR201 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.

QY 2045 AAGCGAAGATCTATCATTTTATATAGTATTAATTTCAATCAACATTCCTTAATTAATTTCT 2104
Db 14893 TTAAACTAAATATTAGTAAATGGTATAGATATTT - AATTATATAATAAACTAATTAATC 14836
QY 2105 AAATTAATCTGTAGTTTATTAATCTTAAATGAAATGAGTATTAATTAATGAAATAG 2164
Db 14835 ATAAAAAATATATTTAAATTTATTTATTTCTTAATTTTACATAGTATTTTATCATTTGA 14776
QY 2165 TCGAATCATGAAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTGTATCAATGATCTTA 2224
Db 14775 TATTTAAATCAACAACAGCTAGAAATTAATTAATTAATTAATTAATTAATTAATGCTAG 14716
QY 2225 CATTTGGATGATACAGTTGGGAAGCTGGGTTCGAAATCGAATGAGTTCGCTCGAGTT 2284
Db 14715 TATATCATCTTACATGTTCCGATCAAAATTCATTTAAATAATATATCTACTCTCAACTTTT 14656
QY 2285 ATCATCATCATATAGA --- CACAGAAATATAAGTAATCAAGATTAATCAAGTTAAAGCTATG 2341
Db 14655 ATCTTCTCGCTTTACATCATCTGTGTATTTTTCATTTTTCATTTATGTTTGTATGTA 14596
QY 2342 TAATATTTGCGCATAAACCAATCAATTAATAAATAGATCAGTTTAAAGAAAGATCAAAAGC 2401
Db 14595 AACATATATTTATAAATTTATTTTTCACAAATTAATAAACAATATATTAATAATCAATC 14536
QY 2402 TCAAAAAATATAAGAGAAAGGTCCTAAACAGAAATGAAAGGAAAGAACTAGAA 2461
Db 14535 TAATTAACATCACTTAACATATTTTATTAATAAGGAAAGAAATAATATTTTCCCTTA 14476
QY 2462 TTATCTGCGACAGCTTGGATCCTCTAGACCCTTTGTACAGAAAGCTTGAACGAGAAAC 2521
Db 14475 CNAAGCTGGGTACCGAAT - TCCTCGAGACCCTTTGTACAGAAAGCTTGAACGAGAAAC 14417
QY 2522 GTAAATGATATAAATPATCAATATATTAATATAGATTTTGATTAATAAACAAGATCATATA 2581
Db 14416 GTAAATGATATAAATPATCAATATATTAATATAGATTTTGATTAATAAACAAGATCATATA 14357
QY 2582 ATACTGTAAACACACATPATCAAGTCACTCAATCAATCAATCAATCAATCAATCAATCAAT 2641
Db 14356 ATACTGTAAACACACATPATCAAGTCACTCAATCAATCAATCAATCAATCAATCAATCAAT 14297
QY 2642 CTTGTAGTCACTAAGTTGGCAGCATCACCGCAGCATCTTGGCGCGAATAAATACCTGT 2701
Db 14296 CTTGTAGTCACTAAGTTGGCAGCATCACCGCAGCATCTTGGCGCGAATAAATACCTGT 14237
QY 2702 GACGGAAGATCACTTCGCGAATAAATAAATCTCGGTGCTCTTGTGATACCGGGAAGCC 2761
Db 14236 GACGGAAGATCACTTCGCGAATAAATAAATCTCGGTGCTCTTGTGATACCGGGAAGCC 14177
QY 2762 CTGGGCCAATTTTGGCGAAATGAGAGCTTGTATCGGATTTCAACTCTTATACCTTTTC 2821
Db 14176 CTGGGCCAATTTTGGCGAAATGAGAGCTTGTATCGG --- CACTACCGGAAGTATGTCA 14121
QY 2822 TCTTACAAGTCGTTGGCTTCATCTGGATTTTCAGCCTCTATATCTTAATAACGATGATA 2881
Db 14120 AAAAGAGGTGTGTATGAAGCAGGTATTAACAGTGACAGTTGACAGGACAGCTATCAGT 14061
QY 2882 AGTTCTGTATTTCTACTGTATCGACTCGAGACTGG --- CTTGTATTAAGG 2932
Db 14060 TGCTCAAGGCATATATGATGTCAATATCTCGGTCTGTGAAGCACAACCATGCGAATGA 14001
QY 2933 AGCTGTACATTTATTTCCCGCAACATCAGTTTAAATGGGTTTTTTGATGTCAATTTTCGC 2992
Db 14000 AGCCCGTGTCTGGTGCC --- GAACGCTGAAAGCGGAAATCAGGAAGGATGGCTGA 13944
QY 2993 GGTGGCTGAGATCAGCCACTTTCTTCCCGATTAACGAGACCGGCACACTGCGCCATATCGG 3052
Db 13943 GGTCCCGGTTTATTTGAATGAAACGCTCTTTTGTCTGACGAGAACAGGG --- ACTG 13890
QY 3053 TGGTCATCATCGCCAGCTTTCATCCCGATATGCAACCGCGGTAAAGTTCACGGGAGA 3112
Db 13889 GTGAATGACAGTTTAAAGGTTTACACCTATAAAGAGAGAGCCGTTATCGTCTGTTGTGG 13830
QY 3113 CTTTATCTGACAGCAGCTGCACTGGCCAGGGGATCAACCATCGTCCGCCCGCGCTGT 3172

Db 13829 ATGTACAGATGATATTAATTTGACACGCCCGGCGACGATGGTATCCCTCGCCAGTG 13770
QY 3173 CAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGTGT 3232
Db 13769 CACGTCTGCTGCAGATAAAGTCTCCCGTGAACCTTACCCTGGTGGTGCATATCGGGATG 13710
QY 3233 AAACCTTAAATCGATTTTACC --- AGTCCCTGTTCTGTCAGCAAAAGACCGGTTCT 3286
Db 13709 AAAGCTGGCGATGATGATGACACCGGATGCGCAGTGTGCGGGTCTCCGTTATCGGGGAG 13650
QY 3287 ATTTCAATPAACCGGCGACCTCAGCCATCCCTTCTCGATTTTCCGCTTCTCCAGCGTTCTC 3345
Db 13649 AAGTGGCTGATCTCAGCCACCGCGAAATGACATCAAAACGCCATTAACCTGATGTTCT 13590
QY 3346 --GGCAGCAGACGACCGGGTTCAATCTGCAAG --- TTGTCGTTTACAGACCGGAGATA 3400
Db 13589 GGGGAATATAAATGTGAGGCTCCCTTATACACAGCCAGCTCTGACAGTGCATACAGTAGAA 13530
QY 3401 TTGACATCATATATGCTTGGAGCAACTGATAGTGTGCTGCTCACTGCTCACTGTAATAC 3460
Db 13529 ATTACAGAAACTTTTATCAGTTTATAGTATAGAGGCTGAAATCCAGATGAAGCCGAA 13470
QY 3461 GCTGCTCATAGCACACCTCTTTTGTGACATACCTCTGTTCTTGTATGAGTGAATTTTTCAG 3520
Db 13469 CGACTTGTAAAGAAAGATTAAGAGTTGTGAATTTGTTCTTGATGAGATGATTTTCAG 13410
QY 3521 GACTATGACATAGCGTATATGATAGTATGATGTTTATTTTGTCTACACAAAAGAG 3580
Db 13409 GACTATGACATAGCGTATATGATAGTATGATGTTTATTTTGTCTACACAAAAGAG 13350
QY 3581 GCTCGACCTCTTTTCTTATTTTCTTTTATGATTAATACGGCATTCAGGACATAGCG 3640
Db 13349 GCTCGACCTCTTTTCTTATTTTCTTTTATGATTAATACGGCATTCAGGACATAGCG 13290
QY 3641 AGTAGGCTGGATPACACGATTCCTGTTTGAAGAAACATTTGGAAGGCTGTGGTTCGACTA 3700
Db 13289 AGTAGGCTGGATPACACGATTCCTGTTTGAAGAAACATTTGGAAGGCTGTGGTTCGACTA 13230
QY 3701 AGTTGGAGCATPACCCGAGAAACATTTGGAAGGCTGTGGTTCGACTACAGTCACTAAT 3760
Db 13229 AGTTGGAGCATPACCCGAGAAACATTTGGAAGGCTGTGGTTCGACTACAGTCACTAAT 13170
QY 3761 ACCATCTAGTATGATTTGATGACTGGATATGTTGTTTACAGTATATGATG 3820
Db 13169 ACCATCTAGTATGATTTGATGACTGGATATGTTGTTTACAGTATATGATG 13110
QY 3821 CTGTTTTTATGCAAAATCAATTTAATATATTTGATATTTATCATATTTACGTTTCTCG 3880
Db 13109 CTGTTTTTATGCAAAATCAATTTAATATATTTGATATTTATCATATTTACGTTTCTCG 13050
QY 3881 TTCAGCTTTTGTACAAACTGTCTAGAG 3910
Db 13049 TTCAGCTTTTGTACAAACTGTCTAGAG 13020

RESULT 6

AA55521
ID AAC55521 standard; DNA; 4470 BP.

XX AAC55521;

XX AC AC

XX AT AT

XX 11-JAN-2001 (first entry)

XX Donor plasmid pDONR201 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

XX mutant; recombinational cloning; entry vector; destination vector;

XX gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

XX OS Synthetic.

XX

CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention

SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

Query Match 25.8%; Score 1208.4; DB 6; Length 17681;

Best Local Similarity 60.4%; Pred. No. 2e-162;

Matches 2374; Conservative 0; Mismatches 1476; Indels 80; Gaps 20;

QY	21	CTCGAGACAGTTTGTCACAAAAGCTGAACGAGAAACGTAAATGATATATAATCAAT	80
DB	16909	CTCTAGCAAGTTTGTCACAAAAGCTGAACGAGAAACGTAAATGATATATAATCAAT	16850
QY	81	ATATTAAATAGATTGTCATAAAAAGACACTACATAATCTGTAAACACCAACATATC	140
DB	16849	ATATTAAATAGATTGTCATAAAAAGACACTACATAATCTGTAAACACCAACATATC	16790
QY	141	CAGTCACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGACAGCCTT	200
DB	16789	CAGTCACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGACAGCCTT	16730
QY	201	CCAAATGTTCTTCGGGTGATGTCGCAACTAGTTCGACCGCAGCCTTCCAAATGTTCTT	260
DB	16729	CCAAATGTTCTTCGGGTGATGTCGCAACTAGTTCGACCGCAGCCTTCCAAATGTTCTT	16670
QY	261	CTCAACCGGAATCGTCTGATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAATCA	320
DB	16669	CTCAACCGGAATCGTCTGATCCAGCCTACTCGCTATTGTCTCAATGCGGTATTAATCA	16610
QY	321	TAAAAGAAATTAAGAAAAGAGGTGGAGCCTCTTTTGTGTGACAAAATTAACAATC	380
DB	16609	TAAAAGAAATTAAGAAAAGAGGTGGAGCCTCTTTTGTGTGACAAAATTAACAATC	16550
QY	381	TACCTATTCAATACGCTAGTCTCATAGTCTCGTAAATCATCTGATCAAGAACATATC	440
DB	16549	TACCTATTCAATACGCTAGTCTCATAGTCTCGTAAATCATCTGATCAAGAACATATC	16490
QY	441	ACAACTCTTATCTTTCTTTACAAAGTCTTTCGGCTTCATCTGGATTTTCAGCCTCTAT	500
DB	16489	ATGTCAAAAAGAGGTCTGTATGAA---GCAGGTATTATACGTGACAGTTGACGGACA	16433
QY	501	ACTTACTAAACGTGATAAAGTTCTGTAAATTTCTACTGTATCGACTCGAGACTGGCTGT	560
DB	16432	GCTATCAGTTGTCTAAGGCATATATGATGTCATATCTCCGGTCTGGTAAAGCACACCAT	16373
QY	561	GTATAAGGAGCCTGCACATTTATTTCCCGAAGACATCAGGTTAATGGCGTTTTGTATGT	620
DB	16372	GCAGATGAAGCCCGTCTGCTGGTGCC---GAACTGGAAGCGGAAATCAGGAAGG	16316
QY	621	CATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGG	680
DB	16315	GATGGCTGAGGTGCGCCCGTTTATTGAATGAACGCTCTTTTGTCTGACGAGAACAGGG-	16257
QY	681	CCATATCGGTGTCATCATGGCAGCTTTCATCCCGGATATGACACCGGGTAAAGTT	740
DB	16256	-----ACTGGTGAATGCAATTTAAGGTTTACACCTATATAAAGAGAGACCGGTATCGTC	16202
QY	741	CACGGGAGACTTTATCTGACAGCAGCTGCTGCTGCGGCGGGGATCAACATCCGTCGCC	800
DB	16201	TGTTTGTGATGTACAGATGATATTATTGACAGCGCCCGGGACGGATGGTGTATCCCC	16142
QY	801	CGGGCGTGTCAATAATATCACTGTACATCCCAAAACAGACGATAAACGGCTCTCTCTTT	860
DB	16141	TGGCCAGTGCAGCTCTGCTGCAGATAAAGTCTCCCGTGAACCTTTACC CGGTGTGCATA	16082
QY	861	TATAGGTAAACCTTAAACCTGATTTTACC-----AGTCCCTGTTCTCGTCAGCAAAA	914
DB	16081	TCGGGATGAAGCTGGCGCATGATGACCAACCGATATGSCCAGTGTGCGCGTCTCGTTA	16022
QY	915	GAGCCGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTTC	974
DB	16021	TCGGGGAAGAGTGGCTGATCTCAGCCACCGCGGAAATGACATCAAAAAGCCCATTAACC	15962

QY	975	CAGGGTTC---GGCACGACGACGACGGGCTTCAATCTTCATGGTGTGCTTACAGACCG	1031
DB	15961	TGAATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACACAG-----CCAGTCTG	15911
QY	1032	GAGATATTGACATCATATATATGCTTGTAGCAACTGATAGCTGTGCTGTCACTGTCACTG	1091
DB	15910	CAGTGCATACAGPAGAAATTTACAGAAACTTTTATCACGTTTAGTAAAGTATAGAGCTGAA	15851
QY	1092	TAATACGCTGCTTCATAGCACACCTCTTTTGCATACACTTCGGGTAGTG-----CCGATCA	1147
DB	15850	AATCCAGATGAGCGACGACGCTGTGAAGAGAAAAGTATAGAGTGTGGAATCCGATCA	15791
QY	1148	ACGCTCTCATTTTCCGCAAAAGTTGGCCGACGGCTTCCCGGATCAACAGGGACCCAGGA	1207
DB	15790	ACGCTCTCATTTTCCGCAAAAGTTGGCCGACGGCTTCCCGGATCAACAGGGACCCAGGA	15731
QY	1208	TTTATTTATTTCTGCGAAGTGTCTTCGCTACAGGTTATTTTCCGCGCAAGTGCGCTCG	1267
DB	15730	TTTATTTATTTCTGCGAAGTGTCTTCGCTACAGGTTATTTTCCGCGCAAGTGCGCTCG	15671
QY	1268	GGTCAATGCTGCAACTTAGTCCGACTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCAT	1327
DB	15670	GGTCAATGCTGCAACTTAGTCCGACTACAGGTCACCTAATACCATCTAAGTAGTGTGATTCAT	15611
QY	1328	AGTCACTGGATATGTTGTTTTACAGTATTTAGTGTCTGTTTTTATGCAAAATCTAA	1387
DB	15610	AGTCACTGGATATGTTGTTTTACAGTATTTAGTGTCTGTTTTTATGCAAAATCTAA	15551
QY	1388	TTTATATATTTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTCTCTGACAAAGTG	1447
DB	15550	TTTATATATTTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTCTCTGACAAAGTG	15491
QY	1448	GTCTCGAGGA-ATTCTGGTACCCGACCTTGGTAAAGGAATAATTTATTTCTTTTCTCTT	1506
DB	15490	GTCTAGAGGATCCAGCTTGTGCGAGTAAATTTCTAGTTTTTCTCTCTCTCTCTCTCT	15431
QY	1507	TAGTATAAAATAGTTAAGTGTAAATAGTATGATTTATATATATATATAGTTGTATATAT	1566
DB	15430	TAGGACCCCTTTCTCTTTTATTTTGTAGCTTTGATCTTTCTTTTAACTGATCTATTT	15371
QY	1567	TGTGAAAAATAATTTAATAATATTTTACATAAAACAACATAGTATGTAAAAAAT	1626
DB	15370	TTTAAATGATTTGGTTATGCGGCAATAATTTACATAGCTTTAACTGATATCTGATTTACTTT	15311
QY	1627	ATGCAAGTGTGTGTAAAGACGAGAAAGTAAAAGTTTGAGAGTAAAGTATATTTATTTTAA	1686
DB	15310	ATTTCTGTG---TGTCTATGATGATGATGATAACTGCGACGCAAGCTTATCGATTTTGAAC	15254
QY	1687	TGAATTTGATCGAACATGTAAGATGATATACATAGATTAATATTTGTTTAACTAATAA	1746
DB	15253	CCAGCTTCCCACTGTAATCAATCCAAATGTAAGATCAATGATAACACAAATGACATGATC	15194
QY	1747	GTAATTTCTAGCTGGTTTCGATGAAATTAATAATCAATGATAAAATACTATAGTAAAAAATAG	1806
DB	15193	TATCATGTTTACCTGTTTATTTCACTGCTGATATTTCAATTTAATTAAGTCAATCCAT	15134
QY	1807	AATAAATAAATTAATAATATTTTATGATTAATAGTTTATTTATATTAATTT---AATAA	1864
DB	15133	TAGAAGTTAAATAAACTCAAGTATTAATTAAGAAATTAATAAGAAATGTTGATGAATAA	15074
QY	1865	TCATATACCATTTACTAAATATTTTAGTTTAAAGTTTAAATAATTTTGTGTAGAAATTC	1924
DB	15073	ATFACTATATAAATGATAGATCTTCGCTTTGTTATTTAGCATTTAGATTTATGTTTGT	15014
QY	1925	ATCTGCTTGTAAATTTATCAATAAATAAATAATTTAAATAACAGCTAAAGTAAACAATAAT	1984
DB	15013	ACATTAGATTACTGTTCTATTTAGTTGATATTTTGTGTTTACTTTTGTGTTTATTTAAT	14954
QY	1985	ATCAAACTAATAAGAACAGTATCTAATGTAAACAAAACATAATCTAATGCTAATAATA	2044
DB	14953	ATTTGTTTATTTGATAAATTAACAAGCAGATTCGAATTTCTCAACAAAATATTTATTAAC	14894


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QY 3476 ACCTCTTTTTCACATACCTCTGTTCTTTCATGACAGATGATTTTTCAGGACTATGACACTAGC 3535
Db 17388 ACCCTTTTTCACATACCTCTGTTCTTTCATGACAGATGATTTTTCAGGACTATGACACTAGC 17447
QY 3536 GTATATGAATAGGTAGATGTTTATTTTGTGTCACACAAAAAGAGGCTCGACCTCTTTT 3595
Db 17448 GTATATGAATAGGTAGATGTTTATTTTGTGTCACACAAAAAGAGGCTCGACCTCTTTT 17507
QY 3596 TCTTATTTCTTTTATGATGATTTTAAATACGCGCATTTAGGACAAATAGCGAGTAGGCTGGATACG 3655
Db 17508 TCTTATTTCTTTTATGATGATTTTAAATACGCGCATTTAGGACAAATAGCGAGTAGGCTGGATACG 17567
QY 3656 ACGATTCGGTTTGAAGAAACATTTTGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCAC 3715
Db 17568 ACGATTCGGTTTGAAGAAACATTTTGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCAC 17627
QY 3716 CCGAAGAACATTTGAAGGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTT 3775
Db 17628 CCGAAGAACATTTGAAGGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTT 17687
QY 3776 GATTCATAGTCACTCGATATGTTGTTTACAGTATTAATGATGATGTTTATGCA 3835
Db 17688 GATTCATAGTCACTCGATATGTTGTTTACAGTATTAATGATGATGTTTATGCA 17747
QY 3836 AATCTAATTAATATTAATGATATTAATGATATTAATGATATTAATGATATTAATGAT 3895
Db 17748 AATCTAATTAATATTAATGATATTAATGATATTAATGATATTAATGATATTAATGAT 17807
QY 3896 CAAACTTG----- 3903
Db 17808 CAAAGTGGCATTAATAAAAGCATTTGCTCATTAATTTGTTGCAACGACAGGTCACTAT 17867
QY 3904 -----TCTAGAGTCTGCTT 3918
Db 17868 CAGTCAAAATAAATCAATTAATTTGGGCGCGAGATCCATGCTAGTCTAGAGTCTGCTT 17927
QY 3919 TAATGAGATATCGGAGACGCTATGATCGATGATATTTGCTTTCAATCTGTTGTCAC 3978
Db 17928 TAATGAGATATCGGAGACGCTATGATCGATGATATTTGCTTTCAATCTGTTGTCAC 17987
QY 3979 GTTGTAAATAAACTGAGATGTTAGTCTCAGATCCTTACCGCGGTTTCGGTTCAATCTTA 4038
Db 17988 GTTGTAAATAAACTGAGATGTTAGTCTCAGATCCTTACCGCGGTTTCGGTTCAATCTTA 18047
QY 4039 ATGAATATATACCGGTTACTATCGTATTTTATGAATAATATTCCTCGTTCAATTTACT 4098
Db 18048 ATGAATATATACCGGTTACTATCGTATTTTATGAATAATATTCCTCGTTCAATTTACT 18107
QY 4099 GATTGTACCTACTACTATATGATCAATATTAATAATGAAACAAATATATTTGCTGAT 4158
Db 18108 GATTGTACCTACTACTATATGATCAATATTAATAATGAAACAAATATATTTGCTGAT 18167
QY 4159 AGGTTTATAGCAGATCTATGATAGAGCGCCCAATAACAAACAAATTTGGTTTATTTAT 4218
Db 18168 AGGTTTATAGCAGATCTATGATAGAGCGCCCAATAACAAACAAATTTGGTTTATTTAT 18227
QY 4219 ACAATATCCAAATTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGATTAACATTA 4278
Db 18228 ACAATATCCAAATTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGATTAACATTA 18287
QY 4279 ATCTTATTCAAATTTAAAAAGGCCCCAGGGCTAGTATCTACGACACACCGAGCGCGAA 4338
Db 18288 ATCTTATTCAAATTTAAAAAGGCCCCAGGGCTAGTATCTACGACACACCGAGCGCGAA 18347
QY 4339 CTAATAACGTTTCACTAAGGAACTCCGGTTCCCGCGCGGCGGATGGGTGAGATTCTT 4398
Db 19348 CTAATAACGTTTCACTAAGGAACTCCGGTTCCCGCGCGGCGGATGGGTGAGATTCTT 18407
QY 4399 TGAAGTTGATATTTGGCCGCTCTACCGAAAGTTACGGGACCAATTCACACCGGCTCC 4458
Db 18408 TGAAGTTGATATTTGGCCGCTCTACCGAAAGTTACGGGACCAATTCACACCGGCTCC 18467
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QY 4459 AGCACGGCGCCGGGTAAACCGACTTGTGCTCCCGAGAAATATGACGATTTTGTGTGT 4518
Db 18468 AGCACGGCGCCGGGTAAACCGACTTGTGCTCCCGAGAAATATGACGATTTTGTGTGT 18527
QY 4519 ATGTGGSCCCCAATGAAGTGCAGGTCAAAACCTTGCAGTGACGACAAATCGTTGGGCGG 4578
Db 19528 ATGTGGSCCCCAATGAAGTGCAGGTCAAAACCTTGCAGTGACGACAAATCGTTGGGCGG 18587
QY 4579 GTCCAGGCGCAATTTTTCGCAACAATGTGAGGCTCAGCAGGACCTGCAGGCGATGCAAGC 4638
Db 18588 GTCCAGGCGCAATTTTTCGCAACAATGTGAGGCTCAGCAGGACCTGCAGGCGATGCAAGC 18647
QY 4639 TAGCTTACTAGTCAATGATATTTCTATAGTGTCACTAAATCTGC 4682
Db 18648 TAGCTTACTAGTCAATGATATTTCTATAGTGTCACTAAATCTGC 18691
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RESULT 5
ABQ82143/C
ID ABQ82143 standard; DNA; 17681 BP.
XX ABQ82143;
XX AC
XX AC
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
XX WO200259294-A1.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU000073.
XX
XX 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
PI
XX
XX WPI; 2002-692669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 17; Page 93-102; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a

Db 15280 CGTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTGGAGTGAATACACGACGATTT 15339
Qy 1727 ----- 1726
Db 15340 CCGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAAACCTGGGCTA 15399
Qy 1727 ----- 1726
Db 15400 TTTCCCTAAAGGGTTTATTGAGATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTT 15459
Qy 1727 ----- 1726
Db 15460 CACCAGTTTGAATTTAAACGTGGCCAAATATGGACAACACTTCTTCGCCCCCGCTTTTACCAT 15519
Qy 1727 ----- 1726
Db 15520 GGGGMAATATTATACGMAAGGGACAAGGTGCTGATGCCGTGGGATTCAGGTTTCATCA 15579
Qy 1727 ----- 1726
Db 15580 TGGCGTCTGTGATGCTCCATGTCGGCAGAACTGCTTAATGAATTTACAACAGTACTGGGA 15639
Qy 1727 ----- 1726
Db 15640 TGAGTGGCAGGGCGGGCGGTAATCGCGTGGATCGCGCTTACTAAAGCCAGATAACAGTA 15699
Qy 1727 ----- 1743
Db 15700 TGGCTATTGGCGCTGATTTTTGGGTTAAGAAATATATCTGATGTAATGTCGGGCCATA 15759
Qy 1744 ATAGTAATCTAGCTGGTGTGATGAATTAATATCAATGATAAATACTATAGTAAAAAT 1803
Db 15760 ATAGTAATCTAGCTGGTGTGATGAATTAATATCAATGATAAATACTATAGTAAAAAT 15819
Qy 1804 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1863
Db 15820 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15879
Qy 1864 ATCTATACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1923
Db 15880 ATCTATACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15939
Qy 1924 AATCTGCTGTAATTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1983
Db 15940 AATCTGCTGTAATTTATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15999
Qy 1984 TATCAAACTTAATAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGTAAATTAAC 2043
Db 16000 TATCAAACTTAATAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGTAAATTAAC 16059
Qy 2044 AAAGCGCAAGATCTATCAATTTATATAGTATTTTCAATCAACATTTCTTATTAATTTTC 2103
Db 16060 AAAGCGCAAGATCTATCAATTTATATAGTATTTTCAATCAACATTTCTTATTAATTTTC 16119
Qy 2104 TAAATTAATCTGTAGTTTATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAAT 2163
Db 16120 TAAATTAATCTGTAGTTTATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAAT 16179
Qy 2164 GTCGAATCAATTAACAAAGGTAACATGATGATCATGTCATGTTGTTATCATCTTATCTT 2223
Db 16180 GTCGAATCAATTAACAAAGGTAACATGATGATCATGTCATGTTGTTATCATCTTATCTT 16239
Qy 2224 ACATTTGGATTTGATTTACAGTTGGGAGCTGGGTTGAAATCGAATAGCTTGGCTGCGAGT 2283
Db 16240 ACATTTGGATTTGATTTACAGTTGGGAGGTTGGGTTGAAATCGAATAGCTTGGCTGCGAGT 16293
Qy 2284 TATCATCATCATCATAGACACAGGAAATTAAGTAATCATGATTAATCAATTAAGCTTATGTA 2343
Db 16294 CCTCTAGAGAGCTGACGCTGGATGGCAATAATGATTTTATTTTGAATGATGATGATGATG 16353
Qy 2344 ATATTGGCCCATTAACCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2403

Db 16354 TTCTGTGCAACAAA----- 16367
Qy 2404 AAAAAAATAAAGAGAGAAAAGGTCCTTAACCAAGAAAATGAAGAGAAAACCTAGAAAT 2463
Db 16368 ----- 16367
Qy 2464 TACCTGCACAAGCTTGGATCCTCTAGACCACTTTGTATCAAGAAAGCTGGAACAGAAACGT 2523
Db 16368 TTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTATCAAGAAAGCTGGAACAGAAACGT 16427
Qy 2524 AATATGATATAATATCAATATATTAATTTAGATTTTGCATATAAATAACAGACTACATAAT 2583
Db 16428 AATATGATATAATATCAATATATTAATTTAGATTTTGCATATAAATAACAGACTACATAAT 16487
Qy 2584 ACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 2643
Db 16488 ACTGTAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 16547
Qy 2644 TGTAGTCGATTAAGTTGGCAGCATCACCGACGCACTTTGGCGGCAATAAATACCTGTGA 2703
Db 16548 TGTAGTCGATTAAGTTGGCAGCATCACCGACGCACTTTGGCGGCAATAAATACCTGTGA 16607
Qy 2704 CGGAAGATCACTTCGCAAGATAAATAAATCTCTGTGTCTCTGTGTATACCGGGAAGCCT 2763
Db 16508 CGGAAGATCACTTCGCAAGATAAATAAATCTCTGTGTCTCTGTGTATACCGGGAAGCCT 16667
Qy 2764 GGGCCAACTTTTGGCGAAAATGAGACGTTTGTATCGG-----ATTTTCACAACTCTTATA 2815
Db 16668 GGGCCAACTTTTGGCGAAAATGAGACGTTTGTATCGGCACTACCCATTTTCACAACTCTTATA 16727
Qy 2816 CTTTTCCTTACAAGTCTGTTCCGGTTCATCTGGATTTTCAGCCTCTATCTACTATAACG 2875
Db 16728 CTTTTCCTTACAAGTCTGTTCCGGTTCATCTGGATTTTCAGCCTCTATCTACTATAACG 16787
Qy 2876 TGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGCTGTGTATAGGGAGC 2935
Db 16788 TGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGCTGTGTATAGGGAGC 16847
Qy 2936 CTGACATTTATPATTTCCCGAACAATCAGGTTTAATGGCGTTTTTGTATGTCATTTTCGCGGT 2995
Db 16848 CTGACATTTATPATTTCCCGAACAATCAGGTTTAATGGCGTTTTTGTATGTCATTTTCGCGGT 16907
Qy 2996 GGTGAGATCAGCCACTCTTCCCGGATAACGGAGACGGGCACTGGCCATATCGGTG 3055
Db 16908 GGTGAGATCAGCCACTCTTCCCGGATAACGGAGACGGGCACTGGCCATATCGGTG 16967
Qy 3056 TCATCATGCGGCGAGCTTTTCATCCCGGATATGACACACCGGGTAAAGTTTACGGGAGACTT 3115
Db 16968 TCATCATGCGGCGAGCTTTTCATCCCGGATATGACACACCGGGTAAAGTTTACGGGAGACTT 17027
Qy 3116 TATCTGACAGCAGCTGTCACCTGGCCAGGGGGATCACTATCCGTGCGCCGGCGGTGTCAA 3175
Db 17028 TATCTGACAGCAGCAGCTGTCACCTGGCCAGGGGGATCACTATCCGTGCGCCGGCGGTGTCAA 17087
Qy 3176 TAAATATCACTCTGTATACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3235
Db 17088 TAAATATCACTCTGTATACCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 17147
Qy 3236 CTTTAAACTGATTTTCAACAGTCCCTGTTCTCTGTCAGCAAAAGAGCGGCTTCAATTTCAATA 3295
Db 17148 CTTTAAACTGATTTTCAACAGTCCCTGTTCTCTGTCAGCAAAAGAGCGGCTTCAATTTCAATA 17207
Qy 3296 AACCGGGCGACCTCAGGCAATCCCTTCTGTAATTTTCCGCTTTCCAGCGGTCGGCGACGAGA 3355
Db 17208 AACCGGGCGACCTCAGGCAATCCCTTCTGTAATTTTCCGCTTTCCAGCGGTCGGCGACGAGA 17267
Qy 3356 CGACGGGCTTCAATTTCTGATGTTGTCTTACAGACCGGAGATATTTGACATCATATATG 3415
Db 17268 CGACGGGCTTCAATTTCTGATGTTGTCTTACAGACCGGAGATATTTGACATCATATATG 17327
Qy 3416 CTTTGAGCAACTGATGATGCTGCTGTCACCTGTCACCTGTCATGATAGCTGCTTCAAGCAC 3475
Db 17328 CTTTGAGCAACTGATGATGCTGCTGTCACCTGTCACCTGTCATGATAGCTGCTTCAAGCAC 17387

QY	26	GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATAATATCAATATATT	85	QY	1106	ATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTCCGATCAACGCTCTCATTTTCGCAA	1165
Db	13121	GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATAATATCAATATATT	13180	Db	14201	ATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTCCGATCAACGCTCTCATTTTCGCAA	14260
QY	86	AAATTAGATTTTGCATAAAAAAGACACTACATAATACCTGTAAAAACACACATATCCAGTC	145	QY	1166	AAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACACAGGATTTATTTATCTTCGGAAG	1225
Db	13181	AAATTAGATTTTGCATAAAAAAGACACTACATAATACCTGTAAAAACACACATATCCAGTC	13240	Db	14261	AAGTTGGCCAGGGCTTCCCGGTATCAACAGGGACACACAGGATTTATTTATCTTCGGAAG	14320
QY	146	ACTATGAATCAACTACTTAGATGGTATTAGTACACCTGTAGTCGACGAGCGCTTCCAAA	205	QY	1226	TGATCTTCGGTCAACAGGTATTTATTCGGCGCAAAAGTGGCTCGGGTATGCTGCCAATTA	1285
Db	13241	ACTATGAATCAACTACTTAGATGGTATTAGTACACCTGTAGTCGACGAGCGCTTCCAAA	13300	Db	14321	TGATCTTCGGTCAACAGGTATTTATTCGGCGCAAAAGTGGCTCGGGTATGCTGCCAATTA	14380
QY	206	TGTTCTTCGGGTGATCTCCAACTTATGTCGACGAGCGCTTCCAAATGTTCTCTCAA	265	QY	1286	GTGACTACAGGTCACTAATACCATCTAAGTAGTTGATTTCATGCTAGCTGATATGTTGT	1345
Db	13301	TGTTCTTCGGGTGATCTCCAACTTATGTCGACGAGCGCTTCCAAATGTTCTCTCAA	13360	Db	14381	GTGACTACAGGTCACTAATACCATCTAAGTAGTTGATTTCATGCTAGCTGATATGTTGT	14440
QY	266	ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATCGCGTATTAAATCATATAA	325	QY	1346	GTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATATGATATTT	1405
Db	13361	ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATCGCGTATTAAATCATATAA	13420	Db	1441	GTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATATGATATTT	14500
QY	326	AGAAATAAGAAAAAGGTGCGAGCGCTCTTTTTTGTGTGACAAAAAATAAATCATCTACCT	385	QY	1406	ATAICATTTTACGTTTCGCTTCAGCTTCTTTGTACAAAGTGG	1448
Db	13421	AGAAATAAGAAAAAGGTGCGAGCGCTCTTTTTTGTGTGACAAAAAATAAATCATCTACCT	13480	Db	14501	ATAICATTTTACGTTTCGCTTCAGCTTCTTTGTACAAAGTGG	14560
QY	386	ATTCATATACGTTAGTGTATAGTCTGTAATAATCATCTGATCAAGAAATTTCAAAAC	445	QY	1449	-----	1448
Db	13481	ATTCATATACGTTAGTGTATAGTCTGTAATAATCATCTGATCAAGAAATTTCAAAAC	13540	Db	14561	TGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCAGTCAAAATATAAATCATTTATTTGC	14620
QY	446	TCCTTATACCTTTCTCTTACAGTCTGTTTCGGCTTCTATCTGATTTTCAGGCTCTATACCTA	505	QY	1449	-----	1493
Db	13541	TCCTTATACCTTTCTCTTACAGTCTGTTTCGGCTTCTATCTGATTTTCAGGCTCTATACCTA	13600	Db	14621	CATCCAGCTGCGAGCTCCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAATAATATTT	14679
QY	506	CTAAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTGATA	565	QY	1494	TCCTTTTTCCTTTTAGTATAAAAATAGTTAAGTAGTGTAAATAGTATGATATAATAA	1553
Db	13601	CTAAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGCTGTGATA	13660	Db	14680	TCCTTTTTCCTTTTAGTATAAAAATAGTTAAGTAGTGTAAATAGTATGATATAATAA	14739
QY	566	AGGAGCTTGACATTTATATTCGCCAGACATCAGGTTAATGGCGTTTGTGATGTCATTT	625	QY	1554	TAGTTTGTATATTCGTGAAAAATAATTTATAAATATATTTGTTTACATAAAACACATAGT	1613
Db	13661	AGGAGCTTGACATTTATATTCGCCAGACATCAGGTTAATGGCGTTTGTGATGTCATTT	13720	Db	14740	TAGTTTGTATATTCGTGAAAAATAATTTATAAATATATTTGTTTACATAAAACACATAGT	14799
QY	626	TCGCGTGGCTGAGATCAGCACTTCTTCCCGATAAACGAGACCGGACACTGGCCATA	685	QY	1614	AATGTAAAAAATAATGACAAGTGTGTAAAGCGAAGAAGATAAAAGTTGAGAGTAAGT	1673
Db	13721	TCGCGTGGCTGAGATCAGCACTTCTTCCCGATAAACGAGACCGGACACTGGCCATA	13780	Db	14800	AATGTAAAAAATAATGACAAGTGTGTAAAGCGAAGAAGATAAAAGTTGAGAGTAAGT	14859
QY	686	TCGCGTGGCTGATGCGCCAGCTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG	745	QY	1674	ATATTATTTTATGATGATTTGATCCGACATGTAAAGTGTATGATGATGATGATGATGAT	1726
Db	13781	TCGCGTGGCTGATGCGCCAGCTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG	13840	Db	14860	ATATTATTTTATGATGATTTTGTATCGAATGTATGATGATGATGATGATGATGATGAT	14919
QY	746	GAGACTTTATCTGACAGCAGCTGCACTGCGCAGGGGGATCACCATCGCTCGCCGGGC	805	QY	1727	-----	1726
Db	13841	GAGACTTTATCTGACAGCAGCTGCACTGCGCAGGGGGATCACCATCGCTCGCCGGGC	13900	Db	14920	CAACTTTCACCATATGAAATAAGATCACTACCGGGCGTATTTTGTAGTTATCGAGATT	14979
QY	806	GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG	865	QY	1727	-----	1726
Db	13901	GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG	13960	Db	14980	TTTACGAGCTAAGGAAGCTAAAAATGGAGAAAAAATCACTGGATATACCCCGTTGATAT	15039
QY	866	GTGTAAACCTTAACTGCAATTTTCAAGTCCCTGTTTCTGTCAGCAAAAAGAGCGGTTTAT	925	QY	1727	-----	1726
Db	13961	GTGTAAACCTTAACTGCAATTTTCAAGTCCCTGTTTCTGTCAGCAAAAAGAGCGGTTTAT	14020	Db	15040	ATCCCAATGGCATCGTAAAGAACATTTTGTAGGCAATTTTGTAGGCAATTTTGTAGTGTGCTCAATGACCTTA	15099
QY	926	TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGGTTCCGG	985	QY	1727	-----	1726
Db	14021	TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGGTTCCGG	14080	Db	15100	TAACCCAGCGTTACGTGATATTTACGGCTTTTAAAGACCGTAAAGAAAAATAAGCA	15159
QY	986	ACGAGACGAGGGGCTTCAATCTGATGTTGTGTTTACAGACCGGAGATATTGACATC	1045	QY	1727	-----	1726
Db	14081	ACGAGACGAGGGGCTTCAATCTGATGTTGTGTTTACAGACCGGAGATATTGACATC	14140	Db	15160	CAAGTTTATCCGGCTTTTATTTTACATTTCTTCCCGCTGATGATGATGATGATGATGATGAT	15219
QY	1046	ATATATGCTTGACAACTGATAGCTGTGCTGTTCACTGTCTGATGATGATGATGATGATGAT	1105	QY	1727	-----	1726
Db	14141	ATATATGCTTGACAACTGATAGCTGTGCTGTTCACTGTCTGATGATGATGATGATGATGAT	14200	Db	15220	CGGTATGGCAATGAAAGACGAGCTGGTGTGATATGGGATAGTGTTCACCCCTGTTTACAC	15279
				QY	1727	-----	1726

3541 TGAATAGGTAGATGTTTATTTTATTTTGTACACAAAAAGAGGCTCGCACCTCTTTTCTTA 3600
Db |||||
16317 TGAATAGGTAGATGTTTATTTTGTACACAAAAAGAGGCTCGCACCTCTTTTCTTA 16376
Qy |||||
3601 TTTCTTTTATGATTAATACGGCATTCAGGCAATAGCGATAGGCTGGATACGACAT 3660
Db |||||
16377 TTTCTTTTATGATTAATACGGCATTCAGGCAATAGCGATAGGCTGGATACGACAT 16436
Qy |||||
3661 TCCGTTTGAAGAACATTTGAAGGCTGTCGCTGACCTAAGTTCGGCAGCATCACCCGAA 3720
Db |||||
16437 TCCGTTTGAAGAACATTTGAAGGCTGTCGCTGACCTAAGTTCGGCAGCATCACCCGAA 16496
Qy |||||
3721 GAACATTTGAAGGCTGTCGCTGACCTAAGTTCGGCAGCATCACCCGAA 3780
Db |||||
16497 GAACATTTGAAGGCTGTCGCTGACCTAAGTTCGGCAGCATCACCCGAA 16556
Qy |||||
3781 APAGTACGTGATATGTTGTTTATGATTAATAGTATGTTGTTTATGATTAATGTT 3840
Db |||||
16557 ATAGTACGTGATATGTTGTTTATGATTAATAGTATGTTGTTTATGATTAATGTT 16616
Qy |||||
3841 AATTTAATATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 3900
Db |||||
16617 AATTTAATATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 16676
Qy |||||
3901 TTGCTAGAGTCTCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 3960
Db |||||
16677 TTGCTAGAGTCTCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 16736
Qy |||||
3961 TTCATTTGTTGTCAGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 4020
Db |||||
16737 TTCATTTGTTGTCAGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 16796
Qy |||||
4021 CGTTTTGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 4080
Db |||||
16797 CGTTTTGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 16856
Qy |||||
4081 TTCTCGTTCAATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 4140
Db |||||
16857 TTCTCGTTCAATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 16916
Qy |||||
4141 CAATATATGTTGTCAGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 4200
Db |||||
16917 CAATATATGTTGTCAGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 16976
Qy |||||
4201 CAATTTGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 4260
Db |||||
16977 CAATTTGCTGTTTAAATGAGATATCGAGAGCGCTATGATCGCATGATTTGCT 17036
Qy |||||
4261 AAAAGACTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 4320
Db |||||
17037 AAAAGACTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 17096
Qy |||||
4321 GACACACGAGCGGCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 4380
Db |||||
17097 GACACACGAGCGGCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 17156
Qy |||||
4381 CGATGGGTGAGATTCCTTGAAGTTGATTAATGATTAATGATTAATGATTAATGATTAATGAT 4440
Db |||||
17157 CGATGGGTGAGATTCCTTGAAGTTGATTAATGATTAATGATTAATGATTAATGATTAATGAT 17216
Qy |||||
4441 CACATTTCAACCCGGTCCAGACCGCGCGGTTAAACCGATTCGTCGCCCGGAGATTAAT 4500
Db |||||
17217 CACATTTCAACCCGGTCCAGACCGCGCGGTTAAACCGATTCGTCGCCCGGAGATTAAT 17276
Qy |||||
4501 GCAGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4560
Db |||||
17277 GCAGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 17336
Qy |||||
4561 CGACAAATCGTTGGCGGGTCCAGGCGGAAATTTTGGCAGCAACATGTCGAGGCTCAGCAGG 4620
Db |||||
17337 CGACAAATCGTTGGCGGGTCCAGGCGGAAATTTTGGCAGCAACATGTCGAGGCTCAGCAGG 17396
Qy |||||
4621 ACCTGCGGCGGAGCAAGCTAGCTTACTAGTATGATTAATGATTAATGATTAATGATTAATGAT 4680

Db 17397 ACCTGCGGCGGAGCAAGCTAGCTTACTAGTATGATTAATGATTAATGATTAATGAT 17456
Qy 4681 GC 4682
Db 17457 GC 17458
RESULT 4
ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.
XX
AC ABQ82130;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ds.
XX Synthetic.
XX WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
XX 29-NOV-2001; 2001US-0333743P.
XX
(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX
PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 13; Page 62-72; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention

XX Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

Query Match 68.3%; Score 3199.6; DB 6; Length 18691;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 4460; Conservative 0; Mismatches 84; Indels 1140; Gaps 7;

KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX Synthetic.
OS WO200259294-A1.
PN 01-AUG-2002.
XX 24-JAN-2002; 2002WO-AU000073.
XX 26-JAN-2001; 2001US-0264067P.
XX 29-NOV-2001; 2001US-0333743P.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
XX stranded RNA.
PS Claim 16; Page 83-93; 104pp; English.
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 89.7%; Score 4200; DB 6; Length 17458;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 4449; Conservative 0; Mismatches 10; Indels 223; Gaps 2;
QY 1 TTTTCATTTGGAGGAGGACGCTCGAGCAAGTTTGTACAAAAAGCTGAACGAGAAACGT 60
DB 13000 TTTTCATTTGGAGGAGGACGCTCGAGCAAGTTTGTACAAAAAGCTGAACGAGAAACGT 13059
QY 61 AAAATGATATAAATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 13060 AAAATGATATAAATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 13119
QY 121 ACTGTAAACACCAATATCCAGTCACTATGAATCAACTACTTAGATGTTATTAGTGACC 180
DB 13120 ACTGTAAACACCAATATCCAGTCACTATGAATCAACTACTTAGATGTTATTAGTGACC 13179
QY 181 TGTAGTTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCG 240
DB 13180 TGTAGTTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGTCGCCAACTTAGTCGACCG 13239
QY 241 ACAGCCTTCCAAATGTTCTTCTCAACAGGAAATCGTCGTATCCAGCCTACTCGCTATTGTC 300

DB 13240 ACAGCCTTCCAAATGTTCTTCTCAACAGGAAATCGTCGTATCCAGCCTACTCGCTATTGTC 13299
QY 301 CTCAAATGCGGTATTAATAATCAATAAAGAAATAGAAAAAGAGGTGGAGCCTCTTTTTTGG 360
DB 13300 CTCAAATGCGGTATTAATAATCAATAAAGAAATAGAAAAAGAGGTGGAGCCTCTTTTTTGG 13359
QY 361 TGTGACAAAAATAAAAAACATCTACCTATTATATACGCTAGTGTCAATAGTCTGAAATCA 420
DB 13360 TGTGACAAAAATAAAAAACATCTACCTATTATATACGCTAGTGTCAATAGTCTGAAATCA 13419
QY 421 TCTGATCAAGAAACAAATTTTCAAACTCTTATATCTTTCTTCAAGTCTGTCGGCTTCA 480
DB 13420 TCTGATCAAGAAACAAATTTTCAAACTCTTATATCTTTCTTCAAGTCTGTCGGCTTCA 13479
QY 481 TCTGGATTTTTCAGCCTCTATACCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 540
DB 13480 TCTGGATTTTTCAGCCTCTATACCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 13539
QY 541 TCGACCTGACAGCTGGCTGTGTATAAGGGAGCCTGACATTTATATTTCCCGAGAACATCAG 600
DB 13540 TCGACCTGACAGCTGGCTGTGTATAAGGGAGCCTGACATTTATATTTCCCGAGAACATCAG 13599
QY 601 GTTAATGCGGTGTTTGTAGTGCATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGCAT 660
DB 13600 GTTAATGCGGTGTTTGTAGTGCATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGCAT 13659
QY 661 AACGGAGACGGGCACACTGGCCATATCGGTGGTTCATCATCGCCAGCTTTTATCCCGCAT 720
DB 13660 AACGGAGACGGGCACACTGGCCATATCGGTGGTTCATCATCGCCAGCTTTTATCCCGCAT 13719
QY 721 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAG 780
DB 13720 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAG 13779
QY 781 GGGATCACCATCCGTCGCGCGGCGTCAATAATATCATCTGTATCATCCACAAACAG 840
DB 13780 GGGATCACCATCCGTCGCGCGGCGTCAATAATATCATCTGTATCATCCACAAACAG 13839
QY 841 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGT 900
DB 13840 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACCTGATTTTCAACAGTCCCTGT 13899
QY 901 TCTCGTACGAAAAAGAGCGGTTCATTTCAATAAACCGGCGACCTCAGCATCTCCCTTCT 960
DB 13900 TCTCGTACGAAAAAGAGCGGTTCATTTCAATAAACCGGCGACCTCAGCATCTCCCTTCT 13959
QY 961 GATTTTCGCTTTCCAGGTTTCGCGACGACGAGCGGCTTCATTTTGCATGTTGTGTC 1020
DB 13960 GATTTTCGCTTTCCAGGTTTCGCGACGACGAGCGGCTTCATTTTGCATGTTGTGTC 14019
QY 1021 TTACGACGCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTC 1080
DB 14020 TTACGACGCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTC 14079
QY 1081 AACTGTCACTGTATACGCTGCTTCAAGCACTCTTTTGTGACATCTTGGGTAGTG 1140
DB 14080 AACTGTCACTGTATACGCTGCTTCAAGCACTCTTTTGTGACATCTTGGGTAGTG 14139
QY 1141 CCGATCAACGCTCTCATTTTTCGCCAAAAGTTGCCCGAGGCTTCCCGGTATCAACAGGAC 1200
DB 14140 CCGATCAACGCTCTCATTTTTCGCCAAAAGTTGCCCGAGGCTTCCCGGTATCAACAGGAC 14199
QY 1201 ACCAGATTTATTTATCTGCGAAGTGTCTTCGCTGACAGGTATTTATTCGGCGCAAG 1260
DB 14200 ACCAGATTTATTTATCTGCGAAGTGTCTTCGCTGACAGGTATTTATTCGGCGCAAG 14259
QY 1261 TCGGTGCGGTGATGCTGCCAACTTAGTGCATACAGGTCACTAATACCATCTAAGTAGTT 1320
DB 14260 TCGGTGCGGTGATGCTGCCAACTTAGTGCATACAGGTCACTAATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTCTGATATGTTGTGTTTACAGTATTTATGATGTTGTTTATGTCAT 1380

Db 15495 TGACGGAATCACTTCGCAAGATAAATAATCTCGTGTCCCTGTTGATACGGGAAGC 15554
Qy 2761 CCTGGGCCAATCTTTGGCGAAAATGAGACGTTGATCGGAATTCACAACTCTTATACCTTTT 2820
Db 15555 CCTGGGCCAATCTTTGGCGAAAATGAGACGTTGATCGGAATTCACAACTCTTATACCTTTT 15614
Qy 2821 CTCTTACAAGTCGTTCCGCTTCACTCGATTTTCAAGCCTCTATATCTTACTTAAACGCTGATA 2880
Db 15615 CTCTTACAAGTCGTTCCGCTTCACTCGATTTTCAAGCCTCTATATCTTACTTAAACGCTGATA 15674
Qy 2881 AAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTCGGCTGTGTATAGAGGAGCCTGAC 2940
Db 15675 AAGTTTCTGTAATTTCTACTGTATCGACCTCGACACTCGGCTGTGTATAGAGGAGCCTGAC 15734
Qy 2941 ATTATATATCCCGAAGACATCAGGTAAATGCGGTTTTTGTATGTCATTTTCGCGGTGGCTG 3000
Db 15735 ATTATATATCCCGAAGACATCAGGTAAATGCGGTTTTTGTATGTCATTTTCGCGGTGGCTG 15794
Qy 3001 AGATCAGCCACTTCTTCCCGAATAACGGAGACCGGCACACTGGCCATATCGGTGTCTATC 3060
Db 15795 AGATCAGCCACTTCTTCCCGAATAACGGAGACCGGCACACTGGCCATATCGGTGTCTATC 15854
Qy 3061 ATGCGCCAGCTTTTATCCCGGATATGACACCGGGTAAAGTTTACGGGAGACTTTATCT 3120
Db 15855 ATGCGCCAGCTTTTATCCCGGATATGACACCGGGTAAAGTTTACGGGAGACTTTATCT 15914
Qy 3121 GACGACAGCTGACACTCGCGAGGGGATCACATCCGTCGCGCGGGGTGTCAATAATA 3180
Db 15915 GACGACAGCTGACACTCGCGAGGGGATCACATCCGTCGCGCGGGGTGTCAATAATA 15974
Qy 3181 TCACCTCTGTACATCCACAAACAGACGATAAGCGCTCTCTCTTTTATAGGTGTAAACCTTA 3240
Db 15975 TCACCTCTGTACATCCACAAACAGACGATAAGCGCTCTCTCTTTTATAGGTGTAAACCTTA 16034
Qy 3241 AACTGCATTTACCACTGCTCTTCTGTCAGCAAAAGACCGGTCATTTCAATTAACCG 3300
Db 16035 AACTGCATTTACCACTGCTCTTCTGTCAGCAAAAGACCGGTCATTTCAATTAACCG 16094
Qy 3301 GCGACCTCAGGCATCCCTTCTGATTTTCCGCTTCCAGCGTTCCGACGCGACGACG 3360
Db 16095 GCGACCTCAGGCATCCCTTCTGATTTTCCGCTTCCAGCGTTCCGACGCGACGACG 16154
Qy 3361 GCGCTTCACTTCGATGTTGCTTACACAGACCGAGATATTGAATCATATATATGCTT 3420
Db 16155 GCGCTTCACTTCGATGTTGCTTACACAGACCGAGATATTGAATCATATATATGCTT 16214
Qy 3421 AGCACTGATAGCTGTCGCTGTCACCTGCTAATACGCTGCTTCTATGACACACCTC 3480
Db 16215 AGCACTGATAGCTGTCGCTGTCACCTGCTAATACGCTGCTTCTATGACACACCTC 16274
Qy 3481 TTTTGTACATCTCTGTTCTGATGACAGATATTTTCAGGACTATGACACTAGCGTATA 3540
Db 16275 TTTTGTACATCTCTGTTCTGATGACAGATATTTTCAGGACTATGACACTAGCGTATA 16334
Qy 3541 TGAATAGGTAGATGTTTTTATTTGTACACAAAAGAGGTCGACCTCTTTTCTTA 3600
Db 16335 TGAATAGGTAGATGTTTTTATTTGTACACAAAAGAGGTCGACCTCTTTTCTTA 16394
Qy 3601 TTTCTTTTATGATTTAATACGCAATGAGGACATAGCGAGTAGGCTGGATACGACGAT 3660
Db 16395 TTTCTTTTATGATTTAATACGCAATGAGGACATAGCGAGTAGGCTGGATACGACGAT 16454
Qy 3661 TCGTTTGTAGAGAAACATTTGGAAGCTGTTCGTCGACTAAGTTGGCAGCATCACCCGAA 3720
Db 16455 TCGTTTGTAGAGAAACATTTGGAAGCTGTTCGTCGACTAAGTTGGCAGCATCACCCGAA 16514
Qy 3721 GAACATTTGGAAGCTGTTCGTCGACTACAGGTCACTAATACCATCTAAGTAGTAGTTC 3780
Db 16515 GAACATTTGGAAGCTGTTCGTCGACTACAGGTCACTAATACCATCTAAGTAGTAGTTC 16574
Qy 3781 ATAGTGACTGGATGATGTTGTTTTTACAGTATATGTCGTTTTTATGCAAAATCT 3840

Db 16575 ATAGTGACTGGATATGTTGTTTTTACAGTATATGTCGTTTTTATGCAAAATCT 16634
Qy 3841 AATTTAATAATATGATATTTTATATCAATTTTACGTTTCTCGTTTTCAGCTTTTTCGTACAAAC 3900
Db 16635 AATTTAATAATATGATATTTATATCAATTTTACGTTTCTCGTTTTCAGCTTTTTCGTACAAAC 16694
Qy 3901 TTTCTAGAGTCTGCTCTTTAATGAGATATCGAGACGCTTATGATCGCATGATATTGCT 3960
Db 16695 TTTCTAGAGTCTGCTCTTTAATGAGATATCGAGACGCTTATGATCGCATGATATTGCT 16754
Qy 3961 TTTCAATTTCTGTTGTCAGCTTTTAAACCTGAGCATGTTGAGCTCAGATCCTTACCGC 4020
Db 16755 TTTCAATTTCTGTTGTCAGCTTTTAAACCTGAGCATGTTGAGCTCAGATCCTTACCGC 16814
Qy 4021 CGGTTTCCGTTCTCAATCTTAATGAATATATCACCCGTTTACTACTGATTTTATGAATAATA 4080
Db 16815 CGGTTTCCGTTCTCAATCTTAATGAATATATCACCCGTTTACTACTGATTTTATGAATAATA 16874
Qy 4081 TTTCTCCGTTCAATTTACTGATTTGTAACCTTACTTATATGTAATATTAATAATGAAA 4140
Db 16875 TTTCTCCGTTCAATTTACTGATTTGTAACCTTACTTATATGTAATATTAATAATGAAA 16934
Qy 4141 CAATATATTTGCTGTAATAGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAA 4200
Db 16935 CAATATATTTGCTGTAATAGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAA 16994
Qy 4201 CAATTTGCGTTTTTATTATTACAAATCCAAATTTTAAAAAAGCGGACAAACCGTCAACCT 4260
Db 16995 CAATTTGCGTTTTTATTATTACAAATCCAAATTTTAAAAAAGCGGACAAACCGTCAACCT 17054
Qy 4261 AAAAGACTGATTAATATAATTTTCAAAATTTTCAAAAGGCCCCAGGGCTAGTATCTAC 4320
Db 17055 AAAAGACTGATTAATATAATTTTCAAAATTTTCAAAAGGCCCCAGGGCTAGTATCTAC 17114
Qy 4321 GACACACGAGCGCGCAACTAAATAACCTTCACTGAAGGAACTCCGCTTCCCGCCCGCG 4380
Db 17115 GACACACGAGCGCGCAACTAAATAACCTTCACTGAAGGAACTCCGCTTCCCGCCCGCG 17174
Qy 4381 CGCATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCCGCTCGCTCTACCGAAAGTTACGG 4440
Db 17175 CGCATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCCGCTCGCTCTACCGAAAGTTACGG 17234
Qy 4441 CACCATTAACCCGTCAGACACCGCGCGCGGTAAACCGACTTCTGCTCCCGCAGATTAAT 4500
Db 17235 CACCATTAACCCGTCAGACACCGCGCGCGGTAAACCGACTTCTGCTCCCGCAGATTAAT 17294
Qy 4501 GCAGCATTTTTTGTGTATGTCGGGCCCCCAATGAAGTGCAGGTCAAACTTTGACAGTGA 4560
Db 17295 GCAGCATTTTTTGTGTATGTCGGGCCCCCAATGAAGTGCAGGTCAAACTTTGACAGTGA 17354
Qy 4561 CGCAAAATCGTTGGCGGGTCCAGGGCGAAATTTTTCGCAAAACNTGTCGAGGCTCAGCAGG 4620
Db 17355 CGCAAAATCGTTGGCGGGTCCAGGGCGAAATTTTTCGCAAAACNTGTCGAGGCTCAGCAGG 17414
Qy 4621 ACCTGCAGGCTGAAGCTAGTCTAGTATCATATTTCTATAGTCTCAGCTTAAATCT 4680
Db 17415 ACCTGCAGGCTGAAGCTAGTCTAGTATCATATTTCTATAGTCTCAGCTTAAATCT 17474
Qy 4681 GC 4682
Db 17475 GC 17476

RESULT 3

ABQ82142

ID ABQ82142 standard; DNA; 17458 BP.

XX AC ABQ82142;

XX AC ABQ82142;

DT 11-DEC-2002 (first entry)

XX DE Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.

QY 541 TCGACCTGCAGACTGGCTGTGTATATAAGGAGCCTGCACATTATATCCCGAGACATCAG 600
Db 13540 TCGACCTGCAGACTGGCTGTGTATAAGGAGCCTGCACATTATATCCCGAGACATCAG 13599
QY 601 GTTAATGCGGTTTTGATGTCAATTTTCGCGGTGGCTGAGATCAGCCACTCTTCCCGCAT 660
Db 13600 GTTAATGCGGTTTTGATGTCAATTTTCGCGGTGGCTGAGATCAGCCACTCTTCCCGCAT 13659
QY 661 AACGGAGACCGGCACACTGGCCATATCGTGTGATCATCATGCGCCAGCTTTTCATCCCGCAT 720
Db 13660 AACGGAGACCGGCACACTGGCCATATCGTGTGATCATCATGCGCCAGCTTTTCATCCCGCAT 13719
QY 721 ATGCACACCGGGTAAAGTTTACCGGAGACTTTATCTGCACAGCAGAGCTGCAGTGGCCAG 780
Db 13720 ATGCACACCGGGTAAAGTTTACCGGAGACTTTATCTGCACAGCAGAGCTGCAGTGGCCAG 13779
QY 781 GGGGATCACCATCCGTCCCGCGGGGGTGTCAATATATCATCTGTACATCCACAAACAG 840
Db 13780 GGGGATCACCATCCGTCCCGCGGGGGTGTCAATATATCATCTGTACATCCACAAACAG 13839
QY 841 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAATTCACCAAGTCCCTGT 900
Db 13840 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAATTCACCAAGTCCCTGT 13899
QY 901 TCTCGTACGAAAAGAGCGGTTCAATTTCAATAAACCGGGGACCTCAGCCATCCCTTCCT 960
Db 13900 TCTCGTACGAAAAGAGCGGTTCAATTTCAATAAACCGGGGACCTCAGCCATCCCTTCCT 13959
QY 961 GATTTTCGGCTTCAGAGGTTCCGACGACGACGAGCGGCTTCATCTGCAATGGTGTGC 1020
Db 13960 GATTTTCGGCTTCAGAGGTTCCGACGACGACGAGCGGCTTCATCTGCAATGGTGTGC 14019
QY 1021 TTACAGACCGGAGATATGACATCATATATGCGCTTGAGCAACTGATAGCTGTCCCTGTC 1080
Db 14020 TTACAGACCGGAGATATGACATCATATATGCGCTTGAGCAACTGATAGCTGTCCCTGTC 14079
QY 1081 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGT 1140
Db 14080 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGT 14139
QY 1141 CCGATCAACGTCATTTTCGCCAAAGTTGGCCAGGCTTCCGGTATCAACAGGAC 1200
Db 14140 CCGATCAACGTCATTTTCGCCAAAGTTGGCCAGGCTTCCGGTATCAACAGGAC 14199
QY 1201 ACCAGGATTTATTTATCTCGAAGTGATCTTCCGTCAAGGTATTTATTCGGCGCAAG 1260
Db 14200 ACCAGGATTTATTTATCTCGAAGTGATCTTCCGTCAAGGTATTTATTCGGCGCAAG 14259
QY 1261 TCGGTCCGGGTGATGTCGCAACTTATAGTCGATACAGGTCACTAATACCATCTAAGTAGTT 1320
Db 14260 TCGGTCCGGGTGATGTCGCAACTTATAGTCGATACAGGTCACTAATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTCACTGGATATGTTGTGTTTACAGTATTATGATGATGCTGTTTTTATGCAA 1380
Db 14320 GATTCATAGTCACTGGATATGTTGTGTTTACAGTATTATGATGATGCTGTTTTTATGCAA 14379
QY 1381 AATCTAAATTAATATATTTATATATCAATTTTACGTTTCTCGTTCAGCTTTCTTGTA 1440
Db 14380 AATCTAAATTAATATATTTATATATCAATTTTACGTTTCTCGTTCAGCTTTCTTGTA 14439
QY 1441 CAAAGTGTCTCGAGAAATTCGGTACCCAGCTTCGGTAAGGAAATAATTTATTTCTTTTT 1500
Db 14440 CAAAGTGTCTCGAGAAATTCGGTACCCAGCTTCGGTAAGGAAATAATTTATTTCTTTTT 14499
QY 1501 TCCCTTTAGTAAATAGTTAAGTCACTTAATAGTATGATTAATAATATAGTTGT 1560
Db 14500 TCCCTTTAGTAAATAGTTAAGTCACTTAATAGTATGATTAATAATATAGTTGT 14559
QY 1561 TATAATTTGAAAAAATAATTTTATAAATATATTTTGTATATAAACAACATAGTAATGTAA 1620
Db 14560 TATAATTTGAAAAAATAATTTTATAAATATATTTTGTATATAAACAACATAGTAATGTAA 14619

QY 1621 AAAAAATATGCAAGTGATGTGTAAGCAAGAGATATAAAAGTTGAGAGTAAGTATATAT 1680
Db 14620 AAAAAATATGCAAGTGATGTGTAAGCAAGAGATATAAAAGTTGAGAGTAAGTATATAT 14679
QY 1681 TTTTAAATGAAATTTGATCGACATGTAGATGATATCTAGCATTAATATTTGTTTAAATC 1740
Db 14680 TTTTAAATGAAATTTGATCGAATGTAGATGATATCTAGCATTAATATTTGTTTAAATC 14739
QY 1741 ATAATAGTAATTTCTAGCTGTTTATGAAATTAATATCAATGATATAAATACTATAGTAAA 1800
Db 14740 ATAATAGTAATTTCTAGCTGTTTATGAAATTAATATCAATGATATAAATACTATAGTAAA 14799
QY 1801 AATAAGTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1860
Db 14800 AATAAGTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 14859
QY 1861 AATATCTATACCATTTATCAATATTTTATGTTTAAAGCTTAATAATAATTTGTTTAAAT 1920
Db 14860 AATATCTATACCATTTATCAATATTTTATGTTTAAAGCTTAATAATAATTTGTTTAAAT 14919
QY 1921 TCCAACTGCTGTGTAATTTTATCAATAAACAATAATAATAATAATAATAATAATAATA 1980
Db 14920 TCCAACTGCTGTGTAATTTTATCAATAAACAATAATAATAATAATAATAATAATAATA 14979
QY 1981 TAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAACTAATCTAATGCTAATAT 2040
Db 14980 TAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAACTAATCTAATGCTAATAT 15039
QY 2041 AACAAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATCTTATTAAT 2100
Db 15040 AACAAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATCTTATTAAT 15099
QY 2101 TTTCAATAATACTGTGTAGTTTATTAACCTCTAAATGGATGATGATTAATAATAATA 2160
Db 15100 TTTCAATAATACTGTGTAGTTTATTAACCTCTAAATGGATGATGATTAATAATAATA 15159
QY 2161 TTAGTCGAACATGAAATAAACAAGGTAAACATGATGATGATGATGATGATGATGATGAT 2220
Db 15160 TTAGTCGAACATGAAATAAACAAGGTAAACATGATGATGATGATGATGATGATGATGAT 15219
QY 2221 CTTTACATTTGGATTTGATTTACAGTTTGGGAAGCTGGGTTTCAAAATCGATGATGATGAT 2280
Db 15220 CTTTACATTTGGATTTGATTTACAGTTTGGGAAGCTGGGTTTCAAAATCGAT 15266
QY 2281 AGTTATCATCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db 15267 AGTTATCATCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 15266
QY 2341 GTAAATTTTGGCCCATTAACCAATCAATTAATAAATAAGATGATGATGATGATGATGAT 2400
Db 15267 GTAAATTTTGGCCCATTAACCAATCAATTAATAAATAAGATGATGATGATGATGATGAT 15266
QY 2401 CTCAAAAAATAAAAAAGAGAAAAAGGCTCTTAACCAAAAAATGAAGGAGAAAAAAGTAA 2460
Db 15267 CTCAAAAAATAAAAAAGAGAAAAAGGCTCTTAACCAAAAAATGAAGGAGAAAAAAGTAA 15266
QY 2461 ATTTACCTGCAACAGCTTTGGATCTCTAGACCACTTTGTGCAAGAAAGCTGAAACGAGAAA 2520
Db 15267 ATTTACCTGCAACAGCTTTGGATCTCTAGACCACTTTGTGCAAGAAAGCTGAAACGAGAAA 15314
QY 2521 CGTAAATGATATAAATAATCAATATTAATAATTAAGATTTTGCATAAATAAACAAGTACAT 2580
Db 15315 CGTAAATGATATAAATAATCAATATTAATAATTAAGATTTTGCATAAATAAACAAGTACAT 15374
QY 2581 AATCTGTAAAAACAACAATATCCAGTCACATCAATCAACTACTTACTTACTTACTTACTTACT 2640
Db 15375 AATCTGTAAAAACAACAATATCCAGTCACATCAATCAACTACTTACTTACTTACTTACTTACT 15434
QY 2641 ACCTGTAGTCGACTAAGTTGGCAGATCAACCGCAGCACTTTTGGCCGCAATTAATACCTG 2700
Db 15435 ACCTGTAGTCGACTAAGTTGGCAGATCAACCGCAGCACTTTTGGCCGCAATTAATACCTG 15494
QY 2701 TGACGGAAGATCACTTCGACGAATAATAATAATCTCGTGTCTCTGTTGATACCGGAGAC 2760

QY	4081	TTCTCCGTTTCAATTTACTGATTTGTTACCTTACTTCTATATGTACAAATTTAAATGAAA	4140
Db	17080	TTCTCCGTTTCAATTTACTGATTTGTTACCTTACTTCTATATGTACAAATTTAAATGAAA	17139
QY	4141	CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGCGGCCAATAACAAA	4200
Db	17140	CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGCGGCCAATAACAAA	17199
QY	4201	CAATTCCGTTTATTATTACAAATCCAAATTTTAAAAAGCGGCGAGAACCGGTCAAACCT	4260
Db	17200	CAATTCCGTTTATTATTACAAATCCAAATTTTAAAAAGCGGCGAGAACCGGTCAAACCT	17259
QY	4261	AAAAGACTGATTTACATABAATCTTATTCAAAATTTCAAAGGCCCCACAGGCGCTAGTATCTAC	4320
Db	17260	AAAAGACTGATTTACATABAATCTTATTCAAAATTTCAAAGGCCCCACAGGCGCTAGTATCTAC	17319
QY	4321	GACACACCGAGCGCGGAACTAATAACGGTTCACTGAAGGAACTCCGGTTCCCGCGCGCG	4380
Db	17320	GACACACCGAGCGCGGAACTAATAACGGTTCACTGAAGGAACTCCGGTTCCCGCGCGCG	17379
QY	4381	CGCATGGGTGAGATTCCTTTGAAGTTGAGTATTGGCCGTCGCTCTACCGAAGTTACGGG	4440
Db	17380	CGCATGGGTGAGATTCCTTTGAAGTTGAGTATTGGCCGTCGCTCTACCGAAGTTACGGG	17439
QY	4441	CACATTTCACCCGGTCCAGCAGCGCGCGGGTAAACCGACTTGCTGCCCGAGAAATTAT	4500
Db	17440	CACATTTCACCCGGTCCAGCAGCGCGCGGGTAAACCGACTTGCTGCCCGAGAAATTAT	17499
QY	4501	GCAGCATTTTTTTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGAACGTGA	4560
Db	17500	GCAGCATTTTTTTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGAACGTGA	17559
QY	4561	CGCAAAATCGTTGGGCGGGTCCAGGCGGAATTTTGGCGACAAACATGTCGAGGCTCAGCAGG	4620
Db	17560	CGCAAAATCGTTGGGCGGGTCCAGGCGGAATTTTGGCGACAAACATGTCGAGGCTCAGCAGG	17619
QY	4621	ACCTGCAGGCATGCAAGCTAGCTTACTAGTGTATGCATATTTCTATAGTGTCACTAAATCT	4680
Db	17620	ACCTGCAGGCATGCAAGCTAGCTTACTAGTGTATGCATATTTCTATAGTGTCACTAAATCT	17679
QY	4681	GC 4682	
Db	17680	GC 17681	

RESULT 2
ABQ82141
ID ABQ82141 standard; DNA: 17476 BP.

XX
DE
Accceptor vector pHELLSGATE 8 nucleotide sequence
DE
ID NO:24.

XX Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX

OS Synthetic.

XX PN WO200259294-A1.

XX
PD
01-AUG-2002-

24-JAN-2002 2002W0-AT0000073

26 JAN-2001: 2001US-0364067B

PR 26--JAN-2001; 2001US-0264067P.
 PR 28--NOV-2001; 2001US-0333743P

XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.XX
PT Wesley S. Waterhouse P. Helliwell C:

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 15: Page 74-83; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.

Sequence 17476 BP: 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

every Match 91.0%; Score 4262; DB 6; Length 17476;
 1st Local Similarity 95.6%; Pred. No. 0;
 Matches 4477; Conservative 0; Mismatches 0; Indels 205;

Qy	1	TTTCATTTTGGAGGAGCAGCGCTCGAGACGAGTCTTCTGACAAAGAAAGCTCGAACGAGAAACGT	60
Db	13000	TTTCATTTTGGAGGAGCAGCGCTCGAGACGAGTCTTCTGACAAAGAAAGCTCGAACGAGAAACGT	13059
Qy	61	AAAATGATATAAATATCAATATATTAAATTTAGATTTTGCATAAAAAAGACACTACATAAT	120
Db	13060	AAAATGATATAAATATCAATATATTAAATTTAGATTTTGCATAAAAAAGACACTACATAAT	13119
Qy	121	ACTGTAAAAACACACATATCCAGTCCAGTCACTATGAATCAACTACTATGATCGTATTAGTGACC	180
Db	13120	ACTGTAAAAACACACATATCCAGTCCAGTCACTATGAATCAACTACTATGATCGTATTAGTGACC	13179
Qy	181	TGTAGTTCGACCGACAGCCCTTCCAAATGTGTTCTTTCGGGTGATGTCGCCAACTTAGTGCACCG	240
Db	13180	TGTAGTTCGACCGACAGCCCTTCCAAATGTGTTCTTTCGGGTGATGTCGCCAACTTAGTGCACCG	13239
Qy	241	ACAGCCTTCCAAATGTGTTCTTCCAAACGGAATCGTTCGATACAGCCTACTCGCTATTCTGC	300
Db	13240	ACAGCCTTCCAAATGTGTTCTTCCAAACGGAATCGTTCGATACAGCCTACTCGCTATTCTGC	13299
Qy	301	CTCAATGCCCGTATTAATATCATAAAAAGAAATTAAGAAAAAGAGGTCGAGCCCTCTTTTTTG	360
Db	13300	CTCAATGCCCGTATTAATATCATAAAAAGAAATTAAGAAAAAGAGGTCGAGCCCTCTTTTTTG	13359
Qy	361	TGTGACAAATAAAAAACATCTACCTATTCAATATACGCTAGTGTGCATAGTCTGGAATAACA	420
Db	13360	TGTGACAAATAAAAAACATCTACCTATTCAATATACGCTAGTGTGCATAGTCTGGAATAACA	13419
Qy	421	TCTGCAATCAAGAACAAATTTACAAACCTCTTATACCTTTCTCTTACAAGTCGTTCCGGCTTCA	480
Db	13420	TCTGCAATCAAGAACAAATTTACAAACCTCTTATACCTTTCTCTTACAAGTCGTTCCGGCTTCA	13479
Qy	481	TCTGGATTTTTCAGCCCTCTATACCTACTAAACGCGATATAAGTTCTCTGTAATTTCTACTGTA	540
Db	13480	TCTGGATTTTTCAGCCCTCTATACCTACTAAACGCGATATAAGTTCTCTGTAATTTCTACTGTA	13539

Db 14860 AATATCTATACCAATTAACAATAATTTTAGTTTAAAGTTAAATAATATTTTGTAGAAAT 14919
Qy 1921 TCCAACTCTGCTGTAAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTAACAAA 1980
Db 14920 TCCAACTCTGCTGTAAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTAACAAA 14979
Qy 1981 TAAATATCAAACTAAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAAT 2040
Db 14980 TAAATATCAAACTAAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAAT 15039
Qy 2041 AACAAAGCGCAAGACTATCATTTTATATAGTATTAATTTTCAATCAACATCTTATTAAT 2100
Db 15040 AACAAAGCGCAAGACTATCATTTTATATAGTATTAATTTTCAATCAACATCTTATTAAT 15099
Qy 2101 TTCTAAATTAATCTAGTTTATTAATCTTCTAATGGAATGACTATTAATTAATGA 2160
Db 15100 TTCTAAATTAATCTAGTTTATTAATCTTCTAATGGAATGACTATTAATTAATGA 15159
Qy 2161 TTAGTCGAACATGAATAACAAGGTAAACATGATAGATCATGTGCTATGCTTATGAT 2220
Db 15160 TTAGTCGAACATGAATAACAAGGTAAACATGATAGATCATGTGCTATGCTTATGAT 15219
Qy 2221 CTTACATTTGGATTCATTAACAGTTGGGAAGCTGGGTTGGAATCGATAAGCTTGGCTGC 2280
Db 15220 CTTACATTTGGATTCATTAACAGTTGGGAAGCTGGGTTGGAATCGATAAGCTTGGCTGC 15279
Qy 2281 AGTTATCATCATCATATAGACACAGAAATAAAGTAAATCAAGATTATCAGTTAAAGCTAT 2340
Db 15280 AGTTATCATCATCATATAGACACAGAAATAAAGTAAATCAAGATTATCAGTTAAAGCTAT 15339
Qy 2341 GTATATTTTGGCCATACCAATCAATTAATAAATAAGATCAGTTTAAAGAAAGATCAAG 2400
Db 15340 GTATATTTTGGCCATACCAATCAATTAATAAATAAGATCAGTTTAAAGAAAGATCAAG 15399
Qy 2401 CTCAAAAATAAAGAGAGAAAAGGCTCTAACCAAGAAAATGAAGAGAAAACAGAA 2460
Db 15400 CTCAAAAATAAAGAGAGAAAAGGCTCTAACCAAGAAAATGAAGAGAAAACAGAA 15459
Qy 2461 ATTTACCTGCAAGCTTGGATCTCTAGACAACCTTTGTACAAGAAAGCTGAACAGAAA 2520
Db 15460 ATTTACCTGCAAGCTTGGATCTCTAGACAACCTTTGTACAAGAAAGCTGAACAGAAA 15519
Qy 2521 CGTAAATAGATAAATAATCAATATTAATAATAGATTTTGCATTAATAAACAAGATCAT 2580
Db 15520 CGTAAATAGATAAATAATCAATATTAATAATAGATTTTGCATTAATAAACAAGATCAT 15579
Qy 2581 AATCTGTAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTG 2640
Db 15580 AATCTGTAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTG 15639
Qy 2641 ACCTGTAGTGAATAGTTGGCAGCATCACCGACGCACTTTGCGCGGAATAAATACCTG 2700
Db 15640 ACCTGTAGTGAATAGTTGGCAGCATCACCGACGCACTTTGCGCGGAATAAATACCTG 15699
Qy 2701 TGACGGAAGATCACCTTCGAGAAATAAATAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Db 15700 TGACGGAAGATCACCTTCGAGAAATAAATAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 15759
Qy 2761 CTTGGGCCAACCTTTTGGCGAAATGAGAGCTTTGATCGGATTTTCAAACTCTTATATCTTT 2820
Db 15760 CTTGGGCCAACCTTTTGGCGAAATGAGAGCTTTGATCGGATTTTCAAACTCTTATATCTTT 15819
Qy 2821 CTCCTTACAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 15820 CTCCTTACAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 15879
Qy 2881 AAGTTTCTGTAATTTCTACTGATCGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Db 15880 AAGTTTCTGTAATTTCTACTGATCGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 15939
Qy 2941 ATTTATTTCCCGAGAAACATCAGGTTTAAAGGGTTTTTGAATGCTATTTTTCGGGTGGCTG 3000
Db 15940 ATTTATTTCCCGAGAAACATCAGGTTTAAAGGGTTTTTGAATGCTATTTTTCGGGTGGCTG 15999

Qy 3001 AGATCAGCACTTCTTCCCGATAACGAGACCGGCACACTGGCCATATCGGTGGTCAATC 3060
Db 16000 AGATCAGCACTTCTTCCCGATAACGAGACCGGCACACTGGCCATATCGGTGGTCAATC 16059
Qy 3061 ATGGCCAGCTTTTCATCCCGATATGCAACACCGGGTAAAGTTACGGGAGACTTTATCT 3120
Db 16060 ATGGCCAGCTTTTCATCCCGATATGCAACACCGGGTAAAGTTACGGGAGACTTTATCT 16119
Qy 3121 GACAGCAGCTGTCACCTGGCCAGGGGATCACCATCCGTCCCGCGGCTGCTCAATATA 3180
Db 16120 GACAGCAGCTGTCACCTGGCCAGGGGATCACCATCCGTCCCGCGGCTGCTCAATATA 16179
Qy 3181 TCACCTGTATCATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTAAACCTTA 3240
Db 16180 TCACCTGTATCATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTAAACCTTA 16239
Qy 3241 AACTGCAATTTACAGTCCCTGTTCTCGTCAGAAAAGAGCGGTTCAATTCATAAACC 3300
Db 16240 AACTGCAATTTACAGTCCCTGTTCTCGTCAGAAAAGAGCGGTTCAATTCATAAACC 16299
Qy 3301 GCGCACCTCAGCCATCCCTTCCATTTTCCGCTTCCAGCGTTCCGGCAGCAGACGACG 3360
Db 16300 GCGCACCTCAGCCATCCCTTCCGCTTCCAGCGTTCCGGCAGCAGACGACGACG 16359
Qy 3361 GGCTTCATTTCTGATGCTGTTGCTTACCAGACCGGAGATATTGACATCATATATGCTTTG 3420
Db 16360 GGCTTCATTTCTGATGCTGTTGCTTACCAGACCGGAGATATTGACATCATATATGCTTTG 16419
Qy 3421 AGCAACTGATAGCTGCTGCTGCTCAACTGTCACTGTATACGCTGCTTCATAGCACCTC 3480
Db 16420 AGCAACTGATAGCTGCTGCTGCTCAACTGTCACTGTATACGCTGCTTCATAGCACCTC 16479
Qy 3481 TTTTGTGACATCTTCTGTTCTTGATGACAGATGATTTTTCAGGACTATGACACTAGCGTATA 3540
Db 16480 TTTTGTGACATCTTCTGTTCTTGATGACAGATGATTTTTCAGGACTATGACACTAGCGTATA 16539
Qy 3541 TGAATAGTAGATGTTTTTATTTTGTGTCACAAAAAGAGGCTCGACCTCTTTTCTTTA 3600
Db 16540 TGAATAGTAGATGTTTTTATTTTGTGTCACAAAAAGAGGCTCGACCTCTTTTCTTTA 16599
Qy 3601 TTTCTTTTATGATTTAATACGGCATTGAGACAAATAGCGTAGGCTGGATAGACGAT 3660
Db 16600 TTTCTTTTATGATTTAATACGGCATTGAGACAAATAGCGTAGGCTGGATAGACGAT 16659
Qy 3661 TCCGTTTGAGAAAGCACTTTGGAAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAA 3720
Db 16660 TCCGTTTGAGAAAGCACTTTGGAAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAA 16719
Qy 3721 GAACTTTGGAAGGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTC 3780
Db 16720 GAACTTTGGAAGGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTC 16779
Qy 3781 ATAGTGATGATATGTTGCTTTTACAGATTTATGATGCTGTTTATGCAAAATCT 3840
Db 16780 ATAGTGATGATATGTTGCTTTTACAGATTTATGATGCTGTTTATGCAAAATCT 16839
Qy 3841 AATTAAATATATGATATTTATATCAATTTTACGTTTCTGTTTACGCTTTTGTACAAAC 3900
Db 16840 AATTAAATATATGATATTTATATCAATTTTACGTTTCTGTTTACGCTTTTGTACAAAC 16899
Qy 3901 TTGCTTAGAGCTGCTTTAATAGATATGCGAGCGCTATGATCGCATGATATTTGCT 3960
Db 16900 TTGCTTAGAGCTGCTTTAATAGATATGCGAGCGCTATGATCGCATGATATTTGCT 16959
Qy 3961 TTCAATTTCTGTTGCGAGCTGTAATAAACAAGTGGAGATGCTAGCTCAGATCCTTACCGC 4020
Db 16960 TTCAATTTCTGTTGCGAGCTGTAATAAACAAGTGGAGATGCTAGCTCAGATCCTTACCGC 17019
Qy 4021 CGGTTTTCGTTTCAATCTAATGAATATATCACCGGTTACTACGTTATTTTATGAATATA 4080
Db 17020 CGGTTTTCGTTTCAATCTAATGAATATATCACCGGTTACTACGTTATTTTATGAATATA 17079

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other, or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

XX SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

Query Match 100.0%; Score 4682; DB 6; Length 17681;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4682; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCATTTTGGAGAGACAGCTCGAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGT 60
DB 13000 TTTTCATTTTGGAGAGACAGCTCGAGACAAAGTTTGTACAAAAAGCTGAACGAGAAACGT 13059

QY 61 AAAATGATATAAATATCAATATATTAATAGATTTCGATFAAAAAACAGACTACATTAAT 120
DB 13060 AAAATGATATAAATATCAATATATTAATAGATTTCGATFAAAAAACAGACTACATTAAT 13119

QY 121 ACTGTAAAAACAAACATATCCAGTCACTATGATGAATCAACTACTTAGATGTTAGTGACC 180
DB 13120 ACTGTAAAAACAAACATATCCAGTCACTATGATGAATCAACTACTTAGATGTTAGTGACC 13179

QY 181 TGTAGTCGACGACAGCCCTCCAAATGTTCTTCGGGTGATGTGCCAACTTAGTCGACCG 240
DB 13180 TGTAGTCGACGACAGCCCTCCAAATGTTCTTCGGGTGATGTGCCAACTTAGTCGACCG 13239

QY 241 ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTGTATCCAGCTACTCGCTATTGTC 300
DB 13240 ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTGTATCCAGCTACTCGCTATTGTC 13299

QY 301 CTCATGCGGTATTAATCATAAAAAGAAATGAAGAAAAAGGTGCGAGCCCTCTTTTGTG 360
DB 13300 CTCATGCGGTATTAATCATAAAAAGAAATGAAGAAAAAGGTGCGAGCCCTCTTTTGTG 13359

QY 361 TGTGCAAAATAAAAACATCTACTATTTCATATACGTAGTGTCTAGTCCTGAAAAATCA 420
DB 13360 TGTGCAAAATAAAAACATCTACTATTTCATATACGTAGTGTCTAGTCCTGAAAAATCA 13419

QY 421 TCTGATCAAGAACAAATTTCAACACTCTTATCTTTCTTTTACAAAGTCGTTTCGCTTCA 480
DB 13420 TCTGATCAAGAACAAATTTCAACACTCTTATCTTTCTTTTACAAAGTCGTTTCGCTTCA 13479

QY 481 TCTGATTTTCAGCCCTCTACTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTA 540
DB 13480 TCTGATTTTCAGCCCTCTACTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTA 13539

QY 541 TCGACTCGAGACTGGCTGTATATAGGAGCCTGACATTTATATCCCGAAGACATCAG 600
DB 13540 TCGACTCGAGACTGGCTGTATATAGGAGCCTGACATTTATATCCCGAAGACATCAG 13599

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DB 13600 GTTAATGGCGTTTGTGATGTCATTTTCGCGGTGGCTGAGATCAGACACTTCTTCCCGAT 13659

QY 661 AACGGAGACCGGCACACTCGCCATATFCGGTGTCTATCATCGCCAGCTTTCATCCCGAT 720
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DB 13720 ATGCACACCGGGTAAAGTTCTACGGGAGCTTTATCTGACAGACAGCTGCTAGCCAG 13779

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DB 13780 GGGGATCACCATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTATATCCACAAACAG 13839

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DB 13840 ACGATACGGCTCTCTCTTTTATAGGTGAACCTTAACTGCAATTTACACAGTCCCTGT 13899

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QY 1081 AACTGTCACTGTAAATACGCTGCTTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGTG 1140

DB 14080 AACTGTCACTGTAAATACGCTGCTTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGTG 14139

QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCCGAGGGCTTCGGGTATCAACAGGAC 1200

DB 14140 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCCGAGGGCTTCGGGTATCAACAGGAC 14199

QY 1201 ACCAGGATTTATTTATCTCGGAAGTGTCTTCGGTCAACAGTATTTATTCGGGCAAG 1260

DB 14200 ACCAGGATTTATTTATCTCGGAAGTGTCTTCGGTCAACAGTATTTATTCGGGCAAG 14259

QY 1261 TGCGTCGGGTGATGTCGCCAACTTAGTCGACTACAGGTCACATAACATCAATCAAGTAGTT 1320

DB 14260 TGCGTCGGGTGATGTCGCCAACTTAGTCGACTACAGGTCACATAACATCAATCAAGTAGTT 14319

QY 1321 GATTCATAGTCACGTCGATGCTGTGTTTACAGTATTTATGATGCTGCTTTTATGCA 1380

DB 14320 GATTCATAGTCACGTCGATGCTGTGTTTACAGTATTTATGATGCTGCTTTTATGCA 14379

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DB 14380 AATCTAATTTAATATTTATGATTTATATCAATTTTACGTTTCTCGTTCAGCTTCTTGTA 14439

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DB 14440 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAATAAATATTTCTTTT 14499

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DB 14560 TATAATTTGAAAAAATAAATTTTAAATATATTTTAAATATATTTTAAATAGTAATGTA 14619

QY 1621 AAAAATATGACAGTGTGTGTAAGACGAGATAAAGTTGAGAGTAAGTATATAT 1680

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QY 1681 TTTTAAATGAAATTTGATCGAACATGTAGATCATATCTAGCATTAATAATTTGTTTAAATC 1740

DB 14680 TTTTAAATGAAATTTGATCGAACATGTAGATCATATCTAGCATTAATAATTTGTTTAAATC 14739

QY 1741 ATAATAGTAAATCTAGCTGGTTTGTGAATTTAAATATCAATGATATAAATACTATAGTAAA 1800

DB 14740 ATAATAGTAAATCTAGCTGGTTTGTGAATTTAAATATCAATGATATAAATACTATAGTAAA 14799

QY 1801 AATAGAGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1860

DB 14800 AATAGAGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 14859

QY 1861 AATATCTATACCATCTCTAAATATTTTAGTTTAAAGTTAAATAAATAAATAAATAAATAAATA 1920

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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1078.53 Seconds
(without alignments)
18441.778 Million cell updates/sec

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Perfect score: 4682
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.*

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3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4682	100.0	17681	6	ABQ82143	Abq82143 Acceptor
2	4262	91.0	17476	6	ABQ82141	Abq82141 Acceptor
3	4200	89.7	17458	6	ABQ82142	Abq82142 Acceptor
4	3193.6	68.3	18691	6	ABQ82130	Abq82130 Acceptor
5	1208.4	25.8	17681	6	ABQ82143	Abq82143 Acceptor
6	1108.8	23.7	4470	3	AAc55521	AAc55521 Donor pla
7	1108.8	23.7	4470	7	ABZ58767	ABZ58767 Destinati
8	1108.8	23.7	4892	8	ADA50329	ADA50329 Plasmid v
9	1108.8	23.7	4939	3	AAc55525	AAc55525 Donor pla
10	1108.8	23.7	5584	3	AAc55632	AAc55632 Donor pla
11	1108.8	23.7	5584	7	ABZ58766	ABZ58766 Donor pla
12	1102.4	23.5	4428	7	ABZ58768	ABZ58768 Destinati
13	1102.4	23.5	4627	7	ABZ58769	ABZ58769 Destinati
14	1102.4	23.5	4627	7	ABZ58770	ABZ58770 Destinati
15	1074.8	23.0	17476	6	ABQ82141	Abq82141 Acceptor
16	1074.8	22.9	17458	6	ABQ82142	Abq82142 Acceptor
17	989.6	21.1	4165	3	AAc55524	AAc55524 Donor pla
18	947.8	20.2	4208	3	AAc55523	AAc55523 Donor pla
19	827	17.7	4204	3	AAc55522	AAc55522 Donor pla
20	823.8	17.6	5156	3	AAc55526	AAc55526 Donor pla
21	780	16.7	786	3	AAZ38603	AAZ38603 Flaveria
22	780	16.7	786	9	ADD44386	ADD44386 Flaveria
23	747	16.0	7050	2	AAQ40419	AAQ40419 Sequence

24	728.8	15.6	7566	2	AAQ42160	AAq42160 Plasmid p
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26	713	15.2	4947	3	AAZ60627	Aaz60627 Nucleotid
27	711.4	15.2	3435	8	ACC85049	Acc85049 Nucleotid
28	710.2	15.2	7599	4	AAF25320	Aaf25320 Nucleotid
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31	709.8	15.2	14194	4	AAc66932	AAc66932 Plant sig
32	707	15.1	24596	1	AAAN50182	AAan50182 Complete
33	703.8	15.0	24593	1	AAAN50226	AAan50226 Sequence
34	703	15.0	2867	7	ABZ68391	ABz68391 Nucleotid
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36	597	12.8	1846	6	AAAD44626	AAad44626 Gateway t
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38	597	12.8	5957	3	AAc55467	AAc55467 Destinati
39	597	12.8	5957	3	AAc55464	AAc55464 Destinati
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41	597	12.8	6264	3	AAc55507	AAc55507 Destinati
42	597	12.8	6354	3	AAc55491	AAc55491 Destinati
43	597	12.8	6422	3	AAc55483	AAc55483 Destinati
44	597	12.8	6464	3	AAc55454	AAc55454 Destinati
45	597	12.8	6526	3	AAc55471	AAc55471 Destinati

ALIGNMENTS

RESULT 1
ABQ82143
ID ABQ82143 standard; DNA; 17681 BP.
XX
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector PHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
(CSIR) COMMONWEALTH SCI & IND RES ORG.
Wesley S, Waterhouse P, Helliwell C;
WPI; 2002-682669/73.
New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
Claim 17; Page 93-102; 104pp; English.

The present invention describes a vector (i) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

Db	3932	ATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGCGGCACAAATACAAACA	3991
QY	4203	ATTGCGGTTTTATTATTACAAATCCAAATTTTAAAAAAGCGGCAGAACCGGTCAAACTTA	4262
Db	3992	ATTGCGGTTTTATTATTACAAATCCAAATTTTAAAAAAGCGGCAGAACCGGTCAAACTTA	4051
QY	4263	AAGACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA	4322
Db	4052	AAGACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA	4111
QY	4323	CACACCGAGCGGCGAACTATAATACGTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGG	4382
Db	4112	CACACCGAGCGGCGAACTATAATACGTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGG	4171
QY	4383	CATGGGTGAGATTCTCTTGAAGTTGAGTATTTGGCGCTCTACCGAAGTTACCGGCA	4442
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QY	4443	CCATTCAACCCGGTCCAGCAGCGCGCGGGTAAACCGACTTGTGCCCCGAGAAATTATGC	4502
Db	4232	CCATTCAACCCGGTCCAGCAGCGCGCGGGTAAACCGACTTGTGCCCCGAGAAATTATGC	4291
QY	4503	AGCATTTTTTGGTGTTATGTGGGCCCCAAATGAAGTCAGGTCAAACCTTGCAGTGAACG	4562
Db	4292	AGCATTTTTTGGTGTTATGTGGGCCCCAAATGAAGTCAGGTCAAACCTTGCAGTGAACG	4351
QY	4563	ACAAATCGTTGGGCGGGTCCAGGCGCAATTTTGGCAACAATGTCGAGGCTCAGCAGGAC	4622
Db	4352	ACAAATCGTTGGGCGGGTCCAGGCGCAATTTTGGCAACAATGTCGAGGCTCAGCAGGAC	4411
QY	4623	CTGCAGGCATGC	4634
Db	4412	CTGCAGGAATTC	4423

Search completed: May 9, 2004, 11:29:16
Job time : 11671.2 secs

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4325	CACCGAGCGCGGAACATAAATCAATTCCTTCACTGAAGGGAACCTCCGGTTCCCGCCCGCGCGCA	4384
8352	CACCGAGCGCGGAACATAAATCAATTCCTTCACTGAAGGGAACCTCCGGTTCCCGCCCGCGCGCA	8293
4385	TGGGTCAGAGTTCCTTCAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTTACGGGCACC	4444
8292	TGGGTCAGAGTTCCTTCAAGTTGAGTATTGGCCGCTCCGCTCTACCGAAAGTTTACGGGCACC	8233
4445	ATTCAACCCGGTCCAGACAGCGGCGCGGTAAACCGACTGCTGCCCGCGAATATTGCGAG	4504
8232	ATTCAACCCGGTCCAGACAGCGGCGCGGTAAACCGACTGCTGCCCGCGAATATTGCGAG	8173
4505	CATTTTTTTGGTGATGTATGGGCCCCAAAATGAAGTGCAGGTCAAACTTGCACGTGAGCAC	4564
8172	CATTTTTTTGGTGATGTATGGGCCCCAAAATGAAGTGCAGGTCAAACTTGCACGTGAGCAC	8113
4565	AAATCGTTGGCGGGTCCAGGGCGAAATTTTGGACAAACATGTCCAGGCTCAGCAGGACCT	4624
8112	AAATCGTTGGCGGGTCCAGGGCGAAATTTTGGACAAACATGTCCAGGCTCAGCAGGACCT	8053
4625	GCAGGCATCGAAGCT 4639	
8052	GCAGGCATCGAAGCT 8038	
RESULT 15		
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LOCUS	A24783	7566 bp DNA linear PAT 24-FEB-1995
DEFINITION	plasmid pPS0212 replicable en E.coli.	
ACCESSION	A24783	
VERSION	A24783.1	GI:833505
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	
ORGANISM	artificial sequences.	
REFERENCE	1 (bases 1 to 7566)	
AUTHORS		
TITLE	MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS	
JOURNAL	Patent: WO 9309218-A 23 13-MAY-1993;	
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Best Local Similarity	99.7%;	Pred. No. 1.8e-95;
Matches	730; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
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QY	3963	CAATTCGTGTGTCACGTTGTAAAAAACCTGAGCATGTCTAGCTCAGATCCTTACCGCG 4022
Db	3752	CAATTCGTGTGTCACGTTGTAAAAAACCTGAGCATGTCTAGCTCAGATCCTTACCGCG 3811
QY	4023	GTTCGCGTTTCATTCTAATGAATATATCACCGGTTACTATCGTATTTTATGAATAATTT 4082
Db	3812	GTTCGCGTTTCATTCTAATGAATATATCACCGGTTACTATCGTATTTTATGAATAATTT 3871
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QY	4143	ATATATTGTGCTGAATAGGTTTTATACGCATCTATGATAGACGCGCAACAATAACAAACA 4202

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QY 1892 TAAAGTAAATAAATATTTGTTAGAAATCCAAATCTGCTTGTATATTTATCAATAAACA 1951
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QY 2252 TGGGTTTCAAAATC 2264
Db 8672 AAAGAGCAAAATC 8684

RESULT 13
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DEFINITION pTE4 expression vector.
ACCESSION A23998
VERSION A23998.1 GI:833338
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences
REFERENCE 1 (bases 1 to 7049)
AUTHORS Nazarov, V., Botterman, J., Stanssens, P. and Sevcik, J.
TITLE A novel ribonuclease and its inhibitor
JOURNAL Patent: EP 0537399-A 3 21-APR-1993;
PLANT GENETIC SYSTEMS, N.V
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match 16.0%; Score 747; DB 6; Length 7049;
Best Local Similarity 94.6%; Pred. No. 4.4e-98;
Matches 771; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db 4002 TTTTTCAGCTTTACATATAAAGTGTGTAATAAATTTTCTTCAAACTCTGATCGGTCAAT 4061
QY 3887 TTTTGTGACAACTTGCTAGAGTCCTGCTTAAATGAGATATGCGAGACCGCTATGATC 3946

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QY 4007 CAGATCCTTACCGCGGTTTCCGTTTCATTTCTAAATGAATATATACCCGTTACTATCGTAT 4066
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Db 4242 TTTTATGAATTAATTTCTCCGTTCAATTTACTGATTTGACCTACTACTTATATGACAA 4301
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QY 4607 CGAGGCTCAGCAGGACCTGCGAGGCATCGAAGCTAG 4641
Db 4782 CGAGGCTCAGCAGGACCTGCGAGGCATCGAAGCTAG 4816

RESULT 14
LOCUS AF187951/c 10138 bp DNA linear SYN 11-MAY-2000
DEFINITION Activation-tagging vector pSKI015, complete sequence.
ACCESSION AF187951
VERSION AF187951.1 GI:6537289
KEYWORDS Activation-tagging vector pSKI015
SOURCE Activation-tagging vector pSKI015
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 10138)
AUTHORS Weigel, D., Ahn, J.H., Blazquez, M.A., Borevitz, J.O.,
Christensen, S.K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharuk, E.J., Neff, M.M., Nguyen, J.T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R.A., Harrison, M.J., Lamb, C.J., Yanofsky, M.F. and
Chory, J.
TITLE Activation tagging in Arabidopsis
JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000)
MEDLINE 2023715
PUBMED 10759496
REFERENCE 2 (bases 1 to 10138)

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PLN 15-APR-1996

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PUBMED 11576441
REFERENCE 2 (bases 1 to 6063)
AUTHORS Waterhouse, P.M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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Db 4724 AATATTTGTTTAAATCATATAGTAAATCTAGCTGGTGTGATGAATTAATAATCAATGAT 4783
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Db 4844 GTTATTTATATAAATAAATAATCTATACCATTAATAATTTTATAGTTTAAAGAGTTAATAA 4903
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Db 5264 GATAAGCTTG 5273

RESULT 11
LOCUS BD194641
DEFINITION Method and means of obtaining improved phenotype.
ACCESSION BD194641
VERSION BD194641.1 GI:33004386
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 786)
AUTHORS Waterhouse, P.M., Wang, M.B. and Graham, M.W.
TITLE Method and means of obtaining improved phenotype
JOURNAL Patent: JP 2002511258-A 7 16-APR-2002;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
COMMENT OS Artificial Sequence
PN JP 2002511258-A/7
PD 16-APR-2002
PF 07-APR-1999 JP 2000543598
PR 08-APR-1998 US 09/056767, 03-AUG-1998 US 09/127735 PI
PETER MICHAEL WATERHOUSE, MIN BO WANG, MICHAEL WAIN GRAHAM PC
C12N15/09, A01H5/00, C12N5/10, C12N5/00, C12N5/00 CC Description of

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1905	QY	ATATTTTGTGTAGAAATTTCCAAATCTGCTTGTGTAATTTATCAATAAATAAATAAATAAAT	1964
4665	DB	ATATTTTGTGTAGAAATTTCCAAATCTGCTTGTGTAATTTATCAATAAATAAATAAATAAAT	4724
1965	QY	AAGCTAAGATGACAAATAATATCAACTAATAGAAACAGTAATCTAATGTAAACAAACAT	2024
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LOCUS			
DEFINITION		CVE311873 6063 bp DNA circular SYN 09-JUL-2002	
ACCESSION		Cloning vector pKANNIBAL.	
VERSION		ADJ311873	
KEYWORDS		ADJ311873.1 GI:15982216	
SOURCE		kan gene; kanamycin resistance protein; pdk gene; promoter.	
ORGANISM		Cloning vector pKANNIBAL	
REFERENCE		Cloning vector pKANNIBAL	
AUTHORS		artificial sequences; vectors.	
TITLE		1	
JOURNAL		Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,	
MEDLINE		Gooding, ps., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,	
		Gleave, A.P., Green, A.G. and Waterhouse, P.M.	
		Construct design for efficient, effective and high-throughput gene	
		silencing in plants	
		Plant J. 27 (6), 581-590 (2001)	
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RESULT 8
BD263382/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD263382
5156 bp DNA linear PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of nucleic acids.
BD263382
GI:33073150
JP 2002537790-A/160.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 5156)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of nucleic acids
INVITROGEN CORP
Patent: JP 2002537790-A 160 12-NOV-2002;
OS Artificial Sequence
PN JP 2002537790-A/160
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
00, C12N5/00
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CC May be any nucleotide
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Best Local Similarity 99.8%; Pred. No. 4.2e-109;
Matches 825; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9
CVE311872
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

CVE311872
5824 bp DNA circular SYN 09-JUL-2002
Cloning vector pHANNIBAL.
AJ311872
AJ311872.1 GI:15982214
AMP gene; ampicillin resistance protein; pdk gene; promoter.
Cloning vector pHANNIBAL
Cloning vector pHANNIBAL
artificial sequences; vectors.
1
Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.F.,
Gleave,A.P., Green,A.G. and Waterhouse,P.M.
Construct design for efficient, effective and high-throughput gene

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DEFINITION			
Compositions and methods for use in recombinational cloning of nucleic acids.			
ACCESSION	BD263379		
VERSION	BD263379.1	GI:33073147	
KEYWORDS	JP 2002537790-A/157.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
artificial sequences.			
REFERENCE	1 (bases 1 to 4208)		
AUTHORS	Hartley,J.L., Bransch,M.A., Temple,G.F. and Cheo,D.		
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids		
JOURNAL	Patent: JP 2002537790-A 157 12-NOV-2002;		
COMMENT			
INVITROGEN CORP			
OS Artificial Sequence			
PN	JP 2002537790-A/157		
PD	12-NOV-2002		
PF	02-MAR-2000 JP 2000602252		
PR	02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049		PR
28-MAY-1999 US 60/136744			
PI	JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO		PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/00			
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LOCUS			
DEFINITION			
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ACCESSION			
BD263402.1 GI:33073170			
KEYWORDS			
JP 2002537790-A/180.			
SOURCE			
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ORGANISM			
artificial sequences.			
REFERENCE			
1 (bases 1 to 5584)			
AUTHORS			
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.			
TITLE			
Compositions and methods for use in recombinational cloning of			
nucleic acids			
JOURNAL			
Patent: JP 2002537790-A 180 12-NOV-2002;			
COMMENT			
INVITROGEN CORP			
OS Artificial Sequence			
PN JP 2002537790-A/180			
PD 12-NOV-2002			
PF 02-MAR-2000 JP 2000602252			
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR			
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC			
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/			
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AUTHORS
Compositions and methods for use in recombinational cloning of
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JOURNAL
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PD 12-NOV-2002
PR 02-MAR-2000 JP 200602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
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Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants

JOURNAL
Plant J. 27 (6), 581-590 (2001)

MEDLINE
21461301

PUBMED
11576441

REFERENCE
2 (bases 1 to 18691)

AUTHORS
Waterhouse, P.M.

DIRECT SUBMISSION
Submitted (04-MAY-2001)

JOURNAL
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

LOCATION/QUALIFIERS

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Best Local Similarity 78.5%; Pred. No. 0;
Matches 4460; Conservative 0; Mismatches 84; Indels 1140; Gaps 7;
QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 85
Db 13121 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 13180
QY 86 AAATTAGATTTTGCATATAAAAAAGCTGATACATTAATCTGTAACACACACATATCCAGTC 145
Db 13181 AAATTAGATTTTGCATATAAAAAAGCTGATACATTAATCTGTAACACACACATATCCAGTC 13240
QY 146 ACTATCAATCACTACTTAGATGGTATTAGTACCTGTAGTACCGACGAGCCTTCCAAA 205
Db 13241 ACTATCAATCACTACTTAGATGGTATTAGTACCTGTAGTACCGACGAGCCTTCCAAA 13300
QY 206 TGTTCCTCGGGTGATGCTGCCAACTTGTAGTACCGACGAGCCTTCCAAAATGTTCTTCTCAA 265
Db 13301 TGTTCCTCGGGTGATGCTGCCAACTTGTAGTACCGACGAGCCTTCCAAAATGTTCTTCTCAA 13360
QY 266 ACCGAATCGTCGTATCCAGCCTACTCGCTATTCTCTCAATGCGGTATTAAATCATATAAAA 325
Db 13361 ACCGAATCGTCGTATCCAGCCTACTCGCTATTCTCTCAATGCGGTATTAAATCATATAAAA 13420
QY 326 AGAAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAAAATAAACATCTACCT 385
Db 13421 AGAAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAAAATAAACATCTACCT 13480
QY 386 ATTCATATACGTAGTGTATAGTCTCGAAAAATCATCTGCATCATAGACATTTTCAAC 445
Db 13481 ATTCATATACGTAGTGTATAGTCTCGAAAAATCATCTGCATCATAGACATTTTCAAC 13540
QY 446 TCATTACTTTTCTCTTACAGTGGTTCGGCTTCATCTGGATTTTCAAGCTCTATATCTTA 505
Db 13541 TCATTACTTTTCTCTTACAGTGGTTCGGCTTCATCTGGATTTTCAAGCTCTATATCTTA 13600

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 11650.2 Seconds
(without alignments)
17418.703 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4:	gb.om.*	BD263402 Compositi
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13:	gb.un.*	A23998 pT84 expres
14:	gb.vi.*	AF187951 Activatio
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40:	em.htgo.mus.*	AF433042 Cloning v
41:	em.htgo.other.*	AF433043 Cloning v

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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Cloning vector pHELLSGATE.
AJ311874
AJ311874.1 GI:15982218
kanamycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; spec gene; spectinomycin resistance protein;
transposon Tn7.
Cloning vector pHELLSGATE
Cloning vector pHELLSGATE
artificial sequences; vectors.
1
Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,

Pred. No. is the number of results predicted by chance to have a

New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanopol@med.nyu.edu
No Blast Hits ()

FEATURES
source
1. 1037
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/note="Vector: pCR4.OTOPO; 10 million Plasmodium yoelii
17X sporozoites were isolated from salivary glands of
infected Anopheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
exoerythrocytic malaria parasites does not require host
cells' (J Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."

ORIGIN
Query Match 6.1%; Score 271.8; DB 14; Length 1037;
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Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 571 GCCTGACATTTATATCCCGAGACATCAGGTTAATGGGTTTTGATGTCATTTTCGG 630
Db 496 GCCTGACATTTATATCCCGAGACATCAGGTTAANGGGTTTTGATGTCATTTTCGG 437
QY 631 GTGGCTGAGATCAGCCACTTCTCCCGATACGGAGACCGGACACTGGCCATATCGGT 690
Db 436 GTGGCTGAGATCAGCCACTTCTCCCGATACGGAGACCGGACACTGGCCATATCGGT 377
QY 691 GGTATCATGCGCAGCTTTCTCCCGATACGGAGACCGGACACTGGCCATATCGGT 750
Db 376 GGTATCATGCGCAGCTTTCTCCCGATACGGAGACCGGACACTGGCCATATCGGT 317
QY 751 TTATCTGACAGCAGCGTGCATCGCCAGGGGATCACCATCGGCGCGGGGTGTC 810
Db 316 TTATCTGACAGCAGCGTGCATCGCCAGGGGATCACCATCGGCGCGGGGTGTC 257
QY 811 AATAATATCACTCTGTACATCCACACAG--ACGATAACGGCTCTCTTTTATAGGTG 868
Db 256 AATAAGATCACTCTGTACATCCACATACAGTACGATAACGGCTCTCTTTTATAGGTG 197
QY 869 TAAACCTTAACTGCATTC 888
Db 196 AAACCTTNAACNCCGNTTC 177

RESULT 15
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LOCUS
DEFINITION Homo sapiens genomic DNA, 724 bp DNA linear GSS 06-FEB-1999
survey sequence.
ACCESSION AG000791
VERSION AG000791.1 GI:2579599
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1997)
2 (bases 1 to 724)
Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
Direct Submission
Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@ngc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES
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ORIGIN

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Matches 288; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
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Db 27 ACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAITTCACCACTCCCTGTTCTCG 86
QY 906 TCAGCAAAAGAGCGGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATT 965
Db 87 TCAGCAAAAGAGCGGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATT 146
QY 966 TCCGCTTTCAGCGTTCCGACGAGAGCGGCTTCATTCGATGGTTGCTTACC 1025
Db 147 TCCGCTTTCAGCGTTCCGACGAGAGCGGCTTCATTCGATGGTTGCTTACC 206
QY 1026 AGACGGAGATATTGACATCATATATGCTTGAGCACTGATAGTGTGCTGTCACTG 1085
Db 207 AGACGGAGATATTGACATC--ATATGCTTGAGCACTGATAGTGTGCTGTCACTG 264
QY 1086 TCACGTGAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
Db 265 TCACGTGAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTA 316

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Job time : 6918.79 secs

philippe.vaglio@fci.harvard.edu
POLYA-No.

FEATURES

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ORIGIN

Query Match 7.6%; Score 340.2; DB 12; Length 384;
Best Local Similarity 97.7%; Pred. No. 6.7e-50;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 101 TAAAAACAGACTACATACTGTAACACACACATATCCAGTCACTATGAATCAACTA 160
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QY 221 GTCGCCAATTAGTCGACCGACAGCCTTCCAAATGTTCTTCGAAACGGAATCGTCGAT 280
DB 152 GTCGCCAATTAGTCGACCGACAGCCTTCCAAATGTTCTTCGAAACGGAATCGTCGAT 211
QY 281 CCAGCTCTACTGCTATTCCTCAATGCGGTATTAATCATAAAGAAATGAAGAAAG 340
DB 212 CCAGCTCTACTGCTATTCCTCAATGCGGTATTAATCATAAAGAAATGAAGAAAG 271
QY 341 AGGTGGAGCCTCTTTTGTGTGACAAATATAAACATCTACCTATTCATATACGCTAG 400
DB 272 AGGTGGAGCCTCTTTTGTGTGACAAATATAAACATCTACCTATTCATATACGCTAG 331
QY 401 TGTCTAGTCCTGAAATCATCTGCATCAAGAACAAATTTCAACTCTTTATAC 453
DB 332 TGTCTAGTCCTGAAATCATCTGCATCAAGAACAAATTTCAACTCTTTATAC 384

RESULT 11

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LOCUS OSTF043E11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
DEFINITION F11E1.5, mRNA sequence.
ACCESSION BI174407
VERSION BI174407.1 GI:14640210
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 384)

REFERENCE

AUTHORS Reiboul,J., Vaglio,P., Trellas,N., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-I,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
TITLE Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
JOURNAL Nat. Genet. 27 (3), 332-336 (2001)
MEDLINE 21135099
PUBMED 11242119

COMMENT

Contact: Reiboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome_Reiboul@fci.harvard.edu

FEATURES

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Location/Qualifiers
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 7.3%; Score 325.4; DB 12; Length 384;
Best Local Similarity 98.2%; Pred. No. 2.7e-47;
Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 366 TGTCTTTCATGACGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGATGT 307
QY 3333 TTTTATTTTGTGCACACAAAAGAGGCTCGACCTCTTTTCTTTTCTTTTATGATT 3392
DB 306 TTTTATTTTGTGCACACAAAAGAGGCTCGACCTCTTTTCTTTTCTTTTATGATT 247
QY 3393 TAATACGGCAATTGAGGACATAGCGAGTAGGCTGGATGAGTACGACGATTCGGTTTGAAGAA 3452
DB 246 TAATACGGCAATTGAGGACATAGCGAGTAGGCTGGATGAGTACGACGATTCGGTTTGAAGAA 187
QY 3453 CATTTGGAAGCTGTGCGTGCAGCTTAAGTTGGCAGCATCACCGGAAGACATTTGGAAGGC 3512
DB 186 CATTTGGAAGCTGTGCGTGCAGCTTAAGTTGGCAGCATCACCGGAAGACATTTGGAAGGC 127
QY 3513 TGTGCGTGCAGCTACAGGTCACCTAATACCATCTAAGTAGTTGATTCATAGTACTGGATAT 3572
DB 126 TGTGCGTGCAGCTACAGGTCACCTAAGTAGTTGATTCATAGTACTGGATAT 67
QY 3573 GTTGTGTTTACAGPATTATGATGCTCTTTTATTA 3607
DB 66 GTTGTGTTTACAGPATTATGATGCTCTGTATTA 32

RESULT 12

BIJ555980 337 bp mRNA linear EST 18-DEC-2002
LOCUS BIJ555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil
DEFINITION cDNA clone jml8n08 5', mRNA sequence.
ACCESSION BIJ555980
VERSION BIJ555980.1 GI:27237800
KEYWORDS EST.
SOURCE Ipomoea nil (Japanese morning glory)
ORGANISM Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoea.
1 (bases 1 to 337)

REFERENCE

AUTHORS Hoshino,A., Seki,M., Shin-I,T., Carninci,P., Kamiya,A., Shiraki,T.,
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
TITLE ESTs of Japanese morning glory
JOURNAL Unpublished (2002)

QY 60 TAAATGATATAAATCAATATATTAATAGATTTTGCATATAAAACAGACTACATAA 119
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 Db 487 TAAATGATATAAATCAATATATTAATAGATTTTGCATATAAAACAGACTACATAA 428
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 Db 367 CTGTAGTCACGACGAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTAGTCGACC 308
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 Db 307 GACAGCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACTCGCTATTGT 248
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 QY 300 CTTCAATGCGTATTAATCATATAAAGAAATAGAAAGAGGGTGGAGCTCTTTT 359
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 QY 360 GTGTGACAAAATAAATAATCTAC-CTATTATATACGCTAGTGTATGCTCTGAAAT 418
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 QY 419 CATCTGCATCAAGAAACAATTCACAACTCTTATATCTTTCTCTTCAAG 467
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RESULT 9
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 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

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 /note="The AD-wrmCDNA library was generated with poly(A)+
 RNA isolated from both hermaphrodite and male N2 worms of
 all larval stages, embryos, adults and dauers and the
 subsequent generation of cDNAs by poly(A) priming. The
 cDNAs were cloned into pPC86"

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 Best Local Similarity 96.8%; Pred. No. 3.3e-51;
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 Db 111 TGTTCATGATCGGAAGATACCTCGGACTATGACACTAAAGTATATGAATATCTAGATG 170
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 QY 3332 TTTTATTTTGTGCACAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 3391
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 Db 171 CTTTATTTTGTGCACAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 230
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 QY 3392 TTAATACGGCATTTGAGGACATAGCGAGTAGGCTGGATACGACGATTCGGTTTGAAGA 3451
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 Db 231 TTAATACGGCATTTGAGGACATAGCGAGTAGGCTGGATACGACGATTCGGTTTGAAGA 290
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 QY 3452 ACATTTGGAAGGCTGCTCGTACACTAAGTTGGGAGCATCACCAGAACACTTTTGAAGG 3511
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 QY 3512 CTGTGGTCTGACTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACCTGGATA 3571
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 Db 351 CTGTGGTCTGACTACAGTCACTAATACCATCTAAGTAGTGTGATTCATAGTACCTGGATA 410
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 QY 3572 TGTGTGTTTTACAGTATATATGATGCTGTTTTTATGCAAAATCAATTTAATATATG 3631
 Db 411 TGTGTGTTTTACAGTATATATGATGCTGTTTTTATGCAAAATCAATTTAATATATG 470
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 Db 471 ATATTTATATCATTTTA 487
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RESULT 10
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 DEFINITION
 ACCESSION
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 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
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QY 846 AACGGCTCTCTCTTTTATAGTGTAACACCTTTAAACTGCACTTACACAGTCCCTGTTCTCG 905
Db 323 AACGGCTCTCTC-TTTATAGTGTAACACCTTTAAACTGCACTTACACAGTCCCTGTTCTCG 381
QY 906 TCAGAAAAGAGCGGTTCATTTCAATAAACCGGGGAGCTCAGGCATCC-TTCTGATT 964
Db 382 TCAGAAAAGAGCGGTTCATTTCAATAAACCGGGGAGCTCAGGCATCCCTTCTCTGATT 441
QY 965 TTTCGCTTTCCAGCGTTCCGCGACGACGACGAC 996
Db 442 TTTCGCTTTCCAGCGTTTCGCGACGCGCAGC 473

RESULT 7
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DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000763
VERSION AG000763.1 GI:2579571
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 722)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail: hattori@hgci.ims.u-tokyo.ac.jp, Tel: 0427-78-9732, Fax: 0427-78-9561)

FEATURES
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Best Local Similarity 92.2%; Pred. No. 3e-60;
Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7;

QY 601 GTTAATGGCGTTTGTGATGTCATTTTCGCGTGGCTGAGATCAGCCATCTTCCCGGAT 660
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QY 661 AACGAGACCGGCACACTGGCCATATCGTGGTCATATCGCCAGCTTTCATCCCGAT 720
Db 666 TAAGAGACCGGCACA-TGGGCATAACCGTGGTCATCA-GGCCAGCTTTCATCA-CCCGAT 610
QY 721 ATGACACCGCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 780
Db 609 ATGACACCGCGGTAAAGTTTACGGGAGACTTTACGAGAGACCTTACGACAGCAGACGTGCACTGGCCAG 550
QY 781 GGGATACACCTCCCTCGCCCGCGGTGTCAATAATATATCTCTGTAATCCACAAAACAG 840
Db 549 GGGATACACCTCCCTCGCCCGCGGTGTCAATAATATATCTCTGTATACATCCACAAAACAG 490
QY 841 ACGATAAGCGTCTCTCTTTTATAGTGTAACCTTAACTGCACTTTCACGAGTCCCTGT 900

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Db 489 ACGATAAGCGTCTCTCTTTTATAGTGTAACCTTAAACTGCACTTTCACGAGTCCCTGT 430
QY 901 TCTCGTCAGCAAGAGCGGTTCATTTCAATAAACCGGGGAGCTCAGCCATCCCTTCCCT 960
Db 429 TCTCGTCAGC-AAAGAGCGGTTCATTTCAATAAACCGGGGAGCTCAGCCATCCCTTCCCT 371
QY 961 GATTTTCCGCTTTCCAGCGTTCCGCGACGAGCAGCGGCTTCATTTGTCATGTTGTGC 1020
Db 370 GATTTTCCGCTTTCCAGCGTTCCGCGACGAGCAGCGGCTTCATTTGTCATGTTGTGC 311
QY 1021 TTACCGACCGGAGATTTGACATCATATATATGCTTGAGCACTGATAGTGTGCTGTC 1080
Db 310 TTACCGACCGGAGATTTGACATC--ATATGCTTTGAGCACTGATAG-TGTGCTGTC 254
QY 1081 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTA 1137
Db 253 AACTGTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTCGGGTA 197

RESULT 8
CB395230/c
LOCUS CB395230 487 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION CB395230.1 GI:30736941
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 487)
AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Janna, S., Chevet, E., Papasotiropoulos, V., Tolias, P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, J., Hill, D.E. and Vidal, M.
TITLE C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david.hill@dfci.harvard.edu or marc.vidal@dfci.harvard.edu
POLYA=No.

FEATURES
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    1..487
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    /mol_type="mRNA"
    /strain="N2"
    /db_xref="taxon:6239"
    /sex="Hermaphrodite and male"
    /tissue_type="whole animal"
    /dev_stage="mixed stage"
    /clone_lib="AD-wrmcDNA"
    /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN
Query Match 8.0%; Score 357; DB 14; Length 487;
Best Local Similarity 93.6%; Pred. No. 6.8e-53;
Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic survey sequence.

ACCESSION AG013450 AG005773

VERSION AG013450.1 GI:3549208

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 725)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

TITLE Homo sapiens genomic DNA, chromosome 21q

JOURNAL Published Only in DataBase (1998)

REFERENCE 2 (bases 1 to 725)
Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Direct Submission
Submitted (07-SEP-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).

COMMENT

FEATURES
Location/Qualifiers
1..725
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="f32E9X13"

ORIGIN

Query Match 9.2%; Score 408.4; DB 29; Length 725;
Best Local Similarity 90.2%; Pred. No. 5.2e-62;
Matches 505; Conservative 0; Mismatches 47; Indels 8; Gaps 7;

QY 580 TTATATCCCGAGACATCAGTTAATGCGTTTGTGATGTCATTTTCGGTGGCTGAG 639

DB 723 TTATATCCCGAGACATCAGTTAATGCGTTTGTGATGTCATTTTCGGTGGCTGAG 664

QY 640 ATCAGGCACTTCTTCCCGATACAGGAGACCGGACACCTGGCCATATCGTGGTTCATCAT 699

DB 663 ATCAGGCACTTCTTCCCGATACAGGAGACCGGACACCTGGCCATATCGTGGTTCATCAT 604

QY 700 GCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTCACGGAG-ACCTTATCTG 758

DB 603 GCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTCACGGAG-ACCTTATCTG 545

QY 759 ACAGCAGAGCTGCACCTGGCC-AGGGGATCACCCTCGTCCCGGCGGTGTCATATA 817

DB 544 ACAGCAGAGCTGCACCTGGCC-AGGGGATCACCCTCGTCCCGGCGGTGTCATATA 486

QY 818 TCACCTGTGATATCCCAACAGAGATACCGGCTCTCTTTTATAGGTGTAACCTTA 877

DB 485 TCACCTGTGATATCCCAACAGAGATACCGGCTCTCTTTTATAGGTGTAACCTTA 427

QY 878 AACTGATTTACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTGTCATTTCAATAACCG 937

DB 426 AACTGATTTACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTGTCATTTCAATAACCG 367

QY 938 GCGACCTCAGGACATCCCTTCTGATTTTCGCTTCCAGCGTTCGGCAGCAGACGAG 997

DB 366 GCGACCTCAGGACATCCCTTCTGATTTTCGCTTCCAGCGTTCGGCAGCAGACGAG 307

QY 998 GGCTTCATTTCTGATGGTTGTGTTTACCAGAGCGGAGATATTGACATCATATATGCTTGG 1057

DB 306 GGCTTCATTTCTGATGGTTGTGTTTACCAGAGCGGAGATATTGACATC--ATATGCTTGG 249

QY 1058 AGCACTGATAGTGTGCTGTCACCTGTCATGTAATACGCTGCTTCTATAGCACCTTC 1117

DB 248 AGCACTGATAGTGTGCTGTCACCTGTCATGTAATACGCTGCTTCTATAGCACCTTC 190

QY 1118 TTTTGGACATACCTTCGGGTA 1137

Db 189 TTTTGGACATACCTTCGGGTA 170

RESULT 6
CB997937

LOCUS

DEFINITION CB997937 522 bp mRNA linear EST 01-MAY-2003
AGNCOURT 13894516 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.

ACCESSION CB997937

VERSION CB997937.1 GI:30292457

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 522)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDAM391 row: e column: 05
High quality sequence start: 68
High quality sequence stop: 256.

FEATURES
Location/Qualifiers
1..522
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30348484"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamH; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NHGR1, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 9.1%; Score 404; DB 14; Length 522;
Best Local Similarity 96.2%; Pred. No. 3.5e-61;
Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 546 CTGCAGACTGGCTGTGTATAGGAGCGCTGACATTTATTTCCCGAACAATCAGGTTAA 605

DB 23 CTGCAGACTGGCTGTGTATAGGAGCGCTGACATTTATTTCCCGAACAATCAGTAA 82

QY 606 TGGCGTTTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGGCACCTTCTTCCCGATAACGG 665

DB 83 TGGCGTTTTTGTATGTCATTTTCGCGGTGGCTGAGATCAGGCACCTTCTTCCCGATAACGG 142

QY 666 AGACCGGCACACTGCCCATATCGGTGTCATCATCGCCAGCTTTCATCCCGATATGCA 725

DB 143 AGACCGGCACACTGCCCATATCGGTGTCATCATCGCCAGCTTTCATCCCGATATGCA 202

QY 726 CCACCGGTTAAAGTTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCGAGGGGA 785

DB 203 CCACCGGTTAAAGTTTCACGGAGACTTTTATCTGACAGCAGCTGCTGCTGCGAGGGGA 262

Email: cgapbe-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM387 row: c column: 24
 High quality sequence start: 144
 High quality sequence stop: 251.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:30346919"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 147"
 /note="Torgan: placenta; Vector: pBluescriptR; Site 1:
 all-XhoI; Site 2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTT-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

ORIGIN

Query Match 9.8%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 4.8e-67;
 Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

Qy 546 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATCAGGTAA 605
 Db 23 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATCAGGTAA 82

Qy 606 TGGCGTTTTTGCATCTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 665
 Db 83 TGGCGTTTTTGCATCTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 142

Qy 666 AGACCGGCACACTGGCCATATCGGTGTCATCATCGCCAGCTTTTCATCCCGATATGCA 725
 Db 143 AGACCGGCACACTGGCCATATCGGTGTCATCATCGGTGTCATCTTCCCGATATGCA 202

Qy 726 CCACCGGTAAAGTTCACGGAGACTTTATCTGACAGCAGAGTGCATCGCCAGGGGA 785
 Db 203 CCACCGGTAAAGTTCACGGAGACTTTATCTGACAGCAGAGTGCATCGCCAGGGGA 262

Qy 786 TCACCATCGCTCGCCGGCGGTGTCATTAATATCACTCTGTACATCCCAACACAGCAT 845
 Db 263 TCACCATCGCTCGCCGGCGGTGTCATTAATATCACTCTGTACATCCCAACACAGCAT 322

Qy 846 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 905
 Db 323 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 382

Qy 906 TCAGCAAAAGAGCCGCTTCATTTCAATAACCGGGGAGCTCAGCCATCCCTTCCTGATT 965
 Db 383 TCAGCAAAAGAGCCGCTTCATTTCAATAACCGGGGAGCTCAGCCATCCCTTCCTGATT 442

Qy 966 TCCGCTTTTCCA-GCGTTCGGCAGCAGAG-ACGGGCTTCATTC--TGCAATGTTGTGCT 1021
 Db 443 TCCCTTTCCAGCTTTTCGGCAGCAGAGACGAGGCTTCATCTCTGCATGTTTGTGCT 502

Qy 1022 TACCAGACGG-AGATATTGACATCATATATGCTTT 1056
 Db 503 TACCAGACGGAGATATTGACATCATATATGCTTT 538

RESULT 4
 AG000761/c
 LOCUS
 DEFINITION
 Homo sapiens genomic DNA, 723 bp DNA linear GSS 06-FEB-1999
 survey sequence.
 ACCESSION
 AG000761
 VERSION
 AG000761.1 GI:2579569
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 723)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Homo sapiens genomic DNA, chromosome 21q
 Published Only in DataBase (1997)
 2 (bases 1 to 723)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Direct Submission
 Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@bc.ims.u.tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
 FEATURES
 source
 1. 723
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clones="64E11X4"

ORIGIN

Query Match 9.2%; Score 411.8; DB 25; Length 723;
 Best Local Similarity 98.1%; Pred. No. 1.3e-62;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 546 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATCAGGTAA 605
 Db 450 CTGCAGACTGGCTGTGTATAGGGAGCCTGCACATTATATCCCGCAGAACATCAGGTAA 391

Qy 606 TGGCGTTTTTGCATCTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 665
 Db 390 TGGCGTTTTTGCATCTTCGGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 331

Qy 666 AGACCGGCACACTGGCCATATCGGTGTCATCATCGCCAGCTTTTCATCCCGATATGCA 725
 Db 330 AGACCGGCACACTGGCCATATCGGTGTCATCATCGCCAGCTTTTCATCCCGATATGCA 271

Qy 726 CCACCGGTAAAGTTCACGGAGACTTTATCTGACAGCAGAGTGCATCGCCAGGGGA 785
 Db 270 CCACCGGTAAAGTTCACGGAGACTTTATCTGACAGCAGAGTGCATCGCCAGGGGA 211

Qy 786 TCACCATCGCTCGCCGGCGGTGTCATTAATATCACTCTGTACATCCCAACACAGCAT 845
 Db 210 TCACCATCGCTCGCCGGCGGTGTCATTAATATCACTCTGTACATCCCAACACAGCAT 151

Qy 846 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 905
 Db 150 AACGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTCG 91

Qy 906 TCAGCAAAAGAGCCGCTTCATTTCAATAACCGGGGAGCTCAGCCATCCCTTCCTGATT 965
 Db 90 TCAGCAAAAGAGCCGCTTCATTTCAATAACCGGGGAGCTCAGCCATCCCTTCCTGATA 31

Qy 966 TCCG 969
 Db 30 TCAG 27

RESULT 5

AG013450/c
 LOCUS
 AG013450 725 bp DNA linear GSS 14-APR-1999


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/map="21q"
/clone="f65H12X16"

ORIGIN
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Best Local Similarity 98.9%; Pred. No. 2.2e-81;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

QY 579 TTTATATTTCCCGAGAAATCAGGTTAATGGGTTTTCATGTCATTTTCGGGGTGGCTGA 638
Db 34 TTTATATTTCCCGAGAAATCAGGTTAATGGGTTTTCATGTCATTTTCGGGGTGGCTGA 93
QY 639 GATCAGCCACTTCTTCCCGGATACGAGACCGGCACACTGGCCATATCGGTGGTCATCA 698
Db 94 GATCAGCCACTTCTTCCCGGATACGAGACCGGCACACTGGCCATATCGGTGGTCATCA 153
QY 699 TCGCCAGCTTTCATCCCGGATATGACACACCGGTAAGTTTACGGGAGACTTTATCTG 758
Db 154 TCGGCCA-NTTTCATCCCGGATATGACACACCGGTAAGTTTACGGGAGACTTTATCTG 212
QY 759 ACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCGCCCGCGGTGTCATATAT 818
Db 213 ACAGCAGCTGCACTGGCCAGGGGATCACCATCCGTCGCCCGCGGTGTCATATAT 272
QY 819 CACTCTGTACATCCACAAACAGACGATACCGGCTCTCTCTTTTATAGGTAAACCTTAA 878
Db 273 CACTCTGTACATCCACAAACAGACGATACCGGCTCTCTCTTTTATAGGTAAACCTTAA 332
QY 879 ACTGATTTTACAGCTGCTGTTCTCGTCAGCAAAAGAGCGGTTTCAATTAATACCGG 938
Db 333 ACTGATTTTACAGCTGCTGTTCTCGTCAGCAAAAGAGCGGTTTCAATTAATACCGG 392
QY 939 GCGACTCAGCATCCCTTCCGTGATTTTCCGCTTCCAGCGTTCCGCGACGACGACGCG 998
Db 393 GCGACTCAGCATCCCTTCCGTGATTTTCCGCTTCCAGCGTTCCGCGACGACGACGCG 452
QY 999 GCTTCATTTGATGTTGTGTTTACCGACCGGAGATATGACATCATATATGCTTTGA 1058
Db 453 GCTTCATTTGATGTTGTGTTTACCGACCGGAGATATGACATC--ATATGCTTTGA 510
QY 1059 GCAACTGATAGCTGCTGTCATCTGTCATGTAATAGCTGCTTCATAGCACACCTCT 1118
Db 511 GCAACTGATAGC-GTCGCTGTCACTGTCACTGTATAGCTGCTTCATAGCACACCTCT 569
QY 1119 TTTTGACATCTTCGGGTA 1137
Db 570 TTTTGACATCTTCGGGTA 588

RESULT 2
AG000762/2
LOCUS      Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
DEFINITION survey sequence.
ACCESSION AG000762
VERSION    AG000762.1 GI:2579570
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 713)
            Homo sapiens genomic DNA, chromosome 21q
            Published Only in DataBase (1997)
            2 (bases 1 to 713)
            Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
            Direct Submission
            Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
            Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
            Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,

/clone="64E11X4"

ORIGIN
Query Match      11.1%; Score 496.6; DB 29; Length 713;
Best Local Similarity 94.2%; Pred. No. 1.5e-77;
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

QY 583 TATTCCCGCAGAAATCAGGTTAATGGGTTTTCATGTCATTTTCGGGGTGGCTGAGATC 642
Db 599 TATATCCCGGANCATCNGTTAATGCCGTTTTCGAGGNAATTTTCGCCGTGGCTGAGAAT 540
QY 643 AGCCACTTTCCTCCCGGATACCGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCG 702
Db 539 CACCAACTTTTTCCTCCCGATACGNAGACCGGCACACTGCCATATCGGTGGTCATCATGCG 480
QY 703 CCAGCTTTTCATCCCGGATATGACACACCGGTAAGTTTTCAGGGAGACTTTTATCTGACAG 762
Db 479 CCAGCTTTTCATCCCGGATATGACACACCGGTAAGTTTTCAGGGAGACTTTTATCTGACAG 420
QY 763 CAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGCGGTGTCATATATCACT 822
Db 419 CAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGCGGTGTCATATATCACT 360
QY 823 CTGTACATCCAAACAGACGATTAACGGCTCTCTTTTATAGGTGTAACCTTAAACCTG 882
Db 359 CTGTACATCCAAACAGACGATTAACGGCTCTCTTTTATAGGTGTAACCTTAAACCTG 300
QY 883 CATTTCCACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCAATTAATACCGGGCGA 942
Db 299 CATTTCCACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCAATTAATACCGGGCGA 240
QY 943 CCTCAGCCATCCCTTCCGTGATTTTCGCTTTCAGCGTTTCGCGACGACGACGCGGCTT 1002
Db 239 CCTCAGCCATCCCTTCCGTGATTTTCGCTTTCAGCGTTTCGCGACGACGACGCGGCTT 180
QY 1003 CATTTCCAGTGTGCTGTTACCGACCGGAGATATGACATCATATATGCTTGAACAA 1062
Db 179 CATTTCCAGTGTGCTGTTACCGACCGGAGATATGACATC--ATAAGCTTGAACAA 122
QY 1063 CTGATAGCTGCTGCTGCACTGTCACTGTAATAGCTGCTTCATAGCACACCTCTTTT 1122
Db 121 CTGAATANTGCTGCTGCACTGTCACTGTAATAGCTGCTTCATAGCACACCTCTTTT 62
QY 1123 GACATACCTTCGGGTA 1137
Db 61 GACATACCTTCGGGTA 47

RESULT 3
CD109790
LOCUS      Homo sapiens
DEFINITION IMAGE:30346919 5', mRNA sequence.
ACCESSION CD109790
VERSION    CD109790.1 GI:30753999
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 542)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 6916.59 Seconds
(without alignments)

19251.609 Million cell updates/sec

Title: US-10-055-001b-25_COPY_13000_17458

Perfect score: 4459

Sequence: 1 tttcatttggagagacacg.....atagtgcacctaatactgc 4459

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
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25: em_gss_rtd:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518.4	11.6	698	29 AG012840	AG012840 Homo sapi
c 2	496.6	11.1	713	29 AG000762	AG000762 Homo sapi
3	437.2	9.8	542	14 CD109790	CD109790 AGENCOURT
c 4	411.8	9.2	723	29 AG000761	AG000761 Homo sapi

c	5	408.4	9.2	725	29	AG013450
c	6	404	9.1	522	14	CB997937
c	7	398.4	8.9	722	29	AG000763
c	8	357	8.0	487	14	CB395230
c	9	347.4	7.8	487	14	CB395230
c	10	340.2	7.6	384	12	BI174407
c	11	335.4	7.3	384	12	BI174407
c	12	301.4	6.8	1068	14	BU555980
c	13	273.2	6.1	1037	14	CF469981
c	14	271.8	6.1	1037	14	CF469981
c	15	264.4	5.9	724	29	AG000791
c	16	262.4	5.9	816	14	CF469496
c	17	257.4	5.8	557	12	BG220129
c	18	255.8	5.7	656	14	CK231800
c	19	254	5.7	569	14	CF469084
c	20	252.4	5.7	819	14	CF469247
c	21	247.4	5.5	320	29	CG206516
c	22	246	5.5	329	28	BH739300
c	23	245.4	5.5	1041	14	CF468941
c	24	243.6	5.5	1035	14	CF470036
c	25	242.8	5.4	1017	14	CF470004
c	26	239.2	5.4	659	14	CK287298
c	27	235.6	5.3	859	14	CF468865
c	28	234.8	5.3	506	14	CF468964
c	29	234.8	5.3	657	14	CF468948
c	30	229	5.1	628	14	CF469215
c	31	227.2	5.1	968	14	CF469474
c	32	220	4.9	583	14	CB403882
c	33	220	4.9	583	14	CB403882
c	34	215.2	4.8	393	14	CB403984
c	35	215.2	4.8	1020	14	CF469337
c	36	215.2	4.8	1017	14	CF468787
c	37	214.6	4.8	1042	14	CF468958
c	38	214.2	4.8	945	14	CF468807
c	39	213.8	4.8	509	14	CF468864
c	40	213.2	4.8	716	29	AG000792
c	41	213.2	4.8	398	14	CF974207
c	42	204.6	4.6	1013	14	CF469353
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c	45	200.4	4.5			

ALIGNMENTS

RESULT 1
AG012840
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
TITLE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL

AG012840
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.
AG012840
AG012840.1 GI:3435047
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 698)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published only in DataBase (1998)
2 (bases 1 to 698)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (20-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228 Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

AG012840
Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.

AG012840
AG012840.1 GI:3435047
GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 698)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published only in DataBase (1998)

2 (bases 1 to 698)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission

Submitted (20-AUG-1998) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228 Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:0427-78-9561)

Location/Qualifiers

1. .698

/organism="Homo sapiens"

/mol_type="genomic DNA"

source

features

Db 750 TCGGTGGTTCATCATGCGCCAGCTTTCATCCCGATATGACACCGGGTAAAGTTCACGG 809
Qy 746 GAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCCGTCCGCCCGGC 805
Db 810 GAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCCGTCCGCCCGGC 869
Qy 806 GTGTCAATAATATCACTCTGTACATCCCAACACAGAGATAAAGCTCTCTCTTTATAG 865
Db 870 GTGTCAATAATATCACTCTGTACATCCCAACACAGAGATAAAGCTCTCTCTTTATAG 929
Qy 866 GTGTAAACCTTAAACCTGCACTTACCACTCCCTGTTCTGTCAGCAAAAGAGCGGTTTAT 925
Db 930 GTGTAAACCTTAAACCTGCACTTACCACTCCCTGTTCTGTCAGCAAAAGAGCGGTTTAT 989
Qy 926 TTCATTAACCGGGCGACTCAGCCATCCCTCTCTGATTTTCCGTTTCCAGCGGTTCCGC 985
Db 990 TTCATTAACCGGGCGACTCAGCCATCCCTCTCTGATTTTCCGTTTCCAGCGGTTCCGC 1049
Qy 986 AGCAGACGAGCGGCTTCATTTCTGATGTTGTGCTTACCAGACCGGAGATATTGACATC 1045
Db 1050 AGCAGACGAGCGGCTTCATTTCTGATGTTGTGCTTACCAGACCGGAGATATTGACATC 1109
Qy 1046 ATATATGCTTGGACAACTGATAGTGTGCTGCTCAACTGTCACTGTAAATACGCTGCTTC 1105
Db 1110 ATATATGCTTGGACAACTGATAGTGTGCTGCTCAACTGTCACTGTAAATACGCTGCTTC 1169
Qy 1106 ATAGCACACCTCTTTTGGACATCTTCGGGTA 1137
Db 1170 ATAGCACACCTCTTTTGGACATCTTCGGGTA 1201

RESULT 15

US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R. N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 24.7%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 7.4e-157; Mismatches 6; Indels 0; Gaps 0;
Matches 1106; Conservative 0;
Qy 26 GACAAAGTTTGTACAAAAGCTGAACGAGAAACGTAATAATGATATAATAATATCAATATATT 85
Db 90 GCAACTTTGTACAAAAGCTGATATCGAAAGTAAATGATATAATAATATCAATATATT 149
Qy 86 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAAAAACACACATATCCAGTC 145
Db 150 AAATTAGATTTTGCATAAAAAACAGACTACATAAATCTGTAAAAACACACATATCCAGTC 209
Qy 146 ACTATGAATCAACTACTTATAGTGGTATTAGTGACCTGTAGTACCGGACCGAGCCCTTCCAAA 205

Search completed: May 10, 2004, 00:05:56
Job time : 1230.96 secs

QY 146 ACTATGAATCAACTACTCTAGATGGTATTAGTGAAGCTGTAGTCGACCGACAGCCTTCCAAA 205
Db |
QY 1059 ACTATGAATCAACTACTCTAGATGGTATTAGTGAAGCTGTAGTCGACCGACAGCCTTCCAAA 1118
Db |
QY 206 TGTCTCTCGGTGATGCTGCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCA 265
Db |
QY 1119 TGTCTCTCGGTGATGCTGCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCA 1178
Db |
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
Db |
QY 1179 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 1238
Db |
QY 326 AGAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 385
Db |
QY 1239 AGAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 1298
Db |
QY 386 ATTCTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 445
Db |
QY 1299 ATTCTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 1358
Db |
QY 446 TCTTATACCTTTCTCTTACAAAGCTGTCGGCTTCACTGTGATTTTTCAGCCTCTATCTTA 505
Db |
QY 1359 TCTTATACCTTTCTCTTACAAAGCTGTCGGCTTCACTGTGATTTTTCAGCCTCTATCTTA 1418
Db |
QY 506 CTAACAGTGATAGTGTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 565
Db |
QY 1419 CTAACAGTGATAGTGTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 1478
Db |
QY 566 AGGAGAGCTGTACATTTATTTCCAGAAATCATAGTGTAAATGGGGTTTTTCATGTCAATTT 625
Db |
QY 1479 AGGAGAGCTGTACATTTATTTCCAGAAATCATAGTGTAAATGGGGTTTTTCATGTCAATTT 1538
Db |
QY 626 TCGGGTGGCTGAGATCAGCACTCTTTCCCGATTAACGGAGACGGCACATCGGCCATA 685
Db |
QY 1539 TCGGGTGGCTGAGATCAGCACTCTTTCCCGATTAACGGAGACGGCACATCGGCCATA 1598
Db |
QY 686 TCGGTGGTTCATCATGCGGACAGCTTTCATCCCGATATGACACCGGGTAAAGTTCACGG 745
Db |
QY 1599 TCGGTGGTTCATCATGCGGACAGCTTTCATCCCGATATGACACCGGGTAAAGTTCACGG 1658
Db |
QY 746 GAGACTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCACCATCCGTCGCCCGGGC 805
Db |
QY 1659 GAGACTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCACCATCCGTCGCCCGGGC 1718
Db |
QY 806 GTGTCAATAATATCACTCTGTATATCCCAACAGACGATAAACGGCTCTCTTTTATAG 865
Db |
QY 1719 GTGTCAATAATATCACTCTGTATATCCCAACAGACGATAAACGGCTCTCTTTTATAG 1778
Db |
QY 866 GTGTAAACCTTAACTGATTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCGCTTCAT 925
Db |
QY 1779 GTGTAAACCTTAACTGATTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCGCTTCAT 1838
Db |
QY 926 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGTGATTTTCCGCTTTCCAGCGTTGCGC 985
Db |
QY 1839 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGTGATTTTCCGCTTTCCAGCGTTGCGC 1898
Db |
QY 986 ACGCAGACAGCGGCTTCATCTGTGATGTTGTGCTTACAGACCGGAGATTTGACATC 1045
Db |
QY 1899 ACGCAGACAGCGGCTTCATCTGTGATGTTGTGCTTACAGACCGGAGATTTGACATC 1958
Db |
QY 1046 ATATATGCTTTGAGCACTGATAGTGTGCTGTCACCTGTCACCTGTGATATCGGTTC 1105
Db |
QY 1959 ATATATGCTTTGAGCACTGATAGTGTGCTGTCACCTGTCACCTGTGATATCGGTTC 2018
Db |
QY 1106 ATAGCACACCTCTTTTTCACATCTTCGGGTA 1137
Db |
QY 2019 ATAGCACACCTCTTTTTCACATCTTCGGGTA 2050
Db |

RESULT 14

US-10-151-690-63

; Sequence 63, Application US/10151690

; Publication No. US2003012455A1

; GENERAL INFORMATION:

; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID M
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match

24.7%; Score 1102.4; DB 15; Length 4627;

Best Local Similarity 99.5%; Pred. No. 7.4e-157;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTCTACAAAAAGCTGACGAGAAACGTAATAATGATATAATATCAATATATT 85
Db 90 GCCAACCTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAATATCAATATATT 149
QY 86 AAATTAGATTTTGCATAAAAACAGACTACATATACTGTAAAAACAAACATATCCAGTC 145
Db 150 AAATTAGATTTTGCATAAAAACAGACTACATATACTGTAAAAACAAACATATCCAGTC 209
QY 146 ACTATGAATCAACTACTCTAGATGGTATTAGTGAAGCTGTAGTCGACCGACAGCCTTCCAAA 205
Db 210 ACTATGAATCAACTACTCTAGATGGTATTAGTGAAGCTGTAGTCGACCGACAGCCTTCCAAA 269
QY 206 TGTCTCTCGGTGATGCTGCCAATCTAGTCGACCGACAGCCTTCCAAATGTTCTTCA 265
Db 270 TGTCTCTCGGTGATGCTGCCAATCTAGTCGACCGACAGCCTTCCAAATGTTCTTCA 329
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
Db 330 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 389
QY 326 AGAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 385
Db 390 AGAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 449
QY 386 ATTCTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 445
Db 450 ATTCTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGACAAATTTCAAC 509
QY 446 TCTTATACCTTTCTCTTACAAAGTGGTTCGGCTTCACTGTGATTTTTCAGCCTCTATCTTA 505
Db 510 TCTTATACCTTTCTCTTACAAAGTGGTTCGGCTTCACTGTGATTTTTCAGCCTCTATCTTA 569
QY 506 CTAACAGTGATAGTGTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 565
Db 570 CTAACAGTGATAGTGTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 629
QY 566 AGGAGAGCTGTACATTTATTTCCCGAAACATCAGGTTAATGGGTTTTTGTATGTCATTT 625
Db 630 AGGAGAGCTGTACATTTATTTCCCGAAACATCAGGTTAATGGGTTTTTGTATGTCATTT 689
QY 626 TCGCGTGGCTGAGATCAGCACTCTTTCCCGATTAACGGAGACGGCACATCGGCCATA 685
Db 690 TCGCGTGGCTGAGATCAGCACTCTTTCCCGATTAACGGAGACGGCACATCGGCCATA 749
QY 686 TCGGTGGTTCATCATGCGGACAGCTTTCATCCCGATATGACACCGGGTAAAGTTCACGG 745

Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 24.9%; Score 1108.8; DB 15; Length 5584;
Best Local Similarity 99.8%; Pred. No. 8.6e-158;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	26	GACAAAGTTTGTACAAAAGCTGACGAGAAACGTGAATATGATATATAATATCAATATATT	85
DB	5483	GCCAACTTTGTACAAAAGCTGACGAGAAACGTGAATATGATATATAATATCAATATATT	5424
QY	86	AAATAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACACATATCCAGTC	145
DB	5423	AAATAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACACATATCCAGTC	5364
QY	146	ACTATGAATCAACTTAGTAGTGGTATTAGTGACCTTAGTGACGAGGAGCCCTTCCAAA	205
DB	5363	ACTATGAATCAACTTAGTAGTGGTATTAGTGACCTTAGTGACGAGGAGCCCTTCCAAA	5304
QY	206	TGTTCTTCGGGTGATGCTCCCACTTAGTCGACGAGCCCTTCCAAATGTTCTCTCAA	265
DB	5303	TGTTCTTCGGGTGATGCTCCCACTTAGTCGACGAGCCCTTCCAAATGTTCTCTCAA	5244
QY	266	ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGATTAATCAATAAA	325
DB	5243	ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCGGATTAATCAATAAA	5184
QY	326	AGAAATAAGAAAAGAGGTGCGAGCCCTCTTTTGTGACAAATAAATAACATCTACCT	385
DB	5183	AGAAATAAGAAAAGAGGTGCGAGCCCTCTTTTGTGACAAATAAATAACATCTACCT	5124
QY	386	ATTATATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAATTTTCAACAC	445
DB	5123	ATTATATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAATTTTCAACAC	5064
QY	446	TCTATATCTTTCTCTTACAAGTCGTTCGCTTCATCTGGATTTTCAGGCTCTATCTTA	505
DB	5063	TCTATATCTTTCTCTTACAAGTCGTTCGCTTCATCTGGATTTTCAGGCTCTATCTTA	5004
QY	506	CTAAACGTGTAAAGTTTCTGTAATTTCTATCTGATCGACCTGACACTGGCTGTATA	565
DB	5003	CTAAACGTGTAAAGTTTCTGTAATTTCTATCTGATCGACCTGACACTGGCTGTATA	4944
QY	566	AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTGTATGTCATT	625
DB	4943	AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTGTATGTCATT	4884
QY	626	TGCGGTGCTGAGATCAGCCACTTTCTTCCCGATACCGGAGCCGGGACACTGGGCAATA	685
DB	4883	TGCGGTGCTGAGATCAGCCACTTTCTTCCCGATACCGGAGCCGGGACACTGGGCAATA	4824

QY	686	TCGGTGTCTATCATATGCGCCAGCTTTTATATCCCGATATATGACCAACCGGTTAAAGTTCA	745
DB	4823	TCGGTGTCTATCATATGCGCCAGCTTTTATATCCCGATATATGACCAACCGGTTAAAGTTCA	4764
QY	746	GAGACTTTTATCTGACAGCAGCAGTGCCTGCGCAGGCGGATCACCATCCCTCGCCCGGGC	805
DB	4763	GAGACTTTTATCTGACAGCAGCAGTGCCTGCGCAGGCGGATCACCATCCCTCGCCCGGGC	4704
QY	806	GTGTCAATAATATACATCTGTATCATCCAAAACAGACGATAACGGCTCTCTCTTTTATAG	865
DB	4703	GTGTCAATAATATACATCTGTATCATCCAAAACAGACGATAACGGCTCTCTCTTTTATAG	4644
QY	866	GTGTAAACCTTAACTGCACTTACAGTCCCTGCTTCTGCTCAGCAAAAGAGCGGTTTCA	925
DB	4643	GTGTAAACCTTAACTGCACTTACAGTCCCTGCTTCTGCTCAGCAAAAGAGCGGTTTCA	4584
QY	926	TTCAATAAAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGC	985
DB	4583	TTCAATAAAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGC	4524
QY	986	ACGAGACGAGCGGCTTCACTTCTGATGTTGCTTACAGACCGGAGATATTGACATC	1045
DB	4523	ACGAGACGAGCGGCTTCACTTCTGATGTTGCTTACAGACCGGAGATATTGACATC	4464
QY	1046	ATATATGCTTGTGCAACTGATGCTGCTGCTCAACTGCTAAATACGCTGCTTC	1105
DB	4463	ATATATGCTTGTGCAACTGATGCTGCTGCTCAACTGCTAAATACGCTGCTTC	4404
QY	1106	ATAGCACACCTCTTTTGTGACATATCTCGGGTA	1137
DB	4403	ATAGCACACCTCTTTTGTGACATATCTCGGGTA	4372

RESULT 13

US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match 24.7%; Score 1102.4; DB 15; Length 4428;
Best Local Similarity 99.5%; Pred. No. 7.3e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	26	GACAAAGTTTGTACAAAAGCTGAACGAGAAACGTAAATATGATATAATATCAATATATT	85
DB	939	GCCAACTTTGTACAAAAGCTGATATCGAAACGTAAATATGATATAATATCAATATATT	998
QY	86	AAATAGATTTTGCATATAAAAAACAGACTACATATAATCTGTAAACACACATATCCAGTC	145
DB	999	AAATAGATTTTGCATATAAAAAACAGACTACATATAATCTGTAAACACACATATCCAGTC	1058

Db 1182 ATAGCACACCTCTCTTTTGACATACCTTCGGGTA 1213

|||||

RESULT 11

US-10-357-268-1

; Sequence 1, Application US/10357268

; Publication No. US20030219902A1

; GENERAL INFORMATION:

; APPLICANT: Kahn, Michael L

; APPLICANT: Houshe, Brent L

; APPLICANT: Mortimer, Michael W

; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination

; FILE REFERENCE: WSUR-1-20291

; CURRENT APPLICATION NUMBER: US/10/357,268

; CURRENT FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: 60/354,063

; PRIOR FILING DATE: 2002-01-31

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 4892

; TYPE: DNA

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: terminator

; LOCATION: (73)..(100)

; OTHER INFORMATION: T2

; FEATURE:

; NAME/KEY: terminator

; LOCATION: (232)..(275)

; OTHER INFORMATION: T1

; FEATURE:

; NAME/KEY: terminator

; LOCATION: (232)..(275)

; OTHER INFORMATION: T1

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (332)..(563)

; OTHER INFORMATION: attP1 recombination site

; FEATURE:

; NAME/KEY: gene

; LOCATION: (959)..(1264)

; OTHER INFORMATION: ccdB gene

; FEATURE:

; NAME/KEY: gene

; LOCATION: (1606)..(2265)

; OTHER INFORMATION: Cam(r) gene

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2513)..(2744)

; OTHER INFORMATION: attP2 recombination site

; FEATURE:

; NAME/KEY: gene

; LOCATION: (2868)..(3677)

; OTHER INFORMATION: Kan(r) gene

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (3794)..(4537)

; OTHER INFORMATION: pUC oriV / RK2 oriT

US-10-357-268-1

Query Match 24.9%; Score 1108.8; DB 16; Length 4892;

Best Local Similarity 99.8%; Pred. No. 8.2e-158;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACACGTTCTGACAAAAGCTGACGAGAAAGCTAAAGTATATAATATCAATATAT 85

Db 102 GCCAACTTTGTACAAAAGAGCTGACGAGAAAGCTAAAGTATATAATATCAATATAT 161

QY 86 AAATTAGATTTCATATAAAGACAGACTACATATACTGTAAACACAAACATATCCAGTC 145

Db 162 AAATTAGATTTCATATAAAGACAGACTACATATACTGTAAACACAAACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCGACGAGCCTTCCTCAA 205

Db 222 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCGACGAGCCTTCCTCAA 281

QY 206 TGTTCCTCGGGTGTATGCTGCCAAGTCTAGTCGACGAGCCTTCCTCAAATGTTCTTCTCAA 265

Db 282 TGTTCCTCGGGTGTATGCTGCCAAGTCTAGTCGACGAGCCTTCCTCAAATGTTCTTCTCAA 341

QY 266 ACAGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAA 325

Db 342 ACAGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAA 401

QY 326 AGAAATAGAAAAGAGTGGAGCCTCTTTTGTGTGACAAATATAAATCATATCACT 385

Db 402 AGAAATAGAAAAGAGTGGAGCCTCTTTTGTGTGACAAATATAAATCATATCACT 461

QY 386 ATTCATATACGCTAGTGTATGCTAGTCTGAAATCATCTGCATCAAGAACATTTTCAAC 445

Db 462 ATTCATATACGCTAGTGTATGCTAGTCTGAAATCATCTGCATCAAGAACATTTTCAAC 521

QY 446 TCTTATACCTTTCTCTTCAAGTCTGCTTGGCTTCATCTGGAATTTTCAAGCCTCTATAC 505

Db 522 TCTTATACCTTTCTCTTCAAGTCTGCTTGGCTTCATCTGGAATTTTCAAGCCTCTATAC 581

QY 506 CTAAACGTGATAAAGTTCCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTATA 565

Db 582 CTAAACGTGATAAAGTTCCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTATA 641

QY 566 AGGAGCCTGACATTTATATTTCCAGAACATCAAGTTAATGCGCTTTTGTATGTCATTT 625

Db 642 AGGAGCCTGACATTTATATTTCCAGAACATCAAGTTAATGCGCTTTTGTATGTCATTT 701

QY 626 TCGCGTGGCTGAGATCAGCCACTTTCTTCCCGATTAACGGAGACCGGACACTGCGCAT 685

Db 702 TCGCGTGGCTGAGATCAGCCACTTTCTTCCCGATTAACGGAGACCGGACACTGCGCAT 761

QY 686 TCGGTGGTCAATCATCGCGCAGCTTTTATCCCGATTAACGGAGACCGGATTAAGTTAC 745

Db 762 TCGGTGGTCAATCATCGCGCAGCTTTTATCCCGATTAACGGAGACCGGATTAAGTTAC 821

QY 746 GAGACTTTATCTGACAGCAGCTGCTGCTGCGCAGGGGATCACCATCCGTCGCGCGGC 805

Db 822 GAGACTTTATCTGACAGCAGCTGCTGCTGCGCAGGGGATCACCATCCGTCGCGCGGC 881

QY 806 GTGTCAATAATATCACTCTGTACATCCAAACAGACGATACGGCTCTCTCTTTATAG 865

Db 882 GTGTCAATAATATCACTCTGTACATCCAAACAGACGATACGGCTCTCTCTTTATAG 941

QY 866 GTGTAAACCTTAAAGTGGATTTTCCAGTCCCTGTTCTGTCAGCAAAAAGAGCGTTCA 925

Db 942 GTGTAAACCTTAAAGTGGATTTTCCAGTCCCTGTTCTGTCAGCAAAAAGAGCGTTCA 1001

QY 926 TTCAATAAACCGGGGAGCTTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCTTCGC 985

Db 1002 TTCAATAAACCGGGGAGCTTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCTTCGC 1061

QY 986 ACAGCAGACCGGGCTTCACTTCTGATGTTGCTTACAGACCGGAGATATGACATC 1045

Db 1062 ACAGCAGACCGGGCTTCACTTCTGATGTTGCTTACAGACCGGAGATATGACATC 1121

QY 1046 ATATATGCTTTCAGCAACTGATAGTGTCTGCTCAACTGTCTCACTGTAATACGCTGCTTC 1105

Db 1122 ATATATGCTTTCAGCAACTGATAGTGTCTGCTCAACTGTCTCACTGTAATACGCTGCTTC 1181

QY 1106 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 1137

Db 1182 ATAGCACACCTCTTTTGTACATACCTTCGGGTA 1213

RESULT 12

US-10-151-690-61/c

; Sequence 61, Application US/10151690

3509 AGGCTGTCGCTCGACTACAGCTCACTAATCACTAAGTAGTGTGATTCATAGTACTGG 3568
13198 AGGCTGTCGCTCGACTACAGCTCACTAATCACTAAGTAGTGTGATTCATAGTACTGG 13139
3569 ATATGTTGTTTACAGATATATAGTACTGTTTATGCAAAATCTAATTTAATATA 3628
13138 ATATGTTGTTTACAGATATATAGTACTGTTTATGCAAAATCTAATTTAATATA 13079
3629 TTGATATTATATCATTTTACGTTTCTCGTTCAGCTTTTGTACAAACTTGTCTAGAG 3687
13078 TTGATATTATATCATTTTACGTTTCTCGTTCAGCTTTTGTACAAACTTGTCTAGAG 13020

RESULT 10

US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIRO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI

; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470

TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: plasmid pDONR201
FEATURE:
NAME/KEY: gene
LOCATION: (29)..(260)
OTHER INFORMATION: attP1
FEATURE:
NAME/KEY: gene
LOCATION: (656)..(961)
OTHER INFORMATION: ccdB
FEATURE:
NAME/KEY: gene
LOCATION: (1099)..(1184)
OTHER INFORMATION: ccda
FEATURE:
NAME/KEY: gene
LOCATION: (1303)..(1962)
OTHER INFORMATION: Cmr
FEATURE:
NAME/KEY: gene
LOCATION: (2210)..(2442)
OTHER INFORMATION: attP2
FEATURE:
NAME/KEY: gene
LOCATION: (2565)..(3374)
OTHER INFORMATION: Km^r
FEATURE:
NAME/KEY: gene
LOCATION: (3495)..(4134)
OTHER INFORMATION: ori
US-10-151-690-21

Query Match 24.9%; Score 1108.8; DB 15; Length 4470;
Best Local Similarity 99.8%; Pred. No. 7.9e-159;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTTGTACAAAAAGCTGAACGAGAAACGTAAAAATGATATAAATATCAATATATT 85
Db 102 GCCAACTTTTGTACAAAAAGCTGAACGAGAAACGTAAAAATGATATAAATATCAATATATT 161
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACAACAATATCCAGTC 145
Db 162 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACAACAATATCCAGTC 221
QY 146 ACTATGAATCAACTATAGTATGGTATAGTACCTGTAGTCCGACGACGACGCTTCCAAA 205
Db 222 ACTATGAATCAACTATAGTATGGTATAGTACCTGTAGTCCGACGACGACGCTTCCAAA 281
QY 206 TGTTCCTTCGGTGATGCTGCCAACTTAGTCGACGACGACGCTTCCAAATGTCTTCFAA 265
Db 282 TGTTCCTTCGGTGATGCTGCCAACTTAGTCGACGACGACGCTTCCAAATGTCTTCFAA 341
QY 266 ACGGAATCGTCTATCCAGCCTACTCGCTATTTGCTCAATGCGGTATTTAAATCATAAAA 325
Db 342 ACGGAATCGTCTATCCAGCCTACTCGCTATTTGCTCAATGCGGTATTTAAATCATAAAA 401
QY 326 AGAAATAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAATATAAAACATCTACTCT 385
Db 402 AGAAATAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAATATAAAACATCTACTCT 461
QY 386 ATTCATATACGCTAGTGTCACTAGTCTCTGAAATCATCTGCATCAAGAACATTTTCAAC 445
Db 462 ATTCATATACGCTAGTGTCACTAGTCTCTGAAATCATCTGCATCAAGAACATTTTCAAC 521
QY 446 TCTTATATCTTCTCTTCAAGTGTGCGCTTCTCTGAAATCATCTGCATCAAGAACATTTTCA 505
Db 522 TCTTATATCTTCTCTTCAAGTGTGCGCTTCTCTGAAATCATCTGCATCAAGAACATTTTCA 581
QY 506 CTAAACGTGATAAAGTTTCTGTATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565
Db 582 CTAAACGTGATAAAGTTTCTGTATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 641
QY 566 AGGGAGCCTGCATTTATTTATTTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGCATTT 625
Db 642 AGGGAGCCTGCATTTATTTATTTCCCGAGAACATCAGGTTAATGGCGTTTGTGATGCATTT 701
QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGAGATAACGGAGACCGGCACACTGGCCATA 685
Db 702 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGAGATAACGGAGACCGGCACACTGGCCATA 761
QY 686 TCGGTGTCATCATGCGCCAGCTTTTATCCCGAGATATGCCACCGGGTAAAGTTTCAAGG 745
Db 762 TCGGTGTCATCATGCGCCAGCTTTTATCCCGAGATATGCCACCGGGTAAAGTTTCAAGG 821
QY 746 GAGACTTTATCTGACAGCAGCTGCATCTGGCCAGGGGATCACCATCCGTCGCCCGGGC 805
Db 822 GAGACTTTATCTGACAGCAGCTGCATCTGGCCAGGGGATCACCATCCGTCGCCCGGGC 881
QY 806 GTGTCAATATATCATCTGTATATCCAAACAGACGATACGGCTCTCTTTTATAG 865
Db 882 GTGTCAATATATCATCTGTATATCCAAACAGACGATACGGCTCTCTTTTATAG 941
QY 866 GTGTAAACCTTAACTGCAATTTTCCAGTCCCTGTTTCTCGTCAGCAAAAGAGCCGTTCA 925
Db 942 GTGTAAACCTTAACTGCAATTTTCCAGTCCCTGTTTCTCGTCAGCAAAAGAGCCGTTCA 1001
QY 926 TTCAATAAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCAGGTTCCGC 985
Db 1002 TTCAATAAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCAGGTTCCGC 1061
QY 986 ACGCAGACGACGGGCTTCAATCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1045
Db 1062 ACGCAGACGACGGGCTTCAATCTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1121
QY 1046 ATATATGCCCTTGAGCAACTGATAGTGTCTGCTCAACTGTCTACTGTATACGCTGCTTC 1105
Db 1122 ATATATGCCCTTGAGCAACTGATAGTGTCTGCTCAACTGTCTACTGTATACGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTGTACATATCTTGGGTA 1137

Db 15405 AGTGACTGGATATGTTGTTGTTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAA 15346
QY 1388 TTTAATATATGATATTTATATCATTTTACGTTTCTCGTTACGCTTCTTGTGACAAAGTG 1447
Db 15345 TTTAATATATGATATTTATATCATTTTACGTTTCTCGTTACGCTTCTTGTGACAAAGTG 15286
QY 1448 GTCTGAGAA-----TTGGGTACCAACTGTAAAGAAATAATTTATTTCTT 1493
Db 15285 GTCTAGAGGATCAAGCTTATCGATTTCGAACCCAGCTTCCCAACTGTAATCAATCCAA 15286
QY 1494 TTTTCTTTAGTATATAATAGTTAAGTATGTTAATAGTATGATTAATAATAATAGT 1553
Db 15225 TGTAGATCAATGATAACAATGATCATATCATGTTTACCTGTTTATTCATGTTTC 15166
QY 1554 TGTATTAATTTGTGAAAAATAATTTATATAATATATTTGTTTACATAAACAACATAGTAATG 1613
Db 15165 GACTAATTCATTTAATATAGTCAATCCATTTAGAGTTAATAAATACAGTATTAT 15106
QY 1614 TAAAAAATATGACAGTGTGTAAGACGAGAGATGATAAAGTTGAGAGTAATAT 1673
Db 15105 TTAGAAATTAATAAGAAATGTTGATTGAAATAATACTATATAAATGATAGATCTTGGC 15046
QY 1674 TATTTTAAATGATTTGTCGACATGTAAGATGATATAGTATTAATATTTCTTTTA 1733
Db 15045 TTTGTTATATAGCAATGATTAATGTTTGTGTTACATTAAGATTACTGTTTCTATTAGTTG 14986
QY 1734 ATCAATAATAGTAATTTCTAGCTGTTTGTGATGAATTAATAATCAATGATAAATACTATAGT 1793
Db 14985 ATATTATTGTTTACCTTAGCTGTTTATTAATATTTGTTTATGATAAATACAGCAG 14926
QY 1794 AAAAAAAGATAAATAAATAAATAATTTTTTTATGATTAATAGTTTATTAATAATA 1853
Db 14925 ATGGAAATTCACAAAAATATTTAATTAACCTTAAACTAATAATATTTAGTAATGGTATA 14866
QY 1854 TTAATATCTATACCAATTAATAATTTTGTGTTAAAGTTAATAAATATTTTGTGTTAGA 1913
Db 14865 GATTTTAAATTAATAAATTAATTAATCAATAAATAATATTTTAAATTTATTTAT 14806
QY 1914 AATCCAAATCTGTTGTAATTTATCAATAAACAATAATTAATAACAGCTTAAAGTAAC 1973
Db 14805 CTATTTTACTATAGTATTTTATCATGATATTTAATTTATCAAAACCCAGCTAGAATTAC 14746
QY 1974 AATAATATCAACTAATAAGAACAGTATCTAATGTAACAATAATCTAATGCTAA 2033
Db 14745 TATTATGATTAATAACAATAATTAATGCTAGTATATCATCTTACATGTTGATCAAAATCA 14686
QY 2034 TATAAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAATCAATCTTAT 2093
Db 14685 TTAATAAATAATATCTTACTCTCACTTTTATCTTCTGCTTACACATCACTTGTAT 14626
QY 2094 AATTTCTAAATAATCTTGTAGTTTATTAATCTTAAATGGAATGACTATTAAATAAT 2153
Db 14625 ATTTTTTACATTAATGTTGTTTATGTATGTAACAATAATATTTATAAATATTTTTCACA 14566
QY 2154 GAATTAGTCGACATGAATAACAGGTAACATGATAGTATCATGTGTTGTTATCAT 2213
Db 14565 ATTATAACAATATATTTAATACTAATAATTAACATCACTTAATTTTATTAATACTA 14506
QY 2214 GATCTTACATTTGGATTGATTACAG--TTACTTACCTTTAAGCTTGG--TCCTCAGACC 2269
Db 14505 AAAGGAAAAAAGAAATAATTTTCCITTACCAAGCTGGGTACCGAATTCCTCAGACC 14446
QY 2270 ACTTTGTACAAGAGCTGAACGAGAAAGTAAAAATGATATAAATAATCAATATAATAAT 2329
Db 14445 ACTTTGTACAAGAAAGCTGAACGAGAAAGTAAAAATGATATAAATAATCAATATAATAAT 14386
QY 2330 TAGATTTGATAAATAACAGACTACATAATCTGTAAACAACATATCCAGTCACTA 2389
Db 14385 TAGATTTGATAAATAACAGACTACATAATCTGTAAACAACATATCCAGTCACTA 14326
QY 2390 TGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCC 2449
Db 14325 TGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCC 14266

QY 2450 GACGCACCTTTCGCGCAATAAATACCTGTGACGGAAGATCACTTCGCAAGATAAATAAAT 2509
Db 14265 GACGCACCTTTCGCGCAATAAATACCTGTGACGGAAGATCACTTCGCAAGATAAATAAAT 14206
QY 2510 CTTGGTGTCTCTGTTGTATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAAATGACGCT 2569
Db 14205 CTTGGTGTCTCTGTTGTATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAAATGACGCT 14146
QY 2570 GATCGGATTTTCAACAACCTTATATCTTTTCTCTTCAAGTCTGTTGGCTTCATCTGGATT 2629
Db 14145 GATCGG-----CACTACCCGAAGTATGTCAAAAAGAGTGTCTATGAAGACGCTATTAC 14090
QY 2630 TCAGCCTCTATACTACTATAAAGCTGATAAAGTTTCTGTAATTTCTATCTGATCGACCTGC 2689
Db 14089 AGTGACAGTTGACAGCGACACTATCAGTTGCTCAAGCATATATGATGTCAATATCTCC 14030
QY 2690 AGACTGG-----CTGTGTATAAGGAGCCTGACATTTATATTTCCCAAGAACATCAG 2740
Db 14029 GGTCTGTGTAAAGCACAACCATGAGAAATGAAGCCCGTCTGTCGCTGCC---GAACGCTGG 13973
QY 2741 GTTAATGCGGTTTGTGATGTCATTTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGAT 2800
Db 13972 AAAGCGAAATCAGGAAGGATGGCTGAGTCCGCCGCTTTATTGAATGAACGGCTCT 13913
QY 2801 AACGAGACCGGCACACTGGCCATATCGTGTGTCATCATGCGCCAGCTTTTCATCCCGAT 2860
Db 13912 TTTGCTGACGAGAACAGGG-----ACTGTGMAATGCAGTTTAAGGTTTACACUTATA 13859
QY 2861 ATGCACACCGGGTAAAGTTCAAGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 2920
Db 13858 AAGAGAGACCGGTTATCTGTTTGTGGATGTACAGAGTGATATTTATGACAGCCCGG 13799
QY 2921 GGGGATCACCACTCGTCCCGCGGTGTCATAATAATCACTGTCATCATCAACAACAG 2980
Db 13798 GCGACGATGTTGATCCCGCTGGCCAGTGCAGCTGCTGTCAGATAAAGTCTCCCGTGA 13739
QY 2981 ACGATAACCGGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTGCATTTTCACC-----AGT 3034
Db 13738 ACTTTACCGGTTGTGCATATCGGGATGAAAGCTGGCGCATGATGACCAACGATATGC 13679
QY 3035 CCTGTCTCTGACGAAAAAGAGCGGTTCAATTTCAATMAACGGGGCGACCTGAGCCATCC 3094
Db 13678 CAGTGTGCGGCTCTCCGTTATCGGGGAAGAGTGGCTGATCTCAGCCACCGCGAAAAATGA 13619
QY 3095 CTTCCTGATTTTCCGCTTTCCAGCGGTTTC---GGCAGCGACGACGCGGCTTCATTTCTGCA 3151
Db 13618 CATCAAAAACCCATTAACCTGATGTTCTGGGAATATAAATGTGACGGCTCCCTTATACA 13559
QY 3152 TGG---TTGTGCTTACAGACCGGAGATATTGACATCATATATATGCTTTGACAACTGATA 3208
Db 13558 CAGCGAGTCTCAGGTCGATACAGTAGAAAATACAGAAACTTTTATCAGCTTTAGTAAGTA 13499
QY 3209 GCTGTGCTGTCAACTGTCATCTGTAATACGCTGCTTCAAGCACACCTCTTTTGGACATA 3268
Db 13498 TAGAGCTGAAAATCCAGATGAAGCCGAAACGACTTGTAAAGAGAAAGTATTAAGAGTTGTG 13439
QY 3269 CTTCCTGTTCTTGTGTCAGATGATTTTTCAGGACTATGACACTAGCGGTATATGAATAGGTAG 3328
Db 13438 AAATGTTCTTGTGTCAGATGATTTTTCAGGACTATGACACTAGCGGTATATGAATAGGTAG 13379
QY 3329 ATGTTTTTATTTTGTACACAAAAAGAGGCTCGCACTCTTTTCTTTTCTTTTATTTCTTTTAT 3388
Db 13378 ATGTTTTTATTTTGTACACAAAAAGAGGCTCGCACTCTTTTCTTTTCTTTTATTTCTTTTAT 13319
QY 3389 GATTTAATACGGCAATGAGGCAATAGCGGTAGGCTGGATACACGATTCGCTTTGAGA 3448
Db 13318 GATTTAATACGGCAATGAGGCAATAGCGGTAGGCTGGATACACGATTCGCTTTGAGA 13259
QY 3449 AGAACAATTTGAAGGCTGTCTGCTGCACTAAGTTGGCAGCATCACCCGAGAACATTTTGA 3508
Db 13258 AGAACAATTTGAAGGCTGTCTGCTGCACTAAGTTGGCAGCATCACCCGAGAACATTTTGA 13199

13438	AAATGTTCTTGATCAGATGATTTTCAGGACTATGACCTAGCGTATATGAATAGGTAG	13379
Db		
3329	ATGTTTTATTTTGTGCACACAAAAGGCTCGCACCTCTTTTCTATTCTCTTTTAT	3388
Qy		
13378	ATGTTTTATTTTGTGCACACAAAAGGCTCGCACCTCTTTTCTATTCTCTTTTAT	13319
Db		
3389	GATTTAATACGCATGTAGGACAATPAGCGATGAGCTGGGATACGACGATTCGGTTTGAGA	3448
Qy		
13318	GATTTAATACGCATGTAGGACAATPAGCGATGAGCTGGGATACGACGATTCGGTTTGAGA	13259
Db		
3449	AGAACATTTTGGAGGCTGTCGGTGCACATAAGTTGCGACATCACCCGAAAGACATTGGGA	3508
Qy		
13258	AGAACATTTTGGAGGCTGTCGGTGCACATAAGTTGCGACATCACCCGAAAGACATTGGGA	13199
Db		
3509	AGGCTGTCGGTGCAGCTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTGCCTGG	3568
Qy		
13198	AGGCTGTCGGTGCAGCTACAGGTCACATAACCATCTAAGTAGTTGATTCATAGTGCCTGG	13139
Db		
3569	ATATGTTGTGTTTTACAGTAATATGCTAGCTGCTTTTTATCGAAACTAAATTAATA	3628
Qy		
13138	ATATGTTGTGTTTTACAGTAATATGCTAGCTGCTTTTTATCGAAACTAAATTAATA	13079
Db		
3629	TTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTTTGTACAAACTGTCTAGAG	3687
Qy		
13078	TTTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTTTGTACAAACTGTCTAGAG	13020
Db		

RESULT 9

```

RES001.5
US-10-385-546-7/C
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Hellmwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

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	Query Match	28.7%;	Score 1277.8;	DB 15;	Length 17476;
	Best Local Similarity	62.4%;	Pred. No. 4e-183;		
	Matches 2321;	Conservative	0;	Mismatches 1312;	Indels 86; Gaps 17;
Qy	21	CTCGAGACAGT	TTGTACAAAAAGCTGGAACGAGAAACGTAAATATGATATAATCAAT	80	
Db	16704	CTTCAGACAGT	TTGTACAAAAAGCTGGAACGAGAAACGTAAATATGATATAATCAAT	16645	
Qy	81	ATATTAATTAGAAT	TTTGTCAATAAAAAACGACATACATAATCTGTAAACACAAATATC	140	
Db	16644	ATATTAATTAGAAT	TTTGTCAATAAAAAACGACATACATAATCTGTAAACACAAATATC	165985	
Qy	141	CAGTCATCTAGGAAT	CAACTACTTCTAGATGGTATTAGTGACCTGTGTAGTCGACCGACAGCCTT	200	
Db	16584	CAGTCATCTAGGAAT	CAACTACTTCTAGATGGTATTAGTGACCTGTGTAGTCGACCGACAGCCTT	16525	
Qy	201	CCAAATGTTCTT	CGGGTGATCGCCAACTTAGTCGACCGACGCTTCGCAATGTTCTT	260	
Db	16524	CCAAATGTTCTT	CGGGTGATCGGCCAACTTAGTCGACCGACGCTTCGCAATGTTCTT	16465	
Qy	261	CTCAAAACGGAAAT	CGTCGTATCCAGGCCTACTCGCTATTGTCCTCAATGCGCGTATTAATCA	320	

16464	DB	CTCAAGCGGAATCGTCGATCCAGCCCTACTCGCTATTGTCTCTAATCGCGTATTAAATCA	16405
321	QY	TAAAGAGAAATTAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAAATAAAAAATC	380
16404	DB	TAAAGAGAAATTAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAAATAAAAAATC	16345
381	QY	TACCTATTTCATATAGCTAGTGTCTAGTCTGAATCATCTGCATCAAGACAAATTC	440
16344	DB	TACCTATTTCATATAGCTAGTGTCTAGTCTGAATCATCTGCATCAAGACAAAGT	16285
441	QY	ACAACTCTTATACATTTTCTTTACAAGTCGTTCGGCTTCATCTGGATTTTTCAGCCTCTAT	500
16284	DB	ATGTCAAAAAGAGGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGACA	16228
501	QY	ACTTACTAAACGTGATTAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGT	560
16227	DB	GCTATCAGTTGCTCAAGGCATATATGATGTCAAATATCTCCGGTCTGGTAAGACAAACAT	16168
561	QY	GTATAAGGAGCCTGACATTTATATCCCAAGAACATCAGGTAAATGCGGTTTTTGTGATGT	620
16167	DB	GCAGAAATGAAGCCCGTCTGTCGGTGCC--GAAGCTGGAAAGCGGAAATCAGBAGG	16111
621	QY	CATTTTCCGGTGGCTGAGATCAGCCACTTTTCCCGATTAACGAGACCGGCACACTGG	680
16110	DB	GATGCTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCTTTTCTGCACGAGAACAGG-	16052
681	QY	CCATATCCGTGTCATCATGCGCAGCTTTCATCCCGATATGCACACCGGGTAAAGTT	740
16051	DB	-----ACTGGTGAATGCAGTTTAAGTTTACACTATAAAGAGAGCGGTTATCGTC	15997
741	QY	CACGGGAGACTTTATCTGACAGCAGACGTCACTGGCCAGCGGGATCACCATCCGTCGCC	800
15996	DB	TGTTTGTGGATGTACAGAGTGATATTAATGACACGCCCGCGCGAGGTGATGATCCCCC	15937
801	QY	CGGGCGTGCATATATATCATCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTT	860
15936	DB	TGGCCAGTGCAGTCTGCTGCAGATAAGTCTCCCGTGAATTTTACCCGGTGGTGCAAT	15877
861	QY	TATAGTGTAAACCTTAAACTGCATTTTCAAC-----AGTCCCTGTTTCTCGTCAGCAAAA	914
15876	DB	TCGGGATCAAAAGCTGGCGCATGATGACACCGATATGCCAGTGTGCGGCTCTCCGTTA	15817
915	QY	GAGCCGTTCAATTAATAAACCAGGGGAGCTCAGCCATCCCTTCTGTATTTTCCGCTTTC	974
15816	DB	TGCGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAATTAACATCAAAAACGCAATAACC	15757
975	QY	CAGCGTTTC--GGCAGCAGACGACGCGGCTTCATTCTGCATGGTTGTGCTTACCAGACCG	1031
15756	DB	TGATGTTCTGGGGAATATAAATGTGAGGCTCCCTTATACAG-----CCAAGTCG	15706
1032	QY	GAGATATTCAGATCATATATAGCCTTGAGCAATGATGTGCGTGTCACTGTCACTG	1091
15705	DB	CAGGTCGATACAGTAAATTAACAGAAACTTTATCACGTTTAGTAAGTATAGAGGCTGAA	15646
1092	QY	TAATACGCTGCTTCATAGACACACCTCTTTTTCACATACCTTCCGGTAGTG---CCGATCA	1147
15645	DB	AATCCAGATGAAGCCGACAGCTTGTAAAGAAAAGTATAAGATGTGAAATCCGATCA	15586
1148	QY	ACGTCTCATTTTTCGCCAAAGTTGGCCACAGGCTTCCCGGTATCAACAGGGACACAGGA	1207
15585	DB	ACGTCTCATTTTTCGCCAAAGTTGGCCACAGGCTTCCCGGTATCAACAGGGACACAGGA	15526
1208	QY	TTTTATTATCTCGAAGTGATCTTCCGTCACAGGTATTTATTTCCGCCGAAGTGGCTCG	1267
15525	DB	TTTTATTATCTCGAAGTGATCTTCCGTCACAGGTATTTATTTCCGCCGAAGTGGCTCG	15466
1268	QY	GGTGATGCTGCCAATTTAGTCAGCTACAGGTCACTAAATACCATCTAAAGTAGTTGATTCAT	1327
15465	DB	GGTGATGCTGCCAATTTAGTCAGCTACAGGTCACTAAATACCATCTAAAGTAGTTGATTCAT	15406
1328	QY	AGTGACTGGGATATGTTGTGTTTTACGATATTATGTAGTCTGTTTTTATGCAAAATCTAA	1387

Db 13660 TATCGGGAAGAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAGCCATTAA 13601
Qy 3113 TCCAGCGTTC---GGCAGCAGAGCAGCGGGTTCATCTCGATGG---TTGTGCTTACCA 3166
Db 13600 CCTGATGTTCTGGGGAATATAAATGTCCAGGCTCCCTTATACACAGCCAGTCTGCAGGTG 13541
Qy 3167 GACCGGAGATATTCACATCATATATGCTTGGAGCACTGTAGTAGTGTGCGTGTCAACTGT 3226
Db 13540 ATACAGTAGAAATPACGAAACTTTATACGTTTAGTAGTAGAGGCTGAAATCCAG 13481
Qy 3227 CACTGTATAGCGCTTCATPAGCACACCTCTTTTTCACATPACTTCTGTCTTGTATGACG 3286
Db 13480 ATGAAGCCGACGACTTGTGAAGAAAGATGAAGAGTTGTGAAATTTGTTCTTGATGCAG 13421
Qy 3287 ATGATTTTCAGACTATGACACTAGCTAGCTATATGATATGATAGTAGTGTATTTTGTGCAC 3346
Db 13420 ATGATTTTCAGACTATGACACTAGCTAGCTATATGATATGATAGTAGTGTATTTTGTGCAC 13361
Qy 3347 ACAAAAAGAGCGCTCGACCTCTTTTCTTATTTCTTTTATGATTTTAATAACGGCATTGA 3406
Db 13360 ACAAAAAGAGCGCTCGACCTCTTTTCTTATTTCTTTTATGATTTTAATAACGGCATTGA 13301
Qy 3407 GGCAATAGCAGTAGGTGATGACAGCAGATTCGGTTTGGAGAAGCAATTTGGAGGCTG 3466
Db 13300 GGCAATAGCAGTAGGTGATGACAGCAGATTCGGTTTGGAGAAGCAATTTGGAGGCTG 13241
Qy 3467 TCGGTCGACTAAGTTGGCAGCATCACCCGAGAACATTTGGAAGGCTGCGGTGCATAC 3526
Db 13240 TCGGTCGACTAAGTTGGCAGCATCACCCGAGAACATTTGGAAGGCTGCGGTGCATAC 13181
Qy 3527 AGGTCACATAACCACTAAAGTAGTGTATTCATAGTACTGGATATGTTGTGTTTACAG 3586
Db 13180 AGGTCACATAACCACTAAAGTAGTGTATTCATAGTACTGGATATGTTGTGTTTACAG 13121
Qy 3587 TATATAGTAGTGTGTTTATGCAAAATCTAAATTAATATATGATATATATATATCAATT 3646
Db 13120 TATATAGTAGTGTGTTTATGCAAAATCTAAATTAATATATGATATATATATATCAATT 13061
Qy 3647 TACGTTTCTCGTTACGTTTTTTTGTACAAACTTGTCTAGAG 3687
Db 13060 TACGTTTCTCGTTACGTTTTTTTGTACAAACTTGTCTAGAG 13020

RESULT 8

US-10-055-001A-24/c
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 28.7%; Score 1277.8; DB 15; Length 17476;
Best Local Similarity 62.4%; Pred. No. 4e-183;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;

Qy 21 CTCGAGCAGTGTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAATATCAAT 80

Db 16704 CTCTAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAATATCAAT 16645
Qy 81 ATATTAAATTTAGATTTCATATAAAAAACAGACTACATAATCTGTAAAAACACAACATATC 140
Db 16644 ATATTAAATTTAGATTTCATATAAAAAACAGACTACATAATCTGTAAAAACACAACATATC 16585
Qy 141 CAGTCACTAGTAATCAACTACTTTAGATGGTATTTAGTACCTGTAGTCGACCGACGCCCTT 200
Db 16584 CAGTCACTAGTAATCAACTACTTTAGATGGTATTTAGTACCTGTAGTCGACCGACGCCCTT 16525
Qy 201 CCAAAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACGACAGCCTTCGAAATGTTCTT 260
Db 16524 CCAAAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACGACAGCCTTCGAAATGTTCTT 16465
Qy 261 CTCAAAACGGAATCGTGGTATCCAGCCCTACTCGCTATTGTCCTCAATGCGGTATTAATCA 320
Db 16464 CTCAAAACGGAATCGTGGTATCCAGCCCTACTCGCTATTGTCCTCAATGCGGTATTAATCA 16405
Qy 321 TAAAAAGAAATAGAAAAAGAGGTGGAGCCTCTTTTGTGTGACAAATAAAAACATC 380
Db 16404 TAAAAAGAAATAGAAAAAGAGGTGGAGCCTCTTTTGTGTGACAAATAAAAACATC 16345
Qy 381 TACCTATTATATACGCTAGTGTCAATAGTCTCTGAAATCATCTGCATCAAGAACAGAGT 440
Db 16344 TACCTATTATATACGCTAGTGTCAATAGTCTCTGAAATCATCTGCATCAAGAACAGAGT 16285
Qy 441 ACAACTCTTATATCTTTCTCTTCAAGTCTGGCTTCACTGGATTTTCAGCCTCTAT 500
Db 16284 ATGTCAAAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACGCGACA 16228
Qy 501 ACTTACTAAGCGTATAGAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGT 560
Db 16227 GCTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGGTCTGTATAGCACAACT 16168
Qy 561 GTATAAGGAGCGCTGACATTTATATTTCCGAGAACATCAGGTTAAAGCGCTTTTGTAGT 620
Db 16167 GCAGATGAAGCGCTGCTGTGCGTGC---GAACGCTGGAAGCGGAAATCAGGAAG 16111
Qy 621 CATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGGATTAACGAGACCGGACACTGG 680
Db 16110 GATGGCTGAGTCTCCCGGTTTATTGAATGAACGGCTCTTTTGTGACGAGAACAGGG- 16052
Qy 681 CCATATCGTGGTCTATCATGCGCCAGCTTTTCCATCCCGATATGACCAACCGGGTAAAGTT 740
Db 16051 -----ACTGGTGAATGCGAGTTTAAAGTTTACACTATTAAGAGAGAGCGCTTATGTC 15997
Qy 741 CACGGGAGACTTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGATCACCAATCGCTGCC 800
Db 15996 TGTTTGTGATGTACAGAGTGTATTTATGACACGCGCGGCGAGGATGGTATCCGCC 15937
Qy 801 CGGGGTGTCAATATATCACTCTGTACATCCAAACAGACGATAGCGGCTCTCTCTTT 860
Db 15936 TGGCCAGTGCACGCTGCTGTCAGATAAAGTCTCCCGTGAACCTTACCCGGTGGTGATA 15877
Qy 861 TATAGTGTAAACCTTAACTGCAATTTCAOC-----AGTCCCTGTTCTCGTCAGCAAAA 914
Db 15876 TCGGGATGAAGCTGGCGCATGATGACCAAGATATGGCCAGTGTGCGGTCTCCGTTA 15817
Qy 915 GAGCGGTTTCAATTAATAACCGGGCGACCTTCAGCATCCCTTCTGTATTTTCCGCTTTC 974
Db 15816 TCGGGGAAGAAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAACGCCATTAACC 15757
Qy 975 CAGCGTTC---GGCAGCAGACGAGCGGCTTCATTTCTGATGGTGTGCTTACCAGACCG 1031
Db 15756 TGATGTTCTGGGGAATATAAATGTCCAGGCTCCCTTATACAG-----CCAGTCTG 15706
Qy 1032 GAGATATTGACATCATATATGCTTTGACAACTGATAGCTGTCCGTGTCAACTGTCACTG 1091
Db 15705 CAGGTCGATACAGTAGAATTTACAGAACTTTTATCACGTTTAGTAAGTATAGAGCTGAA 15646
Qy 1092 TAATACGCTGCTTCATAGCACACCTCTTTTGTGACATACCTCTGGGTAGTG-----CCGATCA 1147
Db 15645 AATCCAGATGAAGCGGACGACTTGTGAAGAAAAAGTATAAGAGTTGTGAAATCCGATCA 15586

QY 915 GAGCGTTCATTTCAATAACGGGCGACCTCAGCCATCCCTCTCGATTTTCCGCTTC 974
Db 15798 TCGGGGAAGAAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAACGCCATTAACC 15739
QY 975 CAGCGTTC---GGCAGCGAGACGCGGCTTCATCTCGCATGGTGTGTTACCCAGACCG 1031
Db 15738 TGNATGTTCTGGGGAAATATAAATGTGTCAGGCTCCCTTATACACAG-----CCAGTCTG 15688
QY 1032 GAGATATGACATCATATATGCTTGAGCAACTGATAGCTGCTGCTGCTGCTCAACTGTCACGTG 1091
Db 15687 CAGGTGATACAGTAGAATAATACAGAACTTTATCACGTTTATAGTAAATAGATAGAGGCTGAA 15628
QY 1092 TAATACGCTGCTTCATAGCACACCTCTTTTGACATACCTTCGGGTAGTG---CGATCA 1147
Db 15627 ATCCAGATGAAGCCGAGACGACTTGAAGAGAAAGTATPAAGATTTGCGAAATCCGATCA 15568
QY 1148 AGCTCTCATTTTGGCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACCGAGA 1207
Db 15567 AGCTCTCATTTTGGCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACCGAGA 15508
QY 1208 TTTATTTATTCGCGAAGTATCTCCGTCACAGGTATTTATTTCCGCGCAAGTGGCTG 1267
Db 15507 TTTATTTATTCGCGAAGTATCTCCGTCACAGGTATTTATTTCCGCGCAAGTGGCTG 15448
QY 1268 GGTGATGCTGCCAACTTAGTCGACTACAGTCACTAATACCATCTAAGTAGTTGATTCAT 1327
Db 15447 GGTGATGCTGCCAACTTAGTCGACTACAGTCACTAATACCATCTAAGTAGTTGATTCAT 15388
QY 1328 AGTGAAGTATGTTGTTTACAGTATATGATGCTGTTTATTTGCGCAAAATCTAA 1387
Db 15387 AGTGAAGTATGTTGTTTACAGTATATGATGCTGTTTATTTGCGCAAAATCTAA 15328
QY 1388 TTTAATATATTTGATATATATCAATTTAGTTTCTCGTTCTAGCTTCTGTTGACAAAGTG 1447
Db 15327 TTTAATATATTTGATATATATCAATTTAGTTTCTCGTTCTAGCTTCTGTTGACAAAGTG 15268
QY 1448 GTCTCAGGAATTCGGTACCAGCTGAAGGAATAATATTTTCTTTTCTTTTCTTTAGTA 1507
Db 15267 GTCTCAGGAATTCGGTACCAGCTGAAGGAATAATATTTTCTTTTCTTTTCTTTAGTA 15208
QY 1508 TAAATATGTTAAGTATGTTTAAATAGTATGATTAATAATATAGTGTGTTAATGTTGA 1567
Db 15207 TAAACAATGATGATGATCATCATGTTACCTGTTTATTCATGTTCCGACTAATTTCAATTA 15148
QY 1568 AAAAAATATTTATAATATATTTTACATAAACAACATAGTAATGTAAAAAATATGAC 1627
Db 15147 ATTATATGTCATCCATTTAGAAGTTTAAATACTACAGTATTTATAGAATAATATAA 15088
QY 1628 AAGTATGTTGAAGCAGGAAGATAAAGTTGAGAGTAGTATATTTATTTTAAATGAAT 1687
Db 15087 GAATGTTGATTGAATAATAATATATATAAATGATAGATCTTCGCGCTTTGTTATATAGC 15028
QY 1688 TTGATCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1747
Db 15027 ATTAGATATGTTTGTATATAGATGATGATGATGATGATGATGATGATGATGATGAT 14968
QY 1748 TCTAGCTGGTTTGATGAATTTAAATATCAATGATATAAATATCTAGTAAATAAAGATAA 1807
Db 14967 TTTAGCTGTTTAAATATTTTGTGTTTATGATTAATTAACAGCAGATGGGAATTTCTAA 14908
QY 1808 ATAAATTTAAATATATTTTATTTATGATTAATAGTTTATTTATATAATATAATATCTATAC 1867
Db 14907 CAAAAATTTTAACTTTTAACTAAATAATTTAGTAAATTTAGTAAATTTATTAATTTATA 14848
QY 1868 CATTAATAATTTTATTTTAAAGTTTAAATATTTTGTGTAATAATTTTGTAGAAATTTCCATCTGCT 1927
Db 14847 TAAATAAATAATATATATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 14788
QY 1928 TGTAAATTTTCAATAAACAATAATTAATAACAAGCTAAAGTAAACAATAATATCAAAAC 1987
Db 14787 AGTATTTTATCATTTGATATTTAATTTATCAAAACAGCTAGATTTACTATTTATGATTTAA 14728

QY 1988 TAATAGAAACAGTAAATCTAATGTTAAACAAACATAATCTAATGCTAATAATAACAAAGCGCA 2047
Db 14727 CAAATATTTAAGCTAGTATATCATCTTACATGTTTCGATCAAAATTCATTAAAAATAATATA 14668
QY 2048 AGATCTATCATTTTATATATGATTTATTTTCAATCAACATCTCTTATTTATTTCTAATAAT 2107
Db 14667 CTTACTCTCAACTTTTATCTTTCTGCTTACACATCATCTGTCATATTTTATTTTACATTA 14608
QY 2108 ACTTCTAGTTTTTATTAACCTTCTAATGATGATGATTAATTAATTAATGAATAGTGAACA 2167
Db 14607 CTATGTTGTTTATGTPAAACAATATATTTAATAATTTTATTTTTCACAAATTAACAACTAT 14548
QY 2168 TGAATAAACAAAGGTAAACATGATGATCATGTCATTTGTGTATCATTTGATGATTTTACATTTGG 2227
Db 14547 ATTATTTAATCATACTAATTAATAACATCACTTAACATTTTATTTTACTAAAAAGGAAAAAGAA 14488
QY 2228 ATTGATTACAGTTACTTACTTACCTTGGATTCCTCTAGACCACTTTCTAGCAAGAAAGCT 2287
Db 14487 AATAATTTTCTTCTTACAGTTGGTACCGAATTCCTCGAGACCACTTTTGTACAAAGAAAGCT 14428
QY 2288 GAAACAGAAACGTAATAATGATATAATAATCAATATTAATAATTAATTTTGTGATAAAAA 2347
Db 14427 GAAACAGAAACGTAATAATGATATAATAATCAATATTAATAATTTTGTGATAAAAA 14368
QY 2348 CAGACTACATAATCTGTAAAAACAACATATCCAGTCACTATGATGAATCACTTACTTAGAT 2407
Db 14367 CAGACTACATAATCTGTAAAAACAACATATCCAGTCACTATGATGAATCACTTACTTAGAT 14308
QY 2408 GGTATGATGACCTGTAGTCGACTAAGTTGGCAGCATCACCGACGCACTTTTGGCCCGAA 2467
Db 14307 GGTATGATGACCTGTAGTCGACTAAGTTGGCAGCATCACCGACGCACTTTTGGCCCGAA 14248
QY 2468 TAAATACCTGTGACGGAAGATCACTTTCGAGAAATAATAATAATCCTGGTGTCCCTGTGAT 2527
Db 14247 TAAATACCTGTGACGGAAGATCACTTTCGAGAAATAATAATAATCCTGGTGTCCCTGTGAT 14188
QY 2528 ACCGGAAGCCCTGGGCCAACTTTTGGCGAAATGAGAGCTTGATCGGATTTTCAACAATC 2587
Db 14187 ACCGGAAGCCCTGGGCCAACTTTTGGCGAAATGAGAGCTTGATCGGATTTTCAACAATC 14132
QY 2588 TTATACTTTCTTCTACAAGTGTTCGGCTTCATCTGGATTTTTCAGCCCTATATCTTACT 2647
Db 14131 GAAATGATGCAAAAAGAGGTGTCTATGAGCAGCGTATTACAGTGACAGTTGACAGCA 14072
QY 2648 AAACTGTATAAAGTTTCTGTAATTTCTACTGTATCGACTGACAGCTGG-----CT 2698
Db 14071 CAGCTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGCTCTGTTAAGACACAACC 14012
QY 2699 GTGATAAGGAGGCTGACATTTATTTCCCGAAGACATCAGGTTAATGGCGTTTGTAT 2758
Db 14011 ATGCAAGATGAAGCCGCTGCTGCGTGCC---GAACTGTGAAAGCGGAAATCAGGAA 13955
QY 2759 GTCAATTTTCGCGGTGCTGAGATCAGCACTTCTTCCCGATAACCGAGACCGGCACT 2818
Db 13954 GGGATGGCTGAGTGTGCGCCGGTTTATGAAATGAAGCGTCTTTGCTGACGAGAACAGG 13895
QY 2819 GGCATATACGTTGGTTCATCATCGCCAGCTTTTATCCCGATATGACCAACCGGGTAAAG 2878
Db 13894 GA-----CTGGTGAATGCAAGTTTAAAGTTTACACCTATAAAGAGAGAGCGGTTATCG 13841
QY 2879 TTCACGGGAGACTTTATCTGACAGAGAGCTGCACTGGCGGGGAGATCACCATCCGTCG 2938
Db 13840 TCTGTTTGTGATGACAGAGTATTTATGACAGCCCGCGGCGAGGATGGTGTATCC 13781
QY 2939 CCGGCGGTGTCATAATATCACTCTGTATCATCTCCAAACACAGACGATACGGTCTCTCT 2998
Db 13780 CTTGGCCAGTGCAGCTCTCTGTGATGAAGTCTCTCCGTGAACCTTACCCGGTGTGCA 13721
QY 2999 TTTATAGGTGTAACCTTTAACTGCAATTTTACC-----AGTCCCTGTTTCTCGTACAGAA 3052
Db 13720 TATCGGGGATGAAGCTGGCGCATGATGACCAACCGATATGGCAGTGTGCGGCTCTCCGT 13661
QY 3053 AAGAGCCGTTTCAATTAATAAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTT 3112

17801 TTTTGTACAAAGTTGGCATTATATAAAAGCATCTCATCAATTTGTGTCAACGACAGG 17860
3681 -----TCTAGAGT 3688
17861 TCACATATCACTCAAAATAAAATCATTTATTGGGGCCCGAGATCCATGCTAGCTTAGAGT 17920
3689 CCGCTTTTAATAGATATGGAGACGCTATGATCGCATGATATTTGCTTTCAATTTCTGT 3748
17921 CCGCTTTTAATAGATATGGAGACGCTATGATCGCATGATATTTGCTTTCAATTTCTGT 17980
3749 TGTGCACTGTGTAATAAAACCTGACATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3808
17981 TGTGCACTGTGTAATAAAACCTGACATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 18040
3809 CATTCTAATGAATATATACACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA 3868
18041 CATTCTAATGAATATATACACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA 18100
3869 ATTACTGATTTGATCCCTTACTTATATGATCAATATTTAAATGAAAAAATAATATTTGT 3928
18101 ATTACTGATTTGATCCCTTACTTATATGATCAATATTTAAATGAAAAAATAATATTTGT 18160
3929 GCTGAATAGTTTATAGGACATCTATGATAGCGCCACAAATTAACAAATTTGCGTTT 3988
18161 GCTGAATAGTTTATAGGACATCTATGATAGCGCCACAAATTAACAAATTTGCGTTT 18220
3989 TATTATTACAAATCAATTTTAAAAAAGCGGCGAGAACCGGTCAAACTTAAAGACTGAT 4048
18221 TATTATTACAAATCAATTTTAAAAAAGCGGCGAGAACCGGTCAAACTTAAAGACTGAT 18280
4049 TACATAAATCTATTCAAAATTTAAAAAGCGCCAGGCGCTAGTATCTACGACACACCGAG 4108
18281 TACATAAATCTATTCAAAATTTAAAAAGCGCCAGGCGCTAGTATCTACGACACACCGAG 18340
4109 CGGCGAATCTAATAGTTTCACTGAGGGAATCCGTTTCCCGCGCGCGCATGGGTGA 4168
18341 CGGCGAATCTAATAGTTTCACTGAGGGAATCCGTTTCCCGCGCGCGCATGGGTGA 18400
4169 GATTCCTTTGAGTTTGGCGCTCCGCTCTACCGAAAGTTTACGGGCGCCATTTCAAC 4228
18401 GATTCCTTTGAGTTTGGCGCTCCGCTCTACCGAAAGTTTACGGGCGCCATTTCAAC 18460
4229 CCGGTCGAGCAGCGCGCGGTAACCGACTTGTCTGCCCGGAGAAATATGACGATTTT 4288
18461 CCGGTCGAGCAGCGCGCGGTAACCGACTTGTCTGCCCGGAGAAATATGACGATTTT 18520
4289 TTGGTGTATGTGGGCGCCCAAAATGAAGTGCAGGTCAAACTTGGACAGTGCACCAATCGT 4348
18521 TTGGTGTATGTGGGCGCCCAAAATGAAGTGCAGGTCAAACTTGGACAGTGCACCAATCGT 18580
4349 TGGGCGGTTCCAGGGCGAATTTTGGCAACAATGTCAGGCTCAGCAGACCTGCGAGCA 4408
18581 TGGGCGGTTCCAGGGCGAATTTTGGCAACAATGTCAGGCTCAGCAGACCTGCGAGCA 18640
4409 TCACAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTTAATCTGC 4459
18641 TCACAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTTAATCTGC 18691

RESULT 7

US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellmwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; CURRENT FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 29.3%; Score 1305; DB 15; Length 17458;
Best Local Similarity 62.4%; Pred. No. 3.1e-187;
Matches 2308; Conservative 0; Mismatches 1325; Indels 68; Gaps 14;
QY 21 CTCGACGACAGTTTGTACAAAAGCTGAAACGAGAAACGTAAATATGATATAATCAAT 80
Db CTCTAGCAAGTTTGTACAAAAGCTGAAACGAGAAACGTAAATATGATATAATCAAT 16627
QY 81 ATATTAAATTAGATTTTGCATAAAAAAGACATACATATCTGTAAAAACACACATATC 140
Db ATATTAAATTAGATTTTGCATAAAAAAGACATACATATCTGTAAAAACACACATATC 16567
QY 141 CAGTCACTATGATCAACTACTTATAGATGATTTAGTGAACCTGTAGTCGACGACGCTT 200
Db CAGTCACTATGATCAACTACTTATAGATGATTTAGTGAACCTGTAGTCGACGACGCTT 16507
QY 201 CCAATTTGTTTCGGGTGATGCTGCCAACTTAGTGCACGACGACCTTCCAAATGTTCTT 260
Db CCAATTTGTTTCGGGTGATGCTGCCAACTTAGTGCACGACGACCTTCCAAATGTTCTT 16447
QY 261 CTCAACGGAATCGTCTATCCAGCCTTACTCGCTATTTGTCTCAATGCCGTATTAATCA 320
Db CTCAACGGAATCGTCTATCCAGCCTTACTCGCTATTTGTCTCAATGCCGTATTAATCA 16387
QY 321 TAAAAAGAAATAAGAAAGAGGTGGAGGCTCTTTTGTGTGACAAAATAAAACATC 380
Db TAAAAAGAAATAAGAAAGAGGTGGAGGCTCTTTTGTGTGACAAAATAAAACATC 16327
QY 381 TACCTATTCATACGCTAGTGTCTGAAATCATCTGCAATCATCTGCAATCAAGAAATTC 440
Db TACCTATTCATACGCTAGTGTCTGAAATCATCTGCAATCATCTGCAATCAAGAAATTC 16267
QY 441 ACAACTCTTATCTTTCTTACAACTCGTTCGGCTTCTATCGGATTTTTCAGCTCTAT 500
Db ATGTCAAAAGAGGTGTCTATGAA---GCAGCGTATTTACAGTGCAGGACGACA 16210
QY 501 ACTTACTAAAGCTGATTAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGCT 560
Db GCTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGCTGCTGTAAGCAACAT 16150
QY 561 GTATAAGGAGCCTGACATTTATATTTCCAGAAACATCAGGTTAATGGCGTTTGTATGT 620
Db GCAGAAATGAAGCCGCTGCTGCGTGCC---GAACGCTGAAACGGGAAATCAGGAGG 16093
QY 621 CATTTTTCGGGTGCTGAGATCAGCCACTTTCTCCCGATTAACGAGACCGGCACTGG 680
Db CATGCTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCTTTTGTGACGAGAAACAGGG- 16034
QY 681 CCATATCGGTGCTCATATGCGCCAGCTTTTCATCCCGATATGACCAACCGGGTAAAGTT 740
Db -----ACTGTGAAATGCGAGTTTAAAGTTTACCTATATAAAGAGAGAGCGCTATCGTC 15979
QY 741 CACGGGAGACTTTTATCTGACAGCAGACGTCACCTGGCCAGGGGATCACCATCGCTGCC 800
Db TGTGTGTGATGACAGAGTATATTTATGACAGCCCGGCGAGCGGATGATGATCCCCC 15919
QY 801 CGGGCGTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTT 860
Db TGGCCAGTGACGCTGCTGTCAGATAAAGTCTCCGTGAACCTTTACCCGGTGGTGATA 15859
QY 861 TATAGGTGTAACCTTAACATGCAATTTTCAAC-----AGTCCCTGTTCTCGTCGACAAA 914
Db TCGGGGATGAAAGCTGGCGCATGATGACACCGATATGACCGGATGTCGGGTCTCCGTTA 15799

QY	1723	-----	1722
Db	15641	GAGTGGCAGCGCGGGCGTAATCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGATAT	15700
QY	1723	-----	1740
Db	15701	CGGTATTTGCGCGCTGATTTTTCGGGTATAGAAATATATATCTGCTATGTCGGGCCCATAA	15760
QY	1741	TAGTAATTTCTAGCTAGCTGGTTTGATGAATTAATAATCAATGATTAATAATCTATAGTAAAAATA	1800
Db	15761	TAGTAATTTCTAGCTAGCTGGTTTGATGAATTAATAATCAATGATTAATAATCTATAGTAAAAATA	15820
QY	1801	AGAATAAATAAATTAATAATAATTTTTTTTATGATTAATAGTTTATATATATTAATTAATAA	1860
Db	15821	AGAATAAATAAATTAATAATAATTTTTTTTATGATTAATAGTTTATATATATTAATTAATAA	15880
QY	1861	TCTATACCATTACTATAATAATTTTTAGTTTAAAAAGTTAATAAATAATTTTGTAGTAATTTCCA	1920
Db	15881	TCTATACCATTACTATAATAATTTTTAGTTTAAAAAGTTAATAAATAATTTTGTAGTAATTTCCA	15940
QY	1921	ATCTGCTTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAAATAAT	1980
Db	15941	ATCTGCTTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAGTAACAAATAAT	16000
QY	1981	ATCAAACTAATAGAAACAGTAATCTAATGTAACAAACATATCTAATGCTAATATAACA	2040
Db	16001	ATCAAACTAATAGAAACAGTAATCTAATGTAACAAACATATCTAATGCTAATATAACA	16060
QY	2041	AAGCCCAAGATCTATCATTTTATATAGTATATTTTTCAATCAACATCTTTATTAAATTTCT	2100
Db	16061	AAGCCCAAGATCTATCATTTTATATAGTATATTTTTCAATCAACATCTTTATTAAATTTCT	16120
QY	2101	AAATAATATCTGTAGTTTATTAACCTTCAAATGGATGACTATTAATTAATGAATGAAATAG	2160
Db	16121	AAATAATATCTGTAGTTTATTAACCTTCAAATGGATGACTATTAATTAATGAATGAAATAG	16180
QY	2161	TCGAACATGAATAAACAAGGTAACATGATAGATCATGTCATTTGCTGTTATCATTTGACTTA	2220
Db	16181	TCGAACATGAATAAACAAGGTAACATGATAGATCATGTCATTTGCTGTTATCATTTGACTTA	16240
QY	2221	CATTTGGATTGATTACAGTTACTTACCT-----TAAGCTTGGATCCCTCTAG	2266
Db	16241	CATTTGGATTGATTACAGTTGGGAATTCGGTTTCGAAATCGATAAGCTTGATCCCTCTAG	16300
QY	2267	A-----	2267
Db	16301	AGAGCTGCAGCTGGATGGCAATAATGATTTTATTTGACTGATAGTGAOCTGTGCTTG	16360
QY	2268	-----	2293
Db	16361	CAACAAATTGATAAGCAATGCTTCTTAATGCCCACTTTGTACAGAAAGCTGACGA	16420
QY	2294	GAAACCTAAAAATGATATAAATATCAATATATTAATTAATTAATTTGATTTGCAATAAAAAAGACT	2353
Db	16421	GAAACCTAAAAATGATATAAATATCAATATATTAATTAATTAATTTGATTTGCAATAAAAAAGACT	16480
QY	2354	ACATAATATGTTAAAAACAACAATATCCAGTCACTATGAACTCAACTACTTGTAGTGGTATT	2413
Db	16481	ACATAATATGTTAAAAACAACAATATCCAGTCACTATGAACTCAACTACTTGTAGTGGTATT	16540
QY	2414	AGTGAOCTGTAGTCGAATAAGTTGGCAGCATCACCCGACGCACCTTTCGCCGGAATAATA	2473
Db	16541	AGTGAOCTGTAGTCGAATAAGTTGGCAGCATCACCCGACGCACCTTTCGCCGGAATAATA	16600
QY	2474	CCTGTGACGGAAGATCATCTTCGCAGGAATAATAAATCCTGGTGTCCCTGTTGTATCCGGG	2533
Db	16601	CCTGTGACGGAAGATCATCTTCGCAGGAATAATAAATCCTGGTGTCCCTGTTGTATCCGGG	16660
QY	2534	AAGCCCTGGGCCCAACTTTTTCGCCGAATAATGAGACGTTGATCGGCACTACCCGTTTCCAAAC	2585
Db	16661	AAGCCCTGGGCCCAACTTTTTCGCCGAATAATGAGACGTTGATCGGCACTACCCGTTTCCAAAC	16720

Db	13421	AGAAATAGAAAGAGGTGGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT	13480
Qy	386	ATTCAATATACGTTAGTGTCTAGTCTGTGAATAATCATCTGCATCAAGAACAAATTTACAAAC	445
Db	13481	ATTCAATACGCTAGTGTCTAGTCTGTGAATAATCATCTGCATCAAGAACAAATTTACAAAC	13540
Qy	446	TCCTTATACCTTTCTCTTACAAAGTCGTTCCGCTTCATCTCGATTTTCAGCCCTCTATACTTA	505
Db	13541	TCCTTATACCTTTCTCTTACAAAGTCGTTCCGCTTCATCTCGATTTTCAGCCCTCTATACTTA	13600
Qy	506	CTAAACGTGATAAAGTTTCGTAAATTTCTACTGTATCGACCTGCGACACTGGTGTGTATA	565
Db	13601	CTAAACGTGATAAAGTTTCGTAAATTTCTACTGTATCGACCTGCGACACTGGTGTGTATA	13660
Qy	566	AGGAGCCTGCACATTTATATCCCGAGAACATCAGGTTAAATGGCGTTTTTGATGTCAATTT	625
Db	13661	AGGAGCCTGCACATTTATATCCCGAGAACATCAGGTTAAATGGCGTTTTTGATGTCAATTT	13720
Qy	626	TCGGGTGGCTGAGATCAGCCACTTCTCCCGATAAACGGAGACCGGCAACATCTGGGCCATA	685
Db	13721	TCGGGTGGCTGAGATCAGCCACTTCTCCCGATAAACGGAGACCGGCAACATCTGGGCCATA	13780
Qy	686	TCGGGTGGCTCATGACCGCGAGCTTTCATCCCGATATGACCAACCGGTAAGTTTCAACGG	745
Db	13781	TCGGGTGGCTCATGACCGCGAGCTTTCATCCCGATATGACCAACCGGTAAGTTTCAACGG	13840
Qy	746	GAGACTTTATCTGACAGCAGCTGCTACCTGGCCAGGGGGATCAACATCCGTCCCGCGGGC	805
Db	13841	GAGACTTTATCTGACAGCAGCTGCTACCTGGCCAGGGGGATCAACATCCGTCCCGCGGGC	13900
Qy	806	GTGTCAATAATATCACTCTGTACATCCACAAACAGAGATTAAGGCTCTCTCTTTTATAG	865
Db	13901	GTGTCAATAATATCACTCTGTACATCCACAAACAGAGATTAAGGCTCTCTCTTTTATAG	13960
Qy	866	GTGTAAACCTTTAAACCTGATTTACCACTGCTCTCTCTGTACGAAAGAGCGGTTTCAT	925
Db	13961	GTGTAAACCTTTAAACCTGATTTACCACTGCTCTCTCTGTACGAAAGAGCGGTTTCAT	14020
Qy	926	TTCAATAAACCGGGGGACTCAGGCATCCCTTCTGTGATTTTCCGCTTCCAGCGGTTCGGC	985
Db	14021	TTCAATAAACCGGGGGACTCAGGCATCCCTTCTGTGATTTTCCGCTTCCAGCGGTTCGGC	14080
Qy	986	ACGAGACGACGGGCTTCATTTCTGATGTTGTGCTTACCAGACCGGAGATATTGACATC	1045
Db	14081	ACGAGACGACGGGCTTCATTTCTGATGTTGTGCTTACCAGACCGGAGATATTGACATC	14140
Qy	1046	ATATATGCTTGAGAACTGATAGCTGTGCTGTCACTGTCACTGTAAATACGCTGCTTC	1105
Db	14141	ATATATGCTTGAGAACTGATAGCTGTGCTGTCACTGTCACTGTAAATACGCTGCTTC	14200
Qy	1106	ATAGCACACCTCTTTTTCACATACCTTCCGGTAGTGGCCGATCAACGCTCTCATTTTCGCCAA	1165
Db	14201	ATAGCACACCTCTTTTTCACATACCTTCCGGTAGTGGCCGATCAACGCTCTCATTTTCGCCAA	14260
Qy	1166	AAGTTGGCCCGGGCTCCCGGTATCAACAGGGACACAGGATTTATTTATCTGCGAAG	1225
Db	14261	AAGTTGGCCCGGGCTCCCGGTATCAACAGGGACACAGGATTTATTTATCTGCGAAG	14320
Qy	1226	TGATCTTCGCTCAGAGGATTTTATTCGGCGAAAGTGGTCCGGTGATGCTGCCAACTTA	1285
Db	14321	TGATCTTCGCTCAGAGGATTTTATTCGGCGAAAGTGGTCCGGTGATGCTGCCAACTTA	14380
Qy	1286	GTGCACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTACCTGGATATGTTGT	1345
Db	14381	GTGCACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTACCTGGATATGTTGT	14440
Qy	1346	GTTTTACAGTATATAGTACTGTGTTTTTATGCAAAATCTAAATTAATATATGATATTT	1405
Db	14441	GTTTTACAGTATATAGTACTGTGTTTTTATGCAAAATCTAAATTAATATATGATATTT	14500
Qy	1406	ATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTGTACAAAGTGG-----	1448

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QY 4038 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCGAGGGCTAGTATCTAC 4057
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Db 17441 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCGAGGGCTAGTATCTAC 17500
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|
|
QY 4098 GACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCCGGCG 4157
|
|
|
Db 17501 GACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCCGGCG 17560
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|
|
QY 4158 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGGCCGCTCCCTCTACGAAAGTTACGGG 4217
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|
|
Db 17561 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGGCCGCTCCCTCTACGAAAGTTACGGG 17620
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|
|
QY 4218 CACCAATCAACCGCTCCAGACGCGCGGCTAAACCGACTTGTGCCCCGAGAAATAT 4277
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|
|
Db 17621 CACCAATCAACCGCTCCAGACGCGCGGCTAAACCGACTTGTGCCCCGAGAAATAT 17680
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|
|
QY 4278 GCAGCATTTTTTGGTGTATGTGGCCCCCAATGAAGTGCAGGTCAAAACCTTGACAGTGA 4337
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|
|
Db 17681 GCAGCATTTTTTGGTGTATGTGGCCCCCAATGAAGTGCAGGTCAAAACCTTGACAGTGA 17740
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|
|
QY 4338 CGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGGCGACACATGTCGAGGCTCAGCAGG 4397
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Db 17741 CGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGGCGACACATGTCGAGGCTCAGCAGG 17800
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|
|
QY 4398 ACCTGCAGCATGCAAGCTAGCTTACTAGTGATGCATATTTATAGTGTCACTAAATCT 4457
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|
|
Db 17801 ACCTGCAGCATGCAAGCTAGCTTACTAGTGATGCATATTTATAGTGTCACTAAATCT 17860
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QY 4458 GC 4459
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Db 17861 GC 17862
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RESULT 6
US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector PHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CamV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17850)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13049)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13
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Query Match 71.4%; Score 3182.2; DB 15; Length 18691;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 4406; Conservative 0; Mismatches 28; Indels 1137; Gaps 7;

QY 26 GACAAAGTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATATCAATATATT 85
|
|
|
Db 13121 GCCAACTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATATCAATATATT 13180
|
|
|
QY 86 AAATTAGATTTTGCATAAAAAACAACACTACATAACTGTAAAAACACACATATCCAGTC 145
|
|
|
Db 13181 AAATTAGATTTTGCATAAAAAACAACACTACATAACTGTAAAAACACACATATCCAGTC 13240
|
|
|
QY 146 ACTATGATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACGAGCCTTCCAAA 205
|
|
|
Db 13241 ACTATGATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGACGAGCCTTCCAAA 13300
|
|
|
QY 206 TGTTCCTCGGGTGTGCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTCTCAA 265
|
|
|
Db 13301 TGTTCCTCGGGTGTGCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTCTCAA 13360
|
|
|
QY 266 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCTCAATCCGCTTAAATCATAAA 325
|
|
|
Db 13361 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCTCAATCCGCTTAAATCATAAA 13420
|
|
|
QY 326 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAAAACATCTACCT 385
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Query Match		90.6%;	Score 4042;	DB 15;	Length 17862;
Best Local Similarity		93.2%;	Pred. No. 0;		
Matches 4419;		Conservative	0;	Mismatches 15;	Indels 308; Gaps 6;
QY	26	GACAAAGTTTGTACAAAAAGCTGACGAGAAACGCTAAATGATATAATATCAATATATT	85		
DB	13121	GCCAACTTTGTACAAAAAGCTGACGAGAAACGCTAAATGATATAATATCAATATATT	13180		
QY	86	AAATTAGATTTTGCATAAAAACAGACTACATAATACCTGTAATAACACACACATATCCAGTC	145		
DB	13181	AAATTAGATTTTGCATAAAAACAGACTACATAATACCTGTAATAACACACATATCCAGTC	13240		
QY	146	ACTATGAATCAACTACTTTAGATGGTATTAGTGACCTGTAGTCGACGACGACCTTCCAAA	205		
DB	13241	ACTATGAATCAACTACTTTAGATGGTATTAGTGACCTGTAGTCGACGACGACCTTCCAAA	13300		
QY	206	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA	265		
DB	13301	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA	13360		
QY	266	ACGGAATCGTGATATCCAGCCTACTCGCTATTGCTCCTCAATGCCGTATTAAATCATAAAA	325		
DB	13361	ACGGAATCGTGATATCCAGCCTACTCGCTATTGCTCCTCAATGCCGTATTAAATCATAAAA	13420		
QY	326	AGAAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAAAATAAAAAATCATCTACCT	385		
DB	13421	AGAAATAAGAAAAAGAGTGGAGCCTCTTTTGTGTGACAAAAATAAAAAATCATCTACCT	13480		
QY	386	ATTCATATACGCTAGTGTATAGTCCTCAAAATCATCTGCATCAGAACATTTTCACAC	445		
DB	13481	ATTCATATACGCTAGTGTATAGTCCTCAAAATCATCTGCATCAGAACATTTTCACAC	13540		
QY	446	TCTTATACCTTTCTCTTACAGTCTGTCGGCTTCACTCGAATTTTCAGCCTCTATACCTTA	505		
DB	13541	TCTTATACCTTTCTCTTACAGTCTGTCGGCTTCACTCGAATTTTCAGCCTCTATACCTTA	13600		
QY	506	CTAAACGTGATAAAGTTTCTGTAAATTTCTATGTAATGACCTGCGAGATGCGGTGTATATA	565		
DB	13601	CTAAACGTGATAAAGTTTCTGTAAATTTCTATGTAATGACCTGCGAGATGCGGTGTATATA	13660		
QY	566	AGGGAGCCTGACATTTATATCCCGAGACATCAGTTAATGGCGTTTGTGATGTCATTT	625		
DB	13661	AGGGAGCCTGACATTTATATCCCGAGACATCAGTTAATGGCGTTTGTGATGTCATTT	13720		
QY	626	TGCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCATA	685		
DB	13721	TGCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGGAGACCGGCACACTGGCCATA	13780		
QY	686	TGCGTGGTCTCATCGCGCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTTACGG	745		
DB	13781	TGCGTGGTCTCATCGCGCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTTACGG	13840		
QY	746	GAGCTTTATCTGACAGACAGCTGACCTGGCGCAGGGGATCACCATCGTCGCGCGCGGC	805		
DB	13841	GAGCTTTATCTGACAGACAGCTGACCTGGCGCAGGGGATCACCATCGTCGCGCGCGGC	13900		
QY	806	GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG	865		
DB	13901	GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG	13960		
QY	866	GTGTAACCTTAAACGTGATTTTACAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTCTAT	925		
DB	13961	GTGTAACCTTAAACGTGATTTTACAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTCTAT	14020		
QY	926	TTCAATAAACCCGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCACGCTTCGGC	985		
DB	14021	TTCAATAAACCCGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCACGCTTCGGC	14080		
QY	986	ACGACAGACGGGCTTCAATCTGCAATGGTGTGCTTACAGACCGGAGATATTGACATC	1045		
DB	14081	ACGACAGACGGGCTTCAATCTGCAATGGTGTGCTTACAGACCGGAGATATTGACATC	14140		

QY	1046	ATATATGCCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC	1105		
DB	14141	ATATATGCCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC	14200		
QY	1106	ATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTGGCGATCAACGCTCTCATTTTCGCCAA	1165		
DB	14201	ATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTGGCGATCAACGCTCTCATTTTCGCCAA	14260		
QY	1166	AAAGTTGGCCCGAGGGCTTCCGGTATCAACAGGGACACACAGGATTTATTTATCTCGCAAG	1225		
DB	14261	AAAGTTGGCCCGAGGGCTTCCGGTATCAACAGGGACACACAGGATTTATTTATCTCGCAAG	14320		
QY	1226	TGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTCGTCGGGTGATGCTGCCAATTTA	1285		
DB	14321	TGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTCGTCGGGTGATGCTGCCAATTTA	14380		
QY	1286	GTGCACTACAGGTACACATAACCATCTAAAGTAGTTGATTCATAGTACTCGATATGTTGT	1345		
DB	14381	GTGCACTACAGGTACACATAACCATCTAAAGTAGTTGATTCATAGTACTCGATATGTTGT	14440		
QY	1346	GTTTTACAGTATTTATGTAGTCTGTGTTTTTATGCAAAATCTAAATTAATATATTCATATTT	1405		
DB	14441	GTTTTACAGTATTTATGTAGTCTGTGTTTTTATGCAAAATCTAAATTAATATATTCATATTT	14500		
QY	1406	ATATCATTTTACGTTTCTCGTTTACGCTTTCTTTGTACAAAGTGG-----	1448		
DB	14501	ATATCATTTTACGTTTCTCGTTTACGCTTTCTTTGTACAAAGTGGCATTTAAGAAAGCAT	14560		
QY	1449	-----	1448		
DB	14561	TGCTTATCAATTTGTTGCAACGACAGGTCACTATCAGTCAAAATAAAATCATTTATTTGC	14620		
QY	1449	-----TCTCGAGGAATTCGGTACC-----AACTGTAAGGAAATAATATTTT	1489		
DB	14621	CATCCAGCTGCAGCTCTCGAGGAATTCGGTACCAGCTTGGTAAAGGAAATAATATTTT	14680		
QY	1490	TCTTTTTTCCTTTTGTAGTATAAAATAGTTAAGTGTGATGTTAATAGTATGATTAATAATA	1549		
DB	14681	TCTTTTTTCCTTTTGTAGTATAAAATAGTTAAGTGTGATGTTAATAGTATGATTAATAATA	14740		
QY	1550	TAGTTGTTTATTAATTTGTAAGAAAAATAATTTATAAATAATCTTTTACATAFAAACACATAGT	1609		
DB	14741	TAGTTGTTTATTAATTTGTAAGAAAAATAATTTATAAATAATCTTTTACATAFAAACACATAGT	14800		
QY	1610	AATGTAAAAAATAATGACAGTGTGTAAGACGAAAGATAAAAGTTGAGAGTAAAGT	1669		
DB	14801	AATGTAAAAAATAATGACAGTGTGTAAGACGAAAGATAAAAGTTGAGAGTAAAGT	14860		
QY	1670	ATATTTATTTTAAATGAAATTTGATCGAACATGTAAAGTATATCTAGCATTAATTTTGT	1729		
DB	14861	ATATTTATTTTAAATGAAATTTGATCGAACATGTAAAGTATATCTAGCATTAATTTTGT	14920		
QY	1730	TTTAAATCAATAATAGTAAATTTAGCTGTTTGAATGAAATATAATCAATGATAAAATACTA	1789		
DB	14921	TTTAAATCAATAATAGTAAATTTAGCTGTTTGAATGAAATATAATCAATGATAAAATACTA	14980		
QY	1790	TAGTAAAAAATAAGATAAATAAATAAATAATATTTTTTATGATTAATAGTTTATTTAT	1849		
DB	14981	TAGTAAAAAATAAGATAAATAAATAAATAATATTTTTTATGATTAATAGTTTATTTAT	15040		
QY	1850	ATAATTAATAATCTATACCATTTACTTAATATTTTGTAGTTTAAAGTTAATAATAATTTTGT	1909		
DB	15041	ATAATTAATAATCTATACCATTTACTTAATATTTTGTAGTTTAAAGTTAATAATAATTTTGT	15100		
QY	1910	TAGAAATTTCCAAATCTGCTTGTAAATTTTATCAATAAACAATAATTTAAATAACAAGCTAAAG	1969		
DB	15101	TAGAAATTTCCAAATCTGCTTGTAAATTTTATCAATAAACAATAATTTAAATAACAAGCTAAAG	15160		
QY	1970	TAACAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATTAATCTAATG	2029		
DB	15161	TAACAATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAAACATTAATCTAATG	15220		
QY	2030	CTAATAATAACAAGCGCAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCT	2089		

Db	16420	TTGAGACAATAGCAGTAGGCTGATACGACGATTCGGTTTGAGAGAACAATTTGGAAG	16479
Qy	3463	GCCTGTCGGTGCAGTAAAGTTGGCAGCATCACCCGAAGAACAATTTCCGAAGGCTGTCGGTCGA	3522
Db	16480	GCCTGTCGGTGCAGTAAAGTTGGCAGCATCACCCGAAGAACAATTTCCGAAGGCTGTCGGTCGA	16539
Qy	3523	CTACAGGTCACATAACCACTAAAGTAGTGTGATTCATAGTCAGTCGGATATGTTGTGTTTT	3582
Db	16540	CTACAGGTCACATAACCACTAAAGTAGTGTGATTCATAGTCAGTCGGATATGTTGTGTTTT	16599
Qy	3583	ACAGTATATGTAGTCTGCTTTTTTATGCAAAATCTAAATTAATATATTTATATTTATATC	3642
Db	16600	ACAGTATATGTAGTCTGCTTTTTTATGCAAAATCTAAATTAATATATTTATATTTATATC	16659
Qy	3643	ATTTTACGTTTCTCGTTCAGCTTTTTTTGTACAAAATCTGCTPAGAGTCCTGCTTTAATGAG	3702
Db	16660	ATTTTACGTTTCTCGTTCAGCTTTTTTTGTACAAAATCTGCTPAGAGTCCTGCTTTAATGAG	16719
Qy	3703	ATATGCGAGCGCCTATGATCCATGATATTTGCTTTCAATCTGTTGTGCAACGCTGTAA	3762
Db	16720	ATATGCGAGCGCCTATGATCCATGATATTTGCTTTCAATCTGTTGTGCAACGCTGTAA	16779
Qy	3763	AAAACCTGAGCATGTAGCTCAGATCCCTACCGCGGTTTCGGTTCATCTTAATGAATA	3822
Db	16780	AAAACCTGAGCATGTAGCTCAGATCCCTACCGCGGTTTCGGTTCATCTTAATGAATA	16839
Qy	3823	TATCACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCAATTTACTCATTTGTA	3882
Db	16840	TATCACCGGTTACTATCGTATTTTATGAATAATATCTCCGTTCAATTTACTCATTTGTA	16899
Qy	3883	CCCTACTACTTATATGACAAATTTAAATGAAAAAATAATATGTTGCTGAATAGGTTTA	3942
Db	16900	CCCTACTACTTATATGACAAATTTAAATGAAAAAATAATATGTTGCTGAATAGGTTTA	16959
Qy	3943	TAGGCATCTATGATAGAGCGCCACAATAACAAATGCGTTTATTTATTTACAATC	4002
Db	16960	TAGGCATCTATGATAGAGCGCCACAATAACAAATGCGTTTATTTATTTACAATC	17019
Qy	4003	CAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAAGCTGATTTACATAAATCTTAT	4062
Db	17020	CAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAAGCTGATTTACATAAATCTTAT	17079
Qy	4063	TCAAAATTTCAAAAGGCCCGAGGCTAGTATCTACGACACCGAGCGCGCACTAATAA	4122
Db	17080	TCAAAATTTCAAAAGGCCCGAGGCTAGTATCTACGACACCGAGCGCGCACTAATAA	17139
Qy	4123	CGTTCACTGAAGGGAATCCCGTTCCCGCGCGCGCATGGGTGAGATTCTTTGAAGTT	4182
Db	17140	CGTTCACTGAAGGGAATCCCGTTCCCGCGCGCGCATGGGTGAGATTCTTTGAAGTT	17199
Qy	4183	GAGTATTTGGCGGTCGCTCTACCGAAGTTACGGGCACCATTTCAACCGGTCACACGG	4242
Db	17200	GAGTATTTGGCGGTCGCTCTACCGAAGTTACGGGCACCATTTCAACCGGTCACACGG	17259
Qy	4243	CGGCGCGGTAAACCGACTGTGTCGCCGAGAAATTTATGCAGCAATTTTTTGGTGTATGGG	4302
Db	17260	CGGCGCGGTAAACCGACTGTGTCGCCGAGAAATTTATGCAGCAATTTTTTGGTGTATGGG	17319
Qy	4303	CCCAATATGAAGTGCAGGTCAAACTTTGACAGTGACGACAAATCGTTGGCGGGTCCAGG	4362
Db	17320	CCCAATATGAAGTGCAGGTCAAACTTTGACAGTGACGACAAATCGTTGGCGGGTCCAGG	17379
Qy	4363	CGCAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTTGCAGGCAATGCAAGCTAGCTTA	4422
Db	17380	CGCAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTTGCAGGCAATGCAAGCTAGCTTA	17439
Qy	4423	CTAGTGATGCAATATCTATAGTGTCACTAAATCTGC	4459
Db	17440	CTAGTGATGCAATATCTATAGTGTCACTAAATCTGC	17476

RESULT 4

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US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US2003049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

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RESULT 3

US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan
; APPLICANT: Wesley, Susan
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid PHELLSGATE 8
US-10-385-546-7

Query Match 98.8%; Score 4406.6; DB 15; Length 17476;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;
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Db 13300 CTCAATGCGGTATTAATCATATAAAGAAATAGAAAAGAGGTGGAGGCTCTTTTTT 13359
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US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

Query Match 98.8%; Score 4406.6; DB 15; Length 17476;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;
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DB 13060 AAAATGATATAATATCAATATATTAATTAAGATTTTGTCAATAAAAAACAGACTACATAAT 13119
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RESULT 2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
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2	4406.6	98.8	17476 15	US-10-055-001A-24	Sequence 24, Appl
3	4406.6	98.8	17476 15	US-10-385-546-7	Sequence 7, Appl
4	4200	94.2	17681 15	US-10-055-001A-26	Sequence 26, Appl
5	4042	90.6	17862 15	US-10-055-001A-23	Sequence 23, Appl
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	1305	29.3	17458 15	US-10-055-001A-25	Sequence 25, Appl
C	1277.8	28.7	17476 15	US-10-055-001A-24	Sequence 24, Appl
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	1108.8	24.9	4470 15	US-10-151-690-21	Sequence 21, Appl
C	1108.8	24.9	4892 16	US-10-357-268-1	Sequence 1, Appl
	1108.8	24.9	5584 15	US-10-151-690-61	Sequence 61, Appl
13	1102.4	24.7	4428 15	US-10-151-690-62	Sequence 62, Appl
14	1102.4	24.7	4627 15	US-10-151-690-63	Sequence 63, Appl

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C	737	16.5	3002 15	US-10-353-454-57	Sequence 57, Appl
	736	16.5	2116 12	US-10-644-335-3	Sequence 3, Appl
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23	735.6	16.5	3034 15	US-10-356-088-48	Sequence 48, Appl
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C	710.2	15.9	7599 15	US-10-027-880-5	Sequence 5, Appl
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C	597	13.4	5558 15	US-10-241-596-137	Sequence 137, App
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C	597	13.4	12789 13	US-10-666-778-9	Sequence 9, Appl
C	593.8	13.3	11180 9	US-09-887-576-581	Sequence 581, App
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C	406.8	9.1	5584 15	US-10-151-690-61	Sequence 61, Appl
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C	323.4	7.3	2877 13	US-09-861-925-11	Sequence 11, Appl

ALIGNMENTS

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; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

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Job time : 195.557 secs

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
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; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
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; US-08-379-614-2

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Best Local Similarity 99.7%; Pred. No. 7.9e-59;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANMA10.001CP1

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; CURRENT APPLICATION NUMBER: US/09/225,152A
; CURRENT FILING DATE: 1998-01-04
; PRIOR APPLICATION NUMBER: 08/379614
; PRIOR FILING DATE: 1995-07-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(378)
; OTHER INFORMATION: ccdB gene of pKIL 18.
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; US-09-225-152A-2

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Query Match          7.3%; Score 325.4; DB 3; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.9e-59;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGGAGCCTGACATTTATATCCCCAGAACATCAGGTTAAATGGCGTTTGA 617
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RESULT 15
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; Sequence 3, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE93/00051
; FILING DATE: 02-AUG-1993

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; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 12.7%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.8e-108;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3929 GCTGAATAGTTTATAGGACATCTATGATAGCGGCACATTAACAAATTCGGTT 3988
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QY 4049 TACATAAATCTTATTCAAATTTTAAAAAGCGGCGGCTAGTATCTACGACACACCGAG 4108
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QY 4109 CGGGAACCTAATACGTTTCACTGAAGGAACTCCCGTTCGCGGCGGCGGATCGGTGA 4168
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QY 4169 GATTCCTTGAAGTTGAGTATGCGGCTCTACCGAAAGTTACGGGCGGCGGATTCAC 4228
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QY 4229 CGGTCACGACGCGGCGGCGGTAACCG 4256
Db 13854 CGGTCACGACGCGGCGGCGGTAACCG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM: Diskette
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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US-08-673-768-1			
; Sequence 1, Application US/08673768			
; Patent No. 5952546			
; GENERAL INFORMATION:			
; APPLICANT: Bedbrook, John R.			
; APPLICANT: Dunsmuir, Pamela			
; APPLICANT: Howie, William J.			
; APPLICANT: Joe, Lawrence K.			
; APPLICANT: Lee, Kathleen Y.			
; TITLE OF INVENTION: Delayed Ripening Tomato Plants			
; NUMBER OF SEQUENCES: 1			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/673,768			
; FILING DATE: 27-JUN-1996			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/000,721			
; FILING DATE: 30-JUN-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bastian, Kevin L.			
; REGISTRATION NUMBER: 34,774			
; REFERENCE/DOCKET NUMBER: 012176-005010US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 576-0200			
; TELEFAX: (415) 576-0300			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 15397 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA			
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Best Local Similarity 99.8%; Pred. No. 1.8e-108;			
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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QY	4290	TGCTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAAATCGTT	4349
Db	11941	TGCTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAAATCGTT	11882
QY	4350	GCGCGGGTCCAGGCGGGAATTTTGCACAACATGTCAGAGCTCAGCAG	4396
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RESULT 11			
US-08-673-768-1			
; Sequence 1, Application US/08673768			
; Patent No. 5952546			
; GENERAL INFORMATION:			
; APPLICANT: Bedbrook, John R.			
; APPLICANT: Dunsmuir, Pamela			
; APPLICANT: Howie, William J.			
; APPLICANT: Joe, Lawrence K.			
; APPLICANT: Lee, Kathleen Y.			
; TITLE OF INVENTION: Delayed Ripening Tomato Plants			
; NUMBER OF SEQUENCES: 1			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/673,768			
; FILING DATE: 27-JUN-1996			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/000,721			
; FILING DATE: 30-JUN-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bastian, Kevin L.			
; REGISTRATION NUMBER: 34,774			
; REFERENCE/DOCKET NUMBER: 012176-005010US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 576-0200			
; TELEFAX: (415) 576-0300			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 15397 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA			
US-08-673-768-1			
Query Match 12.7%; Score 566.4; DB 2; Length 15397;			
Best Local Similarity 99.8%; Pred. No. 1.8e-108;			
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	3689	CCTGCTTTAATGAGATATGCGAGACGCTATGATCGCATATATTCGTTCAATTCGT	3748
Db	7110	CCTGCTTTAATGAGATATGCGAGACGCTATGATCGCATATATTCGTTCAATTCGT	7169
QY	3749	TGTGACGTTGTAAAAAACCTTGACATGTGTAGTCTAGATCTTCACCGCGTTTCGGTT	3808

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LOCATION: 2441..3256
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FEATURE:
NAME/KEY: - 3257..4315
LOCATION: 3257..4315
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OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: - 4316..6555
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-025-583-2
Query Match 15.9%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3689 CTTGCTTTAATGAGATATGCGAGACGCTATGATGCGCATGATATTTGCTTTCAATTCGT 3748
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Qy 3749 TGTGACGTTGTAAAAACCTGAGCATGTGATGCTCAGATCCTTACCGCGGTTTCGGTT 3808
Db 3489 TGTGACGTTGTAAAAACCTGAGCATGTGATGCTCAGATCCTTACCGCGGTTTCGGTT 3548
Qy 3809 CATCTTAATGAATATATCACCGCTTACTATCGTATTTTATGAATAATATTTCTCGTTCA 3868
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Db 3729 TATTATTACAAATCCAAATTTTAAAAAAGCGGACGACCGGTCAAACCTTAAAGACTGAT 3788
Qy 4049 TACATAATCTTATTCAAATTTCAAAGGCGGCGGCGGCTAGTATCTACGACACACCGAG 4108
Db 3789 TACATAATCTTATTCAAATTTCAAAGGCGGCGGCGGCTAGTATCTACGACACACCGAG 3848
Qy 4109 CGGCGAATTAATAAGTTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGGCGGCTAGTATCT 4168
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Qy 4169 GATTCTTTGAAGTTGAGTATTTGGCGCTCCGCTCTACCGGAAAGTTTACGGGCAACCAATTC 4228
Db 3909 GATTCTTTGAAGTTGAGTATTTGGCGCTCCGCTCTACCGGAAAGTTTACGGGCAACCAATTC 3968
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RESULT 9

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US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3
Query Match 15.9%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 2.5e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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LOCATION: 3257..4315
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OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: 4316..6555
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OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-351-413-2

Query Match 15.9%; Score 709.8; DB 1; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3689 CTTGCTTTTATGATGATGCGAGACCCCTATGATCGCATGATATTTTCTCAATCTCT 3748
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QY 3749 TGTGCACTGTGTAATAAAACCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3808
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DB 3549 CATTCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATTTCTCCGTTCA 3608
QY 3869 ATTACTGATTTGACCTTACTTATCTATGATGATGATGATGATGATGATGATGATGAT 3928
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DB 3789 TACATAATCTTATTCACAAATTTTAAATAAGCGGAGACCGGTCACCACTTAAAGACTGAT 3848
QY 4109 CGGCGAATTAATACGTTCTGAAAGGAACTCCGTTCCCGCGCGCGGATGGGTGA 4168
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RESULT 8

US-09-025-583-2

; Sequence 2, Application US/09025583

; Patent No. 597433

; GENERAL INFORMATION:

; APPLICANT: Williams, Mark

; APPLICANT: Leemans, Jan

; TITLE OF INVENTION: Maintenance of male-sterile plants

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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025.583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351.413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pVcl44 (replicable in E.coli)
FEATURE:
NAME/KEY: -
LOCATION: 1..396
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US-09-084-889-1
Query Match 15.9%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 1.9e-138;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3689 CCTGCTTTAATGAGATATGCGAGACGCTATGATCGCATGATATTTGCTTTCAATTCTGT 3748
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; Sequence 2, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
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; OTHER INFORMATION: /label= NPRTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
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; FEATURE:
; NAME/KEY: -
; LOCATION: 2101..3160
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; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALUIN, Kathleen
; APPLICANT: Gobel, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
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; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 9040332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: circular
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QY 3809 CATTCTAATGAATATATCAACCGGTTACTATCGTATTTTATGAATAATATTCCTCGTTCA 3868
Db 2393 CATTCTAATGAATATATCAACCGGTTACTATCGTATTTTATGAATAATATTCCTCGTTCA 2452
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; APPLICANT: D'HALLUIN, Kathleen
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
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; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-089
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
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; Query Match 16.3%; Score 728.8; DB 2; Length 7566;
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; Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN AARSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7639 base pairs
; TYPE: nucleic acid

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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28	148.4	3.3	231	4	US-09-489-039A-4117	Sequence 4117, Ap
29	148.4	3.3	4245	2	US-08-929-967-4	Sequence 4, Appli
30	148.4	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
31	148.4	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
32	148.4	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
33	148.4	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
34	148.4	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
35	148.4	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
36	148.4	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli
37	146.2	3.3	231	4	US-09-489-039A-4117	Sequence 4117, Ap
38	146.2	3.3	4245	2	US-08-929-967-4	Sequence 4, Appli
39	146.2	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
40	146.2	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
41	146.2	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
42	146.2	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
43	146.2	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
44	146.2	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
45	146.2	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-232-016-23
; Sequence 23, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN AARSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

us-10-055-001b-25_copy_13000_17458.rng

Wed May 12 08:21:03 2004

Search completed: May 7, 2004, 18:29:07
Job time : 1060.16 secs

746 GAGACCTTTATCTGACAGCAGCGTGCATCGCCAGGGGATCACCATCGCTCGCCCGGGC 805
DB GAGACCTTTATCTGACAGCAGCGTGCATCGCCAGGGGATCACCATCGCTCGCCCGGGC 1718
806 GTGTCAATATATCATCTGTATCATCCAAACAGACGATACGGCTCTCTCTTTTATAG 865
DB GTGTCAATATATCATCTGTATCATCCAAACAGACGATACGGCTCTCTCTTTTATAG 1778
866 GTGTAAACCTTAACTTCACTTTCCAGATCCCTGTCTGTAGCAAAAGAGCGCTTCAT 925
DB GTGTAAACCTTAACTTCACTTTCCAGATCCCTGTCTGTAGCAAAAGAGCGCTTCAT 1838
926 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTGATTTCCGCTTTCCAGCGTTCCGC 985
DB TTCAATAAACCGGGCGACCTCAGCCATCCCTCTGATTTCCGCTTTCCAGCGTTCCGC 1898
986 ACGCAGACGAGCGGCTTCACTTCTGATGTTGTGCTTACAGACCGAGATATTGACATC 1045
DB ACGCAGACGAGCGGCTTCACTTCTGATGTTGTGCTTACAGACCGAGATATTGACATC 1958
1046 ATATATGCTTGTAGCAACTGATAGCTGTCTGCTCAACTGTCACTGTAATACGCTCTTC 1105
DB ATATATGCTTGTAGCAACTGATAGCTGTCTGCTCAACTGTCACTGTAATACGCTCTTC 2018
1106 ATAGCACACCTCTTTTGTGACATCTTCCGGGTA 1137
DB ATAGCACACCTCTTTTGTGACATCTTCCGGGTA 2050

RESULT 14

ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.

XX AC ABZ58769;

XX 01-MAY-2003 (first entry)

DE Destination plasmid pDONR212(F) nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;
XX nucleic acid isolation; ds.

XX Synthetic.

XX WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US015947.

XX 21-MAY-2001; 2001US-0291973P.

XX (INVI-) INVITROGEN CORP.

XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for
XX selecting and isolating nucleic acid molecules by mixing the second
XX population of nucleic acid with a second target nucleic acid.

PS Disclosure; Fig 28B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
XX second target molecule. The method involves (a) mixing a first population
XX of nucleic acid comprising one or more recombination sites with a target
XX nucleic acid; (b) causing some or all of the nucleic acid molecules of
XX the first population to recombine with the first target nucleic acid
XX molecules to form a second population; (c) mixing the second population
XX of nucleic acid with a second target nucleic acid; and (d) causing some
XX or all of the nucleic acid molecules of the second population to

CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence
XX
SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.7%; Score 1102.4; DB 7; Length 4627;

Best Local Similarity 99.5%; Pred. No. 8.9e-148;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAAGTTGTACAAAAGAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATAT 85
DB 90 GCCAACTTTGTACAAAAGAGCTGATATCGAAACGTAATAATGATATAAATATCAATATAT 149
QY 86 AATATAGATTTTGCATATAAAAACAGACTACATACTGTGTAAACACACATATCCAGTC 145
DB 150 AATATAGATTTTGCATATAAAAACAGACTACATACTGTGTAAACACACATATCCAGTC 209
QY 146 ACTATGAATCAACTACTTATAGATGGTATTAGTACCTGTAGTCGACGAGCCTTCCAAA 205
DB 210 ACTATGAATCAACTACTTATAGATGGTATTAGTACCTGTAGTCGACGAGCCTTCCAAA 269
QY 206 TGTCTTCGGGTGATGTGCGCAACTTAGTCGACGAGCCTTCCAAATGTTCTTCTCAA 265
DB 270 TGTCTTCGGGTGATGTGCGCAACTTAGTCGACGAGCCTTCCAAATGTTCTTCTCAA 329
QY 266 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATCGCTATTAAATCATATAAA 325
DB 330 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATCGCTATTAAATCATATAAA 389
QY 326 AGAAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAFAAAAATCTTACCT 385
DB 390 AGAAATAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAFAAAAATCTTACCT 449
QY 386 ATTCTATACGCTAGTGTCACTAGTCTGTAATCATCTGTCATCAAGAACATTTTCAACAC 445
DB 450 ATTCTATACGCTAGTGTCACTAGTCTGTAATCATCTGTCATCAAGAACATTTTCAACAC 509
QY 446 TCTTATACCTTTCTCTTACAGTCTGCTGGCTTCACTGATTTTTCAGCCTCTTACTACTTA 505
DB 510 TCTTATACCTTTCTCTTACAGTCTGCTGGCTTCACTGATTTTTCAGCCTCTTACTACTTA 569
QY 506 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTATA 565
DB 570 CTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGACAGCTGGCTGTATA 629
QY 566 AGGAGAGCTGACATTTATATTTCCCGACAGCATCAGGTTAATGCGCTTTTGTATGTCATTT 625
DB 630 AGGAGAGCTGACATTTATATTTCCCGACAGCATCAGGTTAATGCGCTTTTGTATGTCATTT 689
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGAGACCGGACACCTGGCCATA 685
DB 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGAGACCGGACACCTGGCCATA 749
QY 686 TCGGTGGCTCATCATCGCCAGCTTTTCATCCCGATATGACACCGCGGTAAAGTTTCAGG 745
DB 750 TCGGTGGCTCATCATCGCCAGCTTTTCATCCCGATATGACACCGCGGTAAAGTTTCAGG 809
QY 746 GAGACTTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCAACATCGCTCGCCCGGC 805
DB 810 GAGACTTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCAACATCGCTCGCCCGGC 869
QY 806 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTTTATAG 865
DB 870 GTGTCAATAATATCACTCTGTACATCCCAAAACAGACGATTAACGGCTCTCTCTTTATAG 929
QY 866 GTGTAAACCTTAACTGATTTACAGCTCCCTGTTCTGTCAGCAAAAGAGCGCTTCAT 925
DB 930 GTGTAAACCTTAACTGATTTACAGCTCCCTGTTCTGTCAGCAAAAGAGCGCTTCAT 989
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCGCG 985

QY 506 CTAACGTCGATAAAGTTCTGTAAATTCATCTGATTCGACCTCGACAGCTGGCTGTGTATA 565
Db |||||
QY 5003 CTAACGTCGATAAAGTTCTGTAAATTCATCTGATTCGACCTCGACAGCTGGCTGTGTATA 4944
Db |||||
QY 566 AGGGAGCCTGCATATTAATTCGCCAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 625
Db |||||
QY 4943 AGGGAGCCTGCATATTAATTCGCCAGACATCAGGTTAATGGCGTTTGTGATGTCATTT 4884
Db |||||
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCACACTGGCCCATTA 685
Db |||||
QY 4883 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCACACTGGCCCATTA 4824
Db |||||
QY 686 TCGGTGGCTCATCATGGCCAGCTTTCATCCCGATATGACACCGCGGTAAGTTTCACGG 745
Db |||||
QY 4823 TCGGTGGCTCATCATGGCCAGCTTTCATCCCGATATGACACCGCGGTAAGTTTCACGG 4764
Db |||||
QY 746 GAGACTTTATCTGACAGACAGTGCACATGGCCAGGGGATCACCATCGTCCGCGGGC 805
Db |||||
QY 4763 GAGACTTTATCTGACAGACAGTGCACATGGCCAGGGGATCACCATCGTCCGCGGGC 4704
Db |||||
QY 806 GTGTCAATTAATATCACTCTGTATATCCACAAACAGACAGTAAACGGCTCTCTCTTTATAG 865
Db |||||
QY 4703 GTGTCAATTAATATCACTCTGTATATCCACAAACAGACAGTAAACGGCTCTCTCTTTATAG 4644
Db |||||
QY 866 GTGTAAACCTTAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTTAT 925
Db |||||
QY 4643 GTGTAAACCTTAACTGCAATTTTACCAGTCCCTGTTCTCGTCAGCAAAAGACCGGTTTAT 4584
Db |||||
QY 926 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGGTTCCGGC 985
Db |||||
QY 4583 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGGTTCCGGC 4524
Db |||||
QY 986 AGCAGACAGACGGGCTTCAATTCGTGATGTTGTGCTTACAGACCGGAGATATTGACATC 1045
Db |||||
QY 4523 AGCAGACAGACGGGCTTCAATTCGTGATGTTGTGCTTACAGACCGGAGATATTGACATC 4464
Db |||||
QY 1046 ATATATGCTTGTAGCAACTGATAGCTGTCGCTGTCAACTGTCATCTAATACGCTGCTTC 1105
Db |||||
QY 4463 ATATATGCTTGTAGCAACTGATAGCTGTCGCTGTCAACTGTCATCTAATACGCTGCTTC 4404
Db |||||
QY 1106 ATAGCACACCTCTTTTGTGACATACCTTCGGGTA 1137
Db |||||
QY 4403 ATAGCACACCTCTTTTGTGACATACCTTCGGGTA 4372
Db |||||

RESULT 13

ABZ58768
ID ABZ58768 standard; DNA; 4428 BP.
XX
AC ABZ58768;
XX
DT 01-MAY-2003 (first entry)
DE
DE Destination plasmid pDONR212 nucleotide sequence.
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
XX WO200295055-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US015947.
PF
XX 21-MAY-2001; 2001US-0291973P.
XX
XX (INVI-) INVITROGEN CORP.
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DR;
PI
XX WPI; 2003-129436/12.
DR

XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 27B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212 nucleotide sequence
XX
SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 24.7%; Score 1102.4; DB 7; Length 4428;
Best Local Similarity 99.5%; Pred. No. 8.9e-148;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 85
Db |||||
QY 939 GCCAACTTTGTACAAAAAAGCTGATATCGAAACGTAATAATGATATAAATATCAATATATT 998
Db |||||
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATATATCTGTAAACACACACATATCCAGTC 145
Db |||||
QY 999 AAATTAGATTTTGCATAAAAAACAGACTACATATATCTGTAAACACACACATATCCAGTC 1058
Db |||||
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACTGTAGTCGACCGACAGCTTCCAAA 205
Db |||||
QY 1059 ACTATGAATCAACTACTTAGATGGTATTAGTACTGTAGTCGACCGACAGCTTCCAAA 1118
Db |||||
QY 206 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACGACAGCTTCCAAATGTTCTCTCAA 265
Db |||||
QY 1119 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACGACAGCTTCCAAATGTTCTCTCAA 1178
Db |||||
QY 266 ACAGAACTCGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAATCATATAAA 325
Db |||||
QY 1179 ACAGAACTCGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAATCATATAAA 1238
Db |||||
QY 326 AGAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
Db |||||
QY 1239 AGAATAAGAAAAAGAGGTGCGAGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 1298
Db |||||
QY 386 ATTCATATACGCTAGTGTCTAGTCTGAAATCATCTGCAATCAAGAACATTTTCAACAC 445
Db |||||
QY 1299 ATTCATATACGCTAGTGTCTAGTCTGAAATCATCTGCAATCAAGAACATTTTCAACAC 1358
Db |||||
QY 446 TCTTATACCTTTCTCTTACAAAGTGTGCGGTCTCATCTGGATTTTACGCTCTTACATTA 505
Db |||||
QY 1359 TCTTATACCTTTCTCTTACAAAGTGTGCGGTCTCATCTGGATTTTACGCTCTTACATTA 1418
Db |||||
QY 506 CTAAACGTCGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGTATA 565
Db |||||
QY 1419 CTAAACGTCGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGTATA 1478
Db |||||
QY 566 AGGGAGCCTGCATTTATATTTCCCGAGAACATCAGGTTTAAATGGCGTTTTCATGTCATTT 625
Db |||||
QY 1479 AGGGAGCCTGCATTTATATTTCCCGAGAACATCAGGTTTAAATGGCGTTTTCATGTCATTT 1538
Db |||||
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACCGAGACCGGCACACTGGCCCATTA 685
Db |||||
QY 1539 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACCGAGACCGGCACACTGGCCCATTA 1598
Db |||||
QY 686 TCGGTGGTCATCATCGCCAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTCACGG 745
Db |||||
QY 1599 TCGGTGGTCATCATCGCCAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTCACGG 1658
Db |||||

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Db 5243 ACCGAATCGTCGATCAGCGCTACTCGCTATGCTCTCAATGCGTATTAAATCATAAA 5184
QY 326 AGAAATAAGAAAAAGAGTCGAGCGCTCTTTTGTGTGACAAAATAAAAAACATCTACCT 385
Db 5183 AGAAATAAGAAAAAGAGTCGAGCGCTCTTTTGTGTGACAAAATAAAAAACATCTACCT 5124
QY 386 ATTCATATACGCTAGTGTCTATAGTCCTGAAATCATCTGCATCAAGAACAAATTTTCAAC 445
Db 5123 ATTCATATACGCTAGTGTCTATAGTCCTGAAATCATCTGCATCAAGAACAAATTTTCAAC 5064
QY 446 TCTTATACCTTTCTCTTACAGCTGCTCGCTTCATCTGGAATTTTTCAGCTCTATCTTA 505
Db 5063 TCTTATACCTTTCTCTTACAGCTGCTCGCTTCATCTGGAATTTTTCAGCTCTATCTTA 5004
QY 506 CTAAACGCTGATAAAGTTTCTGTAAATTTTACTGTATCGACTGCAGCTGGCTGTATA 565
Db 5003 CTAAACGCTGATAAAGTTTCTGTAAATTTTACTGTATCGACTGCAGCTGGCTGTATA 4944
QY 566 AGGAGCTGACATTTATATATCCCGAGAACATCAGGTTAATGGCGTTTGTGATTCATTT 625
Db 4943 AGGAGCTGACATTTATATATCCCGAGAACATCAGGTTAATGGCGTTTGTGATTCATTT 4884
QY 626 TCGCGTGGCTGATCAGACCTCTCTCCCGATACCGAGACCGGACACTGGCCATA 585
Db 4883 TCGCGTGGCTGATCAGACCTCTCTCCCGATACCGAGACCGGACACTGGCCATA 4824
QY 686 TCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAG 745
Db 4823 TCGGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAG 4764
QY 746 GAGACTTTATCTGACAGACGTCGACCTGGCCAGGGGATACCATCCGTCGCGCGGC 805
Db 4763 GAGACTTTATCTGACAGACGTCGACCTGGCCAGGGGATACCATCCGTCGCGCGGC 4704
QY 806 GTGTCAATATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTTTTATAG 865
Db 4703 GTGTCAATATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGGAATTTTCAAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTCA 925
Db 4643 GTGTAAACCTTAACTGGAATTTTCAAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTCA 4584
QY 926 TTCAATAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTCCAGGTTTCGCG 985
Db 4583 TTCAATAACCGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTCCAGGTTTCGCG 4524
QY 986 ACGCAGACGCGGCTTCAATTTCTGATGTTGTGCTTACGACCGGAGATATTGACATC 1045
Db 4523 ACGCAGACGCGGCTTCAATTTCTGATGTTGTGCTTACGACCGGAGATATTGACATC 4464
QY 1046 ATATATGCGCTGAGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db 4463 ATATATGCGCTGAGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4404
QY 1106 ATAGACACCTCTTTTGTGACATCTTCGGGTA 1137
Db 4403 ATAGACACCTCTTTTGTGACATCTTCGGGTA 4372
```

RESULT 12

ABZ58766/c

ID ABZ58766 standard; DNA; 5584 BP.

XX AC ABZ58766;

XX XX

DT 01-MAY-2003 (first entry)

XX XX

DE Donor plasmid pDONR207 nucleotide sequence.

XX XX

KW Nucleic acid insertion; recombination; nucleic acid selection;

XX XX

KW nucleic acid isolation; ds.

XX XX

OS XX
PN WO200295055-A2.
XX 28-NOV-2002.
XX 21-MAY-2002; 2002WO-US015947.
XX 21-MAY-2001; 2001US-0291973P.
XX (INVI-) INVITROGEN CORP.
PI Brach MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
XX Disclosure; Fig 18B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the donor plasmid pDONR207 nucleotide sequence

SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.9%; Score 1108.8; DB 7; Length 5584;
Best Local Similarity 99.8%; Pred. No. 1.1e-148;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAATATATATATAT 85
Db 5483 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAATATATATATAT 5424
QY 86 AAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACAACTATCCAGTC 145
Db 5423 AAATTAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACAACTATCCAGTC 5364
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 205
Db 5363 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 5304
QY 206 TGTTCCTTCGGGTGATGCTGCCAATCTAGTCGACGAGACGCTTCCAAATGTTCTCTCAA 265
Db 5303 TGTTCCTTCGGGTGATGCTGCCAATCTAGTCGACGAGACGCTTCCAAATGTTCTCTCAA 5244
QY 266 ACGGAATCGTCGTATCCAGCGCTTACTCGCTATTGTCTCAATGCCGTATTAAATCATATA 325
Db 5243 ACGGAATCGTCGTATCCAGCGCTTACTCGCTATTGTCTCAATGCCGTATTAAATCATATA 5184
QY 326 AGAATAAGAAAAAGAGTCGAGCGCTCTTTTGTGTGACAAAATAAAAAACATCTACCT 385
Db 5183 AGAATAAGAAAAAGAGTCGAGCGCTCTTTTGTGTGACAAAATAAAAAACATCTACCT 5124
QY 386 ATTCAATACGCTAGTGTCTAGCTAGCTGAAAATCATCTGCAATCAAGAACAAATTTCAAC 445
Db 5123 ATTCAATACGCTAGTGTCTAGCTAGCTGAAAATCATCTGCAATCAAGAACAAATTTCAAC 5064
QY 446 TCTTATACCTTTTCTTACAAAGTCGTCGGCTTCTCATCTGGAATTTTTCAGCCTCTTACTTA 505
Db 5063 TCTTATACCTTTTCTTACAAAGTCGTCGGCTTCTCATCTGGAATTTTTCAGCCTCTTACTTA 5004

QY 266 ACGGAATCGTCTGATCCAGCTACTCGCTATTGTCCTCAATGCGGTATTAATCATATAA 325
Db |||||
QY 3876 ACGGAATCGTCTGATCCAGCTACTCGCTATTGTCCTCAATGCGGTATTAATCATATAA 3935
Db |||||
QY 326 AGAAATAGAAAAGAGGTCGAGCGCTCTTTTGTGTGACAAATATAAAACATCTACCT 385
Db |||||
QY 3936 AGAAATAGAAAAGAGGTCGAGCGCTCTTTTGTGTGACAAATATAAAACATCTACCT 3995
Db |||||
QY 386 ATTATATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAACTTTTCAAC 445
Db |||||
QY 3996 ATTATATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAACTTTTCAAC 4055
Db |||||
QY 446 TCTTATACCTTCTCTTAAGGTCGTCGCTTCAATCTGGAATTTTTCAGCTCTTATCTTA 505
Db |||||
QY 4056 TCTTATACCTTCTCTTAAGGTCGTCGCTTCAATCTGGAATTTTTCAGCTCTTATCTTA 4115
Db |||||
QY 506 CTAAACGCTGATAAGTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGTGTAT 565
Db |||||
QY 4116 CTAAACGCTGATAAGTTCTGTAATTTCTACTGTATCGACCTGCAGCTGGTGTAT 4175
Db |||||
QY 566 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGCTTTTGTATGTCATTT 625
Db |||||
QY 4176 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTAATGCGCTTTTGTATGTCATTT 4235
Db |||||
QY 626 TCGCGTGTGATGATCAGGCTCTTCTCCGATTAACGAGACCGGACACTGGCCATA 685
Db |||||
QY 4236 TCGCGTGTGATGATCAGGCTCTTCTCCGATTAACGAGACCGGACACTGGCCATA 4295
Db |||||
QY 686 TCGCGTGTGATGATGCGGCTCTTCTATCCCGATATGCACACCGGTAAGTTTCAACGG 745
Db |||||
QY 4296 TCGCGTGTGATGATGCGGCTCTTCTATCCCGATATGCACACCGGTAAGTTTCAACGG 4355
Db |||||
QY 746 GAGACTTATCTGACAGAGAGTGATGCGGAGGAGGATCACCATCGTCCCGCGG 805
Db |||||
QY 4356 GAGACTTATCTGACAGAGAGTGATGCGGAGGAGGATCACCATCGTCCCGCGG 4415
Db |||||
QY 806 GTGTCAATATATCACTCTGTATCATCCAGACAGAGATACGGCTCTCTCTTTATAG 865
Db |||||
QY 4416 GTGTCAATATATCACTCTGTATCATCCAGACAGAGATACGGCTCTCTCTTTATAG 4475
Db |||||
QY 866 GTGTCAATATATCACTCTGTATCATCCAGAGTCCCTGTTCTGTGACAAAAGAGCGGTTTAT 925
Db |||||
QY 4476 GTGTCAATATATCACTCTGTATCATCCAGAGTCCCTGTTCTGTGACAAAAGAGCGGTTTAT 4535
Db |||||
QY 926 TTCATTAACCGGCGAGCTCAGCATTCCTCTGATTTTCCGCTTTCCAGGTTCCGCG 985
Db |||||
QY 4536 TTCATTAACCGGCGAGCTCAGCATTCCTCTGATTTTCCGCTTTCCAGGTTCCGCG 4595
Db |||||
QY 986 ACGCAGACGAGCGGCTTCTATCTGATGTTGTTGCTTACAGACCGGAGATTTGACATC 1045
Db |||||
QY 4596 ACGCAGACGAGCGGCTTCTATCTGATGTTGTTGCTTACAGACCGGAGATTTGACATC 4655
Db |||||
QY 1046 ATATATGCTTGTAGCAACTGATAGCTGTGCTGTGTCACCTGTCATGTAATAGCTGCTTC 1105
Db |||||
QY 4656 ATATATGCTTGTAGCAACTGATAGCTGTGCTGTGTCACCTGTCATGTAATAGCTGCTTC 4715
Db |||||
QY 1106 ATAGCACACTCTTTTGTACATCTTCGGGTA 1137
Db |||||
QY 4716 ATAGCACACTCTTTTGTACATCTTCGGGTA 4747
Db |||||

RESULT 11

AC55632/c
ID AAC55632 standard; DNA; 5584 BP.
XX AC AAC55632;
XX AC AAC55632;
XX AC AAC55632;
DT 11-JAN-2001 (first entry)
XX Donor plasmid pDONR207 nucleotide sequence.
XX Bacteriophage lambda; att; recombination site; attB; attP; attL;
KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.

XX WO200052027-A1.
XX 08-SEP-2000.
XX 02-MAR-2000; 2000WO-US005432.
XX 02-MAR-1999; 99US-0122389P.
XX 23-MAR-1999; 99US-0126049P.
XX 28-MAY-1999; 99US-0136744P.
XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.

XX Disclosure; Fig 97; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

XX Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

XX Query Match 24.9%; Score 1108.8; DB 3; Length 5584;
XX Best Local Similarity 99.8%; Pred. No. 1.1e-148;
XX Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAATTTGTACAAAAGCTGAACGAGAAACGTTAAATGATATAATATATATT 85
Db |||||
QY 5483 GCCAACTTTGTACAAAAGCTGAACGAGAAACGTTAAATGATATAATATATATT 5424
Db |||||
QY 86 AAATTAGATTTTGCATAAAACAGACTACATATCTGTAAACACACATATCCAGTC 145
Db |||||
QY 5423 AAATTAGATTTTGCATAAAACAGACTACATATCTGTAAACACACATATCCAGTC 5364
Db |||||
QY 146 ACTATGAATCAACTACTTATAGTGTATTAGTACCTGTAGTCGACGAGCTTCCAAA 205
Db |||||
QY 5363 ACTATGAATCAACTACTTATAGTGTATTAGTACCTGTAGTCGACGAGCTTCCAAA 5304
Db |||||
QY 206 TGTTCCTCGGTGATGCTGCCAATCTAGTCACGACGAGCTTCCAAATGTTCTTCTCA 265
Db |||||
QY 5303 TGTTCCTCGGTGATGCTGCCAATCTAGTCACGACGAGCTTCCAAATGTTCTTCTCA 5244
Db |||||
QY 266 ACGGAATCGTGTGATCCAGCCTACTCGCTATTGTCCTCAATGCGGCTATTAAATCATATAA 325
Db |||||

QY 266 ACGGAATCGTCGATCCAGCTACTCGCTATTGTCCTCAATGCGGATTAATAATCAATAAA 325
Db |||||
QY 342 ACGGAATCGTCGATCCAGCTACTCGCTATTGTCCTCAATGCGGATTAATAATCAATAAA 401
Db |||||
QY 326 AGAATTAAGAAAAGAGGTGGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db |||||
QY 402 AGAATTAAGAAAAGAGGTGGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 461
Db |||||
QY 386 ATTCAATATACGCTAGTCTCATAGTCTCTGAAATCATCTGATCAAGACAAATTTTCAAC 445
Db |||||
QY 462 ATTCAATATACGCTAGTCTCATAGTCTCTGAAATCATCTGATCAAGACAAATTTTCAAC 521
Db |||||
QY 446 TCTTATATCTTTCTCTTACAGTCTGTCGCTTTTCTGATTTTTCAGCCTCTTATCTTA 505
Db |||||
QY 522 TCTTATATCTTTCTCTTACAGTCTGTCGCTTTTCTGATTTTTCAGCCTCTTATCTTA 581
Db |||||
QY 506 CTAAACGTGATAAGTTCTCTGTAATTTCTACTGTATCGACTGAGCTGGCTGTGTATA 565
Db |||||
QY 582 CTAAACGTGATAAGTTCTCTGTAATTTCTACTGTATCGACTGAGCTGGCTGTGTATA 641
Db |||||
QY 566 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTTATGGCGTTTGTGTCATTT 625
Db |||||
QY 642 AGGAGCCTGACATTTATATTCCTCCAGAACATCAGGTTTATGGCGTTTGTGTCATTT 701
Db |||||
QY 626 TCGCGGTGGCTGAGTCAGCCTCTTCTCCCGATTAACGGAGACCGGCACACTGGCCATA 685
Db |||||
QY 702 TCGCGGTGGCTGAGTCAGCCTCTTCTCCCGATTAACGGAGACCGGCACACTGGCCATA 761
Db |||||
QY 686 TCGGTGGTCTATCATGCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTACCGG 745
Db |||||
QY 762 TCGGTGGTCTATCATGCGCAGCTTTTCATCCCGATATGACACCGGTTAAAGTTACCGG 821
Db |||||
QY 746 GAGACTTTATCTGACAGCAGCTGCTGCTGCGCAGGGGATCACCATCCGTCCCGCGGC 805
Db |||||
QY 822 GAGACTTTATCTGACAGCAGCTGCTGCTGCGCAGGGGATCACCATCCGTCCCGCGGC 881
Db |||||
QY 806 GTGTCAATATATCATCTGTATCATCCCAACAGACGATACGGCTCTCTTTTATAG 865
Db |||||
QY 882 GTGTCAATATATCATCTGTATCATCCCAACAGACGATACGGCTCTCTTTTATAG 941
Db |||||
QY 866 GTGTAAACCTTAACTGCAATTTTCAACAGTCCCTGTTCTGTCAGCAAAAGACCGCTCAT 925
Db |||||
QY 942 GTGTAAACCTTAACTGCAATTTTCAACAGTCCCTGTTCTGTCAGCAAAAGACCGCTCAT 1001
Db |||||
QY 926 TTCATATAACCGGGGACCTGACCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC 985
Db |||||
QY 1002 TTCAATAAACCGGGGACCTGACCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCGGC 1061
Db |||||
QY 986 ACGCAGACGACGGGCTTCATTTGCAATGTTGTGCTTACACACCGGAGATTTGACATC 1045
Db |||||
QY 1062 ACGCAGACGACGGGCTTCATTTGCAATGTTGTGCTTACACACCGGAGATTTGACATC 1121
Db |||||
QY 1046 ATATATGCTTTCAGCAACTGATAGTGTGCTGTCACCTGTCACTGTATATGCTGCTTC 1105
Db |||||
QY 1122 ATATATGCTTTCAGCAACTGATAGTGTGCTGTCACCTGTCACTGTATATGCTGCTTC 1181
Db |||||
QY 1106 ATAGCACACCTCTTTTGTGACATCTTTGGGTA 1137
Db |||||
QY 1182 ATAGCACACCTCTTTTGTGACATCTTTGGGTA 1213
Db |||||

RESULT 10

AAC55525

ID AAC55525 standard; DNA; 4939 BP.

XX

AC

AAC55525;

XX

DT 11-JAN-2001 (first entry)

XX

DE Donor plasmid pDONR205 nucleotide sequence.

XX

KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
PN WO200052027-A1.
XX 08-SEP-2000.
XX 02-MAR-2000; 2000WO-US005432.
PF 02-MAR-1999; 99US-012389P.
PR 23-MAR-1999; 99US-012604P.
PR 28-MAY-1999; 99US-0136744P.
XX (LIFE-) LIFE TECHNOLOGIES INC.
PA Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
DR Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX Example 10; Fig 53; 459pp; English.
CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), (IV), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), (IV), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
XX Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;

Query Match

Best Local Similarity 24.9%; Score 1108.8; DB 3; Length 4939;

Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTACAAAAGCTGAACGAGAACCTGAAATGATATATATATCAATATT 85
Db 3636 GCCAACTTTGTACAAAAGCTGAACGAGAACCTGAAATGATATATATCAATATT 3695
QY 86 AAATAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACATATCCAGTC 145
Db 3696 AAATAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACATATCCAGTC 3755
QY 146 ACTATGATCAACTACTTAGATGTTATAGTACTGTAGTCACCGACGCTTCCAAA 205
Db 3756 ACTATGATCAACTACTTAGATGTTATAGTACTGTAGTCACCGACGCTTCCAAA 3815
QY 206 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCAA 265
Db 3816 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCTTCCAAATGTTCTTCAA 3875

Best Local Similarity 99.8%; Pred. No. 1.1e-148; Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 26	GACAAAGTTGTACAAAAGAGCTCAACGAGAAACGTAATAATGATATAAATCAATATATT 85
Db 102	GCCAACTTTGTACAAAAGAGCTCAACGAGAAACGTAATAATGATATAAATCAATATATT 161
QY 86	AAATTAGATTTCATATAAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 145
Db 162	AAATTAGATTTCATATAAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 221
QY 146	ACTATGAATCACTACTAGATGGTATTAGTACCTGTAGTCACGACAGCCTTCCAAA 205
Db 222	ACTATGAATCACTACTAGATGGTATTAGTACCTGTAGTCACGACAGCCTTCCAAA 281
QY 206	TGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTCTCAA 265
Db 282	TGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTCTCAA 341
QY 266	ACGGAATCGTGPATCCAGCCTACTCGCTATTGCTCAATGCGCTATTAAATCATFAAAA 325
Db 342	ACGGAATCGTGPATCCAGCCTACTCGCTATTGCTCAATGCGCTATTAAATCATFAAAA 401
QY 326	AGAAATAGAAAGAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db 402	AGAAATAGAAAGAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAAACATCTACCT 461
QY 386	ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAACAAATTTCAACAC 445
Db 462	ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAACAAATTTCAACAC 521
QY 446	TCATTATCTTTCTCTTAAGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 505
Db 522	TCATTATCTTTCTCTTAAGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
QY 506	CTAAACGCTGATAAGTTCTGTAATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 565
Db 582	CTAAACGCTGATAAGTTCTGTAATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
QY 566	AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGCGCTTTTGTGATGCTATT 625
Db 642	AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGCGCTTTTGTGATGCTATT 701
QY 626	TCGCGTGGCTGAGTACAGCACTTCTTCCCGATTAACGAGACCGGACACTGGCCATA 685
Db 702	TCGCGTGGCTGAGTACAGCACTTCTTCCCGATTAACGAGACCGGACACTGGCCATA 761
QY 686	TCGCTGCTCATCATGCGCCAGCTTTTATCCCGATATGACACCGGCTAAAGTTCAACGG 745
Db 762	TCGCTGCTCATCATGCGCCAGCTTTTATCCCGATATGACACCGGCTAAAGTTCAACGG 821
QY 746	GAGACTTTTATCTGACAGCAGCTGCTGCGGCGGGGATCAACATCCGTCGCCCGGC 805
Db 822	GAGACTTTTATCTGACAGCAGCTGCTGCGGCGGGGATCAACATCCGTCGCCCGGC 881
QY 806	GTGTCATATATACCTCTCTGATCCACAAACAGAGATACAGCTCTCTCTTTTATAG 865
Db 882	GTGTCATATATACCTCTCTGATCCACAAACAGAGATACAGCTCTCTCTTTTATAG 941
QY 866	GTGTAACCTTAACTGCAATTTTACCAGTCCCTGTTCTGCTGACGAAAAGAGCGTTTCA 925
Db 942	GTGTAACCTTAACTGCAATTTTACCAGTCCCTGTTCTGCTGACGAAAAGAGCGTTTCA 1001
QY 926	TTCAATAAACCGGCGACCTCAGGCATCCCTTCTGATTTTCCGCTTTCAGGCTTCGGC 985
Db 1002	TTCAATAAACCGGCGACCTCAGGCATCCCTTCTGATTTTCCGCTTTCAGGCTTCGGC 1061
QY 986	ACGACAGACGAGGCTTCTATCTGATGTTGCTTACACAGCCGAGATATGACATC 1045
Db 1062	ACGACAGACGAGGCTTCTATCTGATGTTGCTTACACAGCCGAGATATGACATC 1121
QY 1046	ATATATGCTTGAGCAACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db 1122	ATATATGCTTGAGCAACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
QY 1106	ATAGCACACCTCTTTTTCACATACCTTTGGGTA 1137
Db 1182	ATAGCACACCTCTTTTTCACATACCTTTGGGTA 1213
RESULT 9	
ADA50329	
ID	ADA50329 standard; DNA; 4892 BP.
XX	ADA50329;
AC	ADA50329;
XX	20-NOV-2003 (first entry)
DT	
XX	Plasmid vector pMK2010 DNA sequence.
DE	
XX	site-specific recombination; array construction; reporter gene fusion;
KW	mutagenesis; protein production; protein characterisation;
KW	plasmid pMK2010; ds.
XX	
OS	Synthetic.
XX	
PN	WO2003064623-A2.
XX	
PD	07-AUG-2003.
XX	
PF	31-JAN-2003; 2003WO-US003176.
XX	
PR	31-JAN-2002; 2002US-0354063P.
XX	
PA	(UNIW) UNIV WASHINGTON STATE RES FOUND.
XX	
PI	Kahn ML, House BL, Mortimer MW;
XX	
XX	WPI; 2003-679497/64.
DR	
XX	Moving an insert nucleic acid between vectors using site-specific
PT	recombination in vivo, useful for studying the biology of the organism,
PT	including array construction, reporter gene fusions, mutagenesis and
PT	protein production.
XX	
PS	Claim 41; Page 47-51; 52pp; English.
XX	
CC	The invention comprises a method for moving an insert nucleic acid
CC	molecule between vectors, the method involves moving an insert nucleic
CC	acid from one vector to another using site-specific recombination. The
CC	method of the invention is useful for studying the biology of an
CC	organism, including array construction, reporter gene fusions, an
CC	organism, protein production and characterisation. The present DNA
CC	sequence represents the plasmid vector pMK2010 of the invention.
XX	
SQ	Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;
Query Match 24.9%; Score 1108.8; DB 8; Length 4892;	
Best Local Similarity 99.8%; Pred. No. 1.1e-148; Indels 0; Gaps 0;	
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 26	GACAAAGTTGTACAAAAGAGCTCAACGAGAAACGTAATAATGATATAAATCAATATATT 85
Db 102	GCCAACTTTGTACAAAAGAGCTCAACGAGAAACGTAATAATGATATAAATCAATATATT 161
QY 86	AAATTAGATTTCATATAAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 145
Db 162	AAATTAGATTTCATATAAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 221
QY 146	ACTATGAATCACTACTAGATGGTATTAGTACCTGTAGTCACGACAGCCTTCCAAA 205
Db 222	ACTATGAATCACTACTAGATGGTATTAGTACCTGTAGTCACGACAGCCTTCCAAA 281
QY 206	TGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTCTCAA 265
Db 282	TGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAAATGTTCTCTCAA 341

comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into plasmids and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.9%; Score 1108.8; DB 3; Length 4470;

Best Local Similarity 99.8%; Pred. No. 1.1e-148;

Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 26 GACAGTTTGTACAAAAAGCTGAACGAGAAACGTTAAATGATATAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTTAAATGATATAATATCAATATATT 161
QY 86 AAATTAGATTTTGCATAAAAAAGACTACATAATCTGTTAAACACACATATCCAGTC 145
DB 162 AAATTAGATTTTGCATAAAAAAGACTACATAATCTGTTAAACACACATATCCAGTC 221
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCAGCCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCAGCCTTCCAAA 281
QY 206 TGTCTTCCGGGTGATGTCGCAACTTAGTCGACGAGCAGCCTTCCAAATGTTCTCTCAA 265
DB 282 TGTCTTCCGGGTGATGTCGCAACTTAGTCGACGAGCAGCCTTCCAAATGTTCTCTCAA 341
QY 266 AGGAATCGTCTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATATAAA 325
DB 342 AGGAATCGTCTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATATAAA 401
QY 326 AGAATAGAAAAAGAGGTGAGAGCCTCTTTTGTGACAAAAATAAAAAATCACTACT 385
DB 402 AGAATAGAAAAAGAGGTGAGAGCCTCTTTTGTGACAAAAATAAAAAATCACTACT 461
QY 386 ATTATATACGCTAGTCATAGTCGTAATATCATCTGATCATCAAGAAACATTTCAAC 445
DB 462 ATTATATACGCTAGTCATAGTCGTAATATCATCTGATCATCAAGAAACATTTCAAC 521
QY 446 TCTTATCTTTTCTTACAACTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATCTTA 505
DB 522 TCTTATCTTTTCTTACAACTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATCTTA 581
QY 506 CTAAACGTGATAAGTTTCTGTAATTTCTGTAATCGACCTGACAGCTGGCTGTGTATA 565
DB 582 CTAAACGTGATAAGTTTCTGTAATTTCTGTAATCGACCTGACAGCTGGCTGTGTATA 641
QY 566 AGGAGCTCTGACATTTATATCCCGACATCAATGAGTAAAGCGCTTTTGTGATCAATT 625
DB 642 AGGAGCTCTGACATTTATATCCCGACATCAATGAGTAAAGCGCTTTTGTGATCAATT 701
QY 626 TCGCGGTGGCTGAGATCAGCCTCTTCTCCCGATAACGGAGACCGGACACCTGGCCATA 685
DB 702 TCGCGGTGGCTGAGATCAGCCTCTTCTCCCGATAACGGAGACCGGACACCTGGCCATA 761
QY 686 TCGGTGGCTCATCGCAGCAGCTTTCTATCCCGATATGACACCGGGTAAAGTTCAAG 745
DB 762 TCGGTGGCTCATCGCAGCAGCTTTCTATCCCGATATGACACCGGGTAAAGTTCAAG 821
QY 746 GAGACTTTATCGACAGAGCTGCTGCTGCGGAGGATCACCATCGCTCGCCGGC 805
DB 822 GAGACTTTATCGACAGAGCTGCTGCTGCGGAGGATCACCATCGCTCGCCGGC 881
QY 806 GTGTCAATAATATCACTCTGTACATCCCAACACAGACGATACGGCTCTCTCTTTATAG 865
DB 882 GTGTCAATAATATCACTCTGTACATCCCAACACAGACGATACGGCTCTCTCTTTATAG 941

QY 866 GTGTAACCTTAAACCTGATTTTCCAGCTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 925
DB 942 GTGTAACCTTAAACCTGATTTTCCAGCTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCA 1001
QY 926 TTCAATAAACCGGGGAGCTTCCAGCCATCCCTTCTCTGATTTTCCAGCGTTCGCG 985
DB 1002 TTCAATAAACCGGGGAGCTTCCAGCCATCCCTTCTCTGATTTTCCAGCGTTCGCG 1061
QY 986 AGCGAGACGAGCGGCTTCAATTTCTGATGTTGCTTACCGAGACCGGAGATTTGACATC 1045
DB 1062 AGCGAGACGAGCGGCTTCAATTTCTGATGTTGCTTACCGAGACCGGAGATTTGACATC 1121
QY 1046 ATATATGCTTTGAGCAACTGATAGCTGCTGCTGCTCACTGTCACCTGATTAACGCTGCTTC 1105
DB 1122 ATATATGCTTTGAGCAACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTC 1181
QY 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1213

RESULT 8

ABZ58767

ID ABZ58767 standard; DNA; 4470 BP.

XX AC ABZ58767;

XX AC ABZ58767;

DT 01-MAY-2003 (first entry)

XX DE Destination plasmid pDONR201 nucleotide sequence.

XX DE Nucleic acid insertion; recombination; nucleic acid selection;

XX KW Nucleic acid isolation; ds.

XX OS Synthetic.

XX PN WO200295055-A2.

XX PD 28-NOV-2002.

XX PF 21-MAY-2002; 2002WO-US015947.

XX PR 21-MAY-2001; 2001US-0291973P.

XX PA (INVI-) INVITROGEN CORP.

XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;

XX DR WPI; 2003-129436/12.

XX Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

XX Disclosure; Fig 26B-C; 273pp; English.

CC The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence

XX Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

XX Query Match

24.9%; Score 1108.8; DB 7; Length 4470;

14445 ACTTTGTACAAGAAAGCTGAACAGAAAGCTAAATGATATAATATCAATATTAAT 14386
14389 TAGATTTTCATAAAAAACAGACTACATATATCTGTAAACACACATATCCAGTCACTA 2389
14385 TAGATTTTCATAAAAAACAGACTACATATATCTGTAAACACACATATCCAGTCACTA 14326
2390 TGAATCAACTACTTAGATGGTATTAGTACCTGTAGTTCGACTAAGTTGGCAGCATCACCC 2449
14325 TGAATCAACTACTTAGATGGTATTAGTACCTGTAGTTCGACTAAGTTGGCAGCATCACCC 14266
2450 GACGCACTTTGGCCGAATAAATACCTGTGAAGAAAGATCACTTCGCGAATAAATAAAT 2509
14265 GACGCACTTTGGCCGAATAAATACCTGTGAAGAAAGATCACTTCGCGAATAAATAAAT 14206
2510 CTTGTGTCTCCCTGTTCATACCGGGAAGCCCTGGCCCAACTTTTGGCGAAATGAGACGTT 2569
14205 CTTGTGTCTCCCTGTTCATACCGGGAAGCCCTGGCCCAACTTTTGGCGAAATGAGACGTT 14146
2570 GATCGGATTTCAACTCTTATCTTTCTCTTCAAGTCTGTTCGGCTTCATCTGGATTT 2629
14145 GATCGG-----CACTACCCGAAGTATGTCAAAAAGAGGTGTGTATGAAGCAGCGATTATC 14090
2630 TCAGCCTCTATCTACTATAACCGTGAATAAGTTCTGTAAATTTCTACTATCGACCTCC 2689
14089 AGTGACAGTTGACGAGCAGCATATCAGTTGCTCAAGGCATATATGATGCTCAATATCTCC 14030
2690 AGACTGG-----CTGTGTATAGGAGCTGACATTTATATTCGCCAGCAATCAG 2740
14029 GGTCTGGTAAGCACACCATGCAGATGAAGCCCTGCTCGTGGTGCC---GAAAGCTGG 13973
2741 GTTAATGGCGTTTGTATGTCATTTTCGGTGGGTGAGATCAGCACTTCCTCCCGAT 2800
13972 AAAGCGGAAATCAGGAAGGATGCTGAGGTGCGCCCGTCTTATTGAATGAACGCTCT 13913
2801 AACGGAGACCGGCACACTGCCATATCGGTGTCTATCATCGCCAGCTTTCATCCCGAT 2860
13912 TTTGCTGACGAGAACAGGG-----ACTGTGAATGCAAGTTAAAGTTTACACCTATAA 13859
2861 ATGCACACCGGTAAGTTCAAGGAGACTTTATCTGACAGCAGCTGCACTGGCCAG 2920
13858 AAGAGAGAGCGGTATCTGCTGTTTGTGATGTACAGAGTGATATTTTGACACGCCCG 13799
2921 GGGATCACATCCGTGCGCCGGGTGTCATATAATATCATCTGTATCATCAACCAAAACAG 2980
13798 GCGACGATGGTGATCCCGCTGCGCCAGTGCAGCTGTCTGTCTAGATAAAGTCTCCCGTGA 13739
2981 ACGATAACCGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTTCAACC-----AGT 3034
13738 ACTTTACCGGTGGTGCATATCGGGATGAAAGCTGGCCGATGATGACACCGATATGGC 13679
3035 CCCTGTTCTCGTACGAAAGACCGCTTCATTTCAATAAACCGGCGACCTCAGCCATCC 3094
13678 CAGTGTGCGGTCTCCGTTATCGGGAAGAGTGGTGTATCTCAGCCACCGCGAAATGA 13619
3095 CTTCTGATTTTCCGCTTTCCAGGCTTC---GGCAGCAGACGAGCGGCTTCATTTCTGCA 3151
13618 CATCAAAACGCCATTAACCTGATGTTTCGGGAATATAAAGTCAAGGCTCCCTTATACA 13559
3152 TGG---TTGTGCTTACAGACCGGAGATTTGACATCATATATGCTTGGAGCACTGTATA 3208
13558 CAGCCAGTCTGCAGTCTGATACAGTAGAATTTACAGAACTTTATCAGCTTTAGTAGTA 13499
3209 GCTGTGCTGCTCACTGTCTGTAATACGCTGCTTCATGACACCTCTTTTTCACATA 3268
13498 TAGAGGCTGAAATCCAGATGAAGCGAAGCAGCTTGTAAAGAAAAAGTAAAGAGTTGTG 13439
3269 CTTCTGTTCTTATGTCAGATGATTTTCAGGACTATGACACTAGCTGATATGATAGTAGT 3328
13438 AAATTTGTTCTTATGTCAGATGATTTTCAGGACTATGACACTAGCTGATATGATAGTAGT 13379
3329 ATGTTTTTATTTGTACAAAAAAGAGGCTCGCACCTCTTTTCTTCTTCTTTTAT 3388

13378 ATGTTTTTATTTGTCAACAAAAAGAGGCTCGCACCTCTTTTCTTTATTTCTTTTAT 13319
3389 GATTTAATACGGCATTTGGGACATATAGCGACTAGCTAGCTGATACGACGATTCGGTTGAGA 3448
13318 GATTTAATACGGCATTTGGGACATATAGCGACTAGCTAGCTGATACGACGATTCGGTTGAGA 13259
3449 AGAATTTGGAAGGCTGTCGGTGCAGCTAAGTGTGCGAGCATCACCGAAGAACATTTTGA 3508
13258 AGAATTTGGAAGGCTGTCGGTGCAGCTAAGTGTGCGAGCATCACCGGAGAACATTTTGA 13199
3509 AGGCTGTGCGTGCAGCTACAGTCTAATATACATCTAAGTAGTGTGATTCATAGTACCTGG 3568
13198 AGGCTGTGCGTGCAGCTACAGTCTAATATACATCTAAGTAGTGTGATTCATAGTACCTGG 13139
3569 ATATGCTGTGTTTACAGTATATGTAGTCTGTTTATGCAAAATCTAATTTAATATA 3628
13138 ATATGCTGTGTTTACAGTATATGTAGTCTGTTTATGCAAAATCTAATTTAATATA 13079
3629 TTGATATTTATATCATTTTACGTTTCTCGTTTCTCGTTTATGCAAACTTGTCTAGAG 3687
13078 TTGATATTTATATCATTTTACGTTTCTCGTTTCTCGTTTATGCAAACTTGTCTAGAG 13020

RESULT 7
AAC55521
ID AAC55521 standard; DNA; 4470 BP.
XX AAC55521;
XX AC AAC55521;
XX AC AAC55521;
DT 11-JAN-2001 (first entry)
XX Donor plasmid pDONR201 nucleotide sequence.
DE Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion gene cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
XX WO200052027-A1.
XX 08-SEP-2000.
XX 02-MAR-2000; 2000WO-US005432.
XX 02-MAR-1999; 99US-0122389P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Chao D;
XX WPI; 2000-543948/49.
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX recombination sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule

2648 AAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGG-----CT 2698
14071 CAGCTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGTTCTGTAAGCACAC 14012
2699 GTGTATAAGGAGCCCTGAATTTATATCCCGAAGACATCAGGTTAATGGCGTTTGTAT 2758
14011 ATGCAATGAAGCCGCTGCTGCTGCGTGC--GAACGCTGGAAGCGGAAATCAGGAA 13955
2759 GTCAATTTCCGCGTGTGATGAGTACGACCTCTCTCCCGATACCGGACCGGACACT 2818
13954 GGGATGGCTGAGTGCCTGCGGTTTATGAAATGAACGGCTCTTTTCTGACGAGAACAG 13895
2819 GGCATATCGGTGCTCATATGCGCAGCTTTTATCCCGATATGACCAACCGGGAAG 2878
13894 GA-----CTGGTGAATCAGTTTAAAGTTTACACCTATAAAGAGAGCGGTTATCG 13841
2879 TTCAGGGAGACTTTATCTGACAGAGAGTGCAGTGGCCAGGGGATCACCATCGGTG 2938
13840 TCTGTTTGTGGATGTACAGAGTATATTTATGACACGCGCGGCGACGGATGGTATGCC 13781
2939 CCGGGCGTGTCAATAATATCACTCTGTATATCCCAACAGACGATAACGGCTCTCTCT 2998
13780 CTGGCCAGTGCAGTCTGCTGTACATAAAGTCTCCCGTGAACCTTACCCGGTGTGCA 13721
2999 TTTATAGGTGTAACCTTAACTGCAATTTACCC-----AGTCCCTGTTTCTCGTCAGCAA 3052
13720 TATCGGGATGAAGCTGGCGCATGATGACCAACCGATATGGCAGTGTGCGGCTCTCCGT 13661
3053 AAGAGCGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCCTCTGATTTTCGGCTT 3112
13660 TATCGGGGAAGAGTGGCTGATCTGACCAACCGGAAATGATCAAAAACGCCATTAA 13601
3113 TCAGAGGTTTC---GGCAGCAGACGAGCGGCTTCATCTCGATGG---TTGTCCTTACCA 3166
13600 CCGTATGTTCTGGGAATATAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGTGC 13541
3167 GACCGAGATATGACATCATATATGCTTGGACCACTGATAGCTGCTGCTCACTGT 3226
13540 ATACAGTGAATATACAGAACTTTATCAGTTTAGTATAGAGGCTGAAATCCAG 13481
3227 CACTGTAATACGCTGCTTCATACACACCTCTTTTGGACATCTCTGTTTGTATGACG 3286
13480 ATGAACCGAGACACTGTGTAAGAGAAAGTATAGAGTGTGAAATGTTCTGATGACG 13421
3287 ATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGTATGTTTATTTGTCAC 3346
13420 ATGATTTTCAGGACTATGACACTAGCGTATATGATAGGTAGTATGTTTATTTTCTCAC 13361
3347 ACAAAAGAGGCTCGCAGCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATGA 3406
13360 ACAAAAGAGGCTCGCAGCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATGA 13301
3407 GGACATAGCGAGTGTGATGACAGCACTTCCGTTTGAAGAGAACATTTGGAAGGCTG 3466
13300 GGACATAGCGAGTGTGATGACAGCACTTCCGTTTGAAGAGAACATTTGGAAGGCTG 13241
3467 TCGGTGCACTAAGTTGCGAGCTATCCCGAAGAACATTTGGAAGGCTGCTGCTGACTAC 3526
13240 TCGGTGCACTAAGTTGCGAGCTATCCCGAAGAACATTTGGAAGGCTGCTGCTGACTAC 13181
3527 AGGTCACTATACATCTAAGTATGATTCATAGTACGCTGATATGTTGTTTACAG 3586
13180 AGGTCACTATACATCTAAGTATGATTCATAGTACGCTGATATGTTGTTTACAG 13121
3587 TATTATGACTCTGTTTTTATGCAAAATCTAATTTAATATATGATTTATATCATTT 3646
13120 TATTATGACTCTGTTTTTATGCAAAATCTAATTTAATATATGATTTATATCATTT 13061
3647 TCGTTTCTGCTGAGCTTTTTTGTACAAACTGTCTAGAG 3687
13060 TCGTTTCTGCTGAGCTTTTTTGTACAAACTGTCTCGAG 13020

RESULT 6

ABQ82141/c
ID ABQ82141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
XX recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
XX
PR 29-NOV-2001; 2001US-0333743P.
XX
PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin of
XX replication, a selectable marker and a chimeric DNA construct, useful for
XX silencing target nucleic acids and for producing large amounts of double-
XX stranded RNA.
XX
PS Claim 15; Page 74-83; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 28.7%; Score 1277.8; DB 6; Length 17476;
Best Local Similarity 62.4%; Pred. No. 1.1e-172;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;

QY 21 CTCGACAGAGTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAAT 80
Db 16704 CTCGACAGAGTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAAT 16645
QY 81 ATATTAAATAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACACATATC 140
Db 16644 ATATTAAATAGATTTTGCATAAAAAACAGACTACATAATCTGTAAACACACATATC 16585

Db 16266 ATGTCAAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGACA 16210
QY 501 ACTTACTAAACGCGATAAAGTTCTGTAATTTCTACTGTATGCAGCTCGAGACTCGCTGT 560
Db 16209 GCTATCAGTTGCTCAGGCGATATATGATCAATATCTCCGCTCTGGTAAGCACAAACCAT 16150
QY 561 GTATAAGGAGCGCTGACATTTATATCCCCGAAACATCAGGTTAATGCGGTTTTTGATGT 620
Db 16149 GCAGAAATGAAGCCGCTCGCTCGCTGCC---GAACGCTGAAAGCGGAAATCAGGAAGG 16093
QY 621 CATTTTCGCGGTGGTGAATCAGCGACATCTTCTTCCCGGATACCGAGACCGGACACTGG 680
Db 16092 GATGGCTGAGTGGCGCCGCTTTATTGAATGAACCGCTCTTTTGTCTGACGAAACAGGG- 16034
QY 681 CCATATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATATGCACCCCGGGTAAAGTT 740
Db 16033 -----ACTGGTGAATGCAAGTTAAGTTTTACCTATAAAGAGAGAGCCGTTATCGTTC 15979
QY 741 CAGGGAGACTTTATCTGACAGCAGCGTGCATCTGGCCAGGGGGATCACCATCCGTCGCC 800
Db 15978 TGTTCGTGATGTACAGAGTGATATTATTGACAGCGCCGGGCGACGGATGGTGATCCGCC 15919
QY 801 CGGGCGTGTCAATATATCACTGTGTACATCCAAACAGACGATACCGGCTCTCTCTTT 860
Db 15918 TGGCCAGTGCAGTCTGCTGTGATGATAAAGTCTCCCGTGAACCTTTACCCGGTGGTGCAAT 15859
QY 861 TATAGGTGTAACCTTAAACTGCAATTTACCC-----AGTCGCTGTCTCTCGTCAGCAAAA 914
Db 15858 TCGGGGATGAAGCTGGCGCATGATGACCAACCGATATGCCAGTGTGCGGCTCTCGTTA 15799
QY 915 GAGCGCTTCATTTCAATAAACCGGGCGAGCTCAGCCATCCCTTCTCTGATTTTCGCGTTTC 974
Db 15798 TCGGGGAAGAGTGGCTGTCTCAGCCACCGCGAATAATGACATCAAAAACGCCATTAAC 15739
QY 975 CAGCGTTC---GGCAGCGAGACGCGGCTTCATCTGCTGATGTTGTGCTTACCGACCG 1031
Db 15738 TGATGTTCTGGGGAATATAAATGTCAGGCTCCCTTATACAG-----CCAGTCTG 15688
QY 1032 GAGATATTGACATCATATATGCTTCAGCAACTGATAGTGTGCTGTCAACTGTCACTG 1091
Db 15687 CAGGTGATACAGTAAGAAATACAGAAACTTTATACGTTTAGTAGTATAGAGCTGAA 15628
QY 1092 TAATACGCTGTTTATAGCACACCTCTTTTGTACATFACCTCGGGTAGTG-----CCGATCA 1147
Db 15627 AATCCAGATGAAGCCGAAACGACTGTGAAGAAAAAGTATAAAGAGTTGTGAAATCCGATCA 15568
QY 1148 ACCTCTCATTTTCGCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGACACCAAGCA 1207
Db 15567 ACCTCTCATTTTCGCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGACACCAAGCA 15508
QY 1208 TTTATTTATTTCTCGAAGTGATCTTCGCTCACAGGTATTTATTCGCGCAAAAGTGGCTCG 1267
Db 15507 TTTATTTATTTCTCGAAGTGATCTTCGCTCACAGGTATTTATTTTCGCGCAAAAGTGGCTCG 15448
QY 1268 GGTGATGCTGCCAACTTAGTCTGACTACAGTCACTATACCATCTAAGTAGTGTATCAT 1327
Db 15447 GGTGATGCTGCCAACTTAGTCTGACTACAGTCACTAATACCATCTAAGTAGTGTATCAT 15388
QY 1328 AGTGACTGGATATGTTGTGTTTACAGTATTTATGTAGTCTGTTTTTATGCAAAATCTAA 1387
Db 15387 AGTGACTGGATATGTTGTGTTTACAGTATTTATGTAGTCTGTTTTTATGCAAAATCTAA 15328
QY 1388 TTTAATATATTTGATATTTATATCATTTTACGTTTCTCGTTTTCGTTTCTGTTACAAAGTG 1447
Db 15327 TTTAATATATTTGATATTTATATCATTTTACGTTTCTCGTTTTCGTTTCTGTTACAAAGTG 15268
QY 1448 GTCTCGAGGAATTCGGTACCACTGTAAAGGAATTAATATTTTCTTTTCTTTTCTTTAGTA 1507
Db 15267 GTCTAGAGGATCCAAAGCTTAAGGTAAGTAACCTGTAATCAATCCAAATGTAAGATCAATGA 15208
QY 1508 TAAAAATAGTTAAGTGATGTTTAAATTTAGTATGATTATATAATATATAGTTGTTTAAATTTGTA 1567
Db 15207 TAACACATGACATGATCTATCATGTTACCTTGTATTATTCATGTTTCGACTAATTCATTTA 15148

QY 1568 AAAAATAATTTTATAATATATATTTGTTTACATAAAACAAACATAGTAAATGTAAAAAATATGAC 1627
Db 15147 ATTAATAGTCAATCCATTTAGAGTTAATAAAACCTACAGTATTATTATTAGAAATTAATA 15088
QY 1628 AAGTGATGTGTAAGCAGGAAGATAAAAGTTGAGAGTAAGTATATATTATTTTAAATGAAT 1687
Db 15087 GAATGTTGATTTGAAATAATACTATATAAATGATAGATCTTGCGCTTTGTTATATTAGC 15028
QY 1688 TTGATCGAACAATGTAAGATGATATACAGCAATTAATATTGTTTAAATCAATAATAGTAAT 1747
Db 15027 ATTAGATTATGTTTGTGTTTACATTAGATTACTGTTTCTATTAGTTTGAATATTATTGTTAC 14968
QY 1748 TCTAGCTGGTTGTGTAATTAATCAATGATAAAATACATATACTATAAAATAAGAAATAA 1807
Db 14967 TTTAGCTTGTATTAAATATTGTTTATTGTAATAATTACAAGCAGATTGGAAATTTCTAA 14908
QY 1808 ATAAATTAATAATATTTTATGATTAATAGTTTATATATAAATTAATAATCTATATAC 1867
Db 14907 CAAAATATTATTAACTTTTAAACTTAAATAATTTAGTAATGGTAPAGATATTTAATTATA 14848
QY 1868 CATTAATAATATTGTTTAAAGTTAAATAATTTTGTAGAAATTCCTCAATCTGCT 1927
Db 14847 TAATAAATCTTAATCAATAAATAATATTATTTAATTTATTTTCTTATTTTACTAT 14788
QY 1928 TGTAAATTTTCAATAAACAATAATTAATAAACAGCTAAAGTAAACAATAATATCAAAAC 1987
Db 14787 AGTATTTTATCATGATATTAAATTCATAAACACAGCTAGAAATTAATATTATGATTAAAA 14728
QY 1988 TAATAAGAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATATTAACAAAGCGCA 2047
Db 14727 CAAATATTAAATGCTAGTATATCATCTTACATGTTTCGATCAAAATTCATTAATAATAATA 14668
QY 2048 AGATCTATCATTTTATATAGTATTATTTTCAATCAACAATCTCTTATTAATTTCTAATAAT 2107
Db 14667 CTTACTCTCAACTTTTATCTTCTGCTTACATCAATCACTGTGATATTTTTCATATA 14608
QY 2108 ACTTGTAGTTTATTAATCTTAAATGGATTGACTATTAAATTAATAANGAATTAGTCCGAACA 2167
Db 14607 CTATGTTGTTATGTAAACAATAATTTTATAAATTTATTTTTCACAATTTATAACAACATAT 14548
QY 2168 TGAATAAACAAGGTAACATGATAGATCAATGTCATTTGTTTATCATTTGATCTTACATTTGG 2227
Db 14547 ATTATTATAATCATACTAATTAACATCACTTAACATATTATTATACATAAAGGAAAAAGAA 14488
QY 2228 ATTGATTACAGTTACTTACCTTAAAGTTGGATCCCTAGACCACTTTGTACAGAAAGCT 2287
Db 14487 AATAATTTTCTTACAGTTGGTACCGAATTCCTCGAGACCACTTTGTACAGAAAGCT 14428
QY 2288 GAACGAGAAACGTAAAAATGATAATAATCAATATTAATAATTAAGATTGTTGATAAAAA 2347
Db 14427 GAACGAGAAACGTAAAAATGATAATAATCAATATTAATAATTAAGATTGTTGATAAAAA 14368
QY 2348 CAGACTACATATCTGTAAAAACACATATCCAGTCACTATGAATCAACTACTTAGAT 2407
Db 14367 CAGACTACATATCTGTAAAAACACATATCCAGTCACTATGAATCAACTACTTAGAT 14308
QY 2408 GGTATTAGTGACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGAGCGCACTTTGCGCCGAA 2467
Db 14307 GGTATTAGTGACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGAGCGCACTTTGCGCCGAA 14248
QY 2468 TAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCTCTGGTGTCCCTGTTGAT 2527
Db 14247 TAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCTCTGGTGTCCCTGTTGAT 14188
QY 2528 ACCGGAGCCCTGGCCAACTTTTGGGAAATGAGAGTTGATCGGATTTTCAACAATC 2587
Db 14187 ACCGGAGCCCTGGCCAACTTTTGGGAAATGAGAGTTGATCGG-----CACTACCC 14132
QY 2588 TTATATCTTTCTTCTACAGTCTGTTGCGCTTCATCTGGATTTTTCAGCTCTTATCTTACT 2647
Db 14131 GAAGTATGTCAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGCA 14072

15761 TAGTAATTCAGCTGGTTGATGAATTAATAATATCAATGATAAATACATATAGTAAATA 15820
1801 AGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1860
15821 AGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 15880
1861 TCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1920
15881 TCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 15940
1921 APTCTGCTGTAATTTATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1980
15941 ATCTGCTGTAATTTATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 16000
1981 ATCAAACTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2040
16001 ATCAAACTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 16060
2041 AAGCGCAAGATCTATCAATTTATATAGTATTAATTTCAATCAACATTTCTTATTAATTTCT 2100
16061 AAGCGCAAGATCTATCAATTTATATAGTATTAATTTCAATCAACATTTCTTATTAATTTCT 16120
2101 AAATAAATCTGTAGTTTATTAATCTTCAATAGGATGACATTAATAAATAAATAAATAA 2160
16121 AAATAAATCTGTAGTTTATTAATCTTCAATAGGATGACATTAATAAATAAATAAATAA 16180
2161 TCGAATGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2220
16181 TCGAATGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 16240
2221 CATTTGGATTTGATTAACAGTTACTTACCT-----TAAGCTTTGGATCCTCTAG 2265
16241 CATTTGGATTTGATTAACAGTTGGGAATTTGGGTTTCGAAATCGAATAAGCTTGGATCCTCTAG 16300
2267 A----- 2267
16301 AGAGCTGCAGCTGGATGGCAATAATGATTTTATTTTGATGATGACCTGTTTCGTTG 16360
2268 -----CCACTTTGTACAAGAAAGCTGAACGA 2293
16361 CAACAAATTTGATAGCAATGCTTTCTTATAATGCGCAACTTTGTACAAGAAAGCTGAACGA 16420
2294 GAAAGTAAATGATTAATAATCAATAATTAATAATTAATAATTTGATTAATAAATAAATAA 2353
16421 GAAAGTAAATGATTAATAATCAATAATTAATAATTAATAATTTGATTAATAAATAAATA 16480
2354 ACATAATGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2413
16481 ACATAATGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 16540
2414 AGTGACCTGTAGTACGACTAAGTTGGCAGCATCACCGACGACTTTGGCCGGAATAAATA 2473
16541 AGTGACCTGTAGTACGACTAAGTTGGCAGCATCACCGACGACTTTGGCCGGAATAAATA 16600
2474 CTTGTGACGGAAGATCACTTCGCAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2533
16601 CTTGTGACGGAAGATCACTTCGCAATAAATAAATAAATAAATAAATAAATAAATAAATAA 16660
2534 AAGCCCTGGGCAACTTTTGGGGAATAAGAGAGGTTGATCGG-----ATTTCACAC 2585
16661 AAGCCCTGGGCAACTTTTGGGGAATAAGAGAGGTTGATCGGCACTTACCCATTTTACACAC 16720
2586 TCTTATACCTTTCTTACAAGTCGTTTCGGCTTCATCTGGATTTTCAGGCTCTTACTACTTA 2645
16721 TCTTATACCTTTCTTACAAGTCGTTTCGGCTTCATCTGGATTTTCAGGCTCTTACTACTTA 16780
2646 CTAAACGATGAATAAGTTTCTGTAATTTCTATGATTCGACCTGCGAGATGGCTGTGTATA 2705
16781 CTAAACGATGAATAAGTTTCTGTAATTTCTATGATTCGACCTGCGAGATGGCTGTGTATA 16840
2706 AAGGACCTGACATTTATTTCCCAAGACATCAGGTTAATGCGGTTTGTGATGATTTT 2765

16841 AGGAGCCTGACATTTATATTCGCCAGAAATCAGGTTAATGGCGTTTTTGTATGATCAATTT 16900
2766 TCGCGTGGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACGGCAGACTGCGCATA 2825
16901 TCGCGTGGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACGGCAGACTGCGCATA 16960
2826 TCGGTGGTCAATCATCGCCAGCTTTTCATCCCGATATGCACACCGGTAAGTTTCAGG 2885
16961 TCGGTGGTCAATCATCGCCAGCTTTTCATCCCGATATGCACACCGGTAAGTTTCAGG 17020
2886 GAGACTTTATCTGACAGACGCTGACCTGCGCAGGGGGATCAATCCGTCGCGCGGCG 2945
17021 GAGACTTTATCTGACAGACGCTGACCTGCGCAGGGGGATCAATCCGTCGCGCGGCG 17080
2946 GTGTCAATAATATCATCTGTACATCCACAAACAGAGATAAACGGCTCTCTCTTTATAG 3005
17081 GTGTCAATAATATCATCTGTACATCCACAAACAGAGATAAACGGCTCTCTCTTTATAG 17140
3006 GTGTAAACCTTTAAACTGCAATTCACCACTGCTCTCTGTCAGCAAAAGAGCGCTTCAT 3065
17141 GTGTAAACCTTTAAACTGCAATTCACCACTGCTCTCTGTCAGCAAAAGAGCGCTTCAT 17200
3066 TTCAATAAACCAGGCGACTCAGGCATCCCTTCCCTGATTTTCCGCTTCCAGCGTTCGCG 3125
17201 TTCAATAAACCAGGCGACTCAGGCATCCCTTCCCTGATTTTCCGCTTCCAGCGTTCGCG 17260
3126 ACGCAGACGACGGCTTCATTTCTGATGTTGCTTACCAAGACGGAGATTAATGACATC 3185
17261 ACGCAGACGACGGCTTCATTTCTGATGTTGCTTACCAAGACGGAGATTAATGACATC 17320
3186 ATATATGCTTTGAGCAACTGATGCTGCTGCTCAACTGCTGCTGTAATACGCTGCTTC 3245
17321 ATATATGCTTTGAGCAACTGATGCTGCTGCTCAACTGCTGCTGTAATACGCTGCTTC 17380
3246 ATAGCAGACCTTTTGGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3305
17381 ATAGCAGACCTTTTGGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 17440
3306 CACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTACACAAAAAGAGGCTCGCAC 3365
17441 CACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTACACAAAAAGAGGCTCGCAC 17500
3366 CTCTTTTCTTATTTTCTTTTATGATTAATAGGATTAAGGATTAAGGATTAAGGATTAAG 3425
17501 CTCTTTTCTTATTTTCTTTTATGATTAATAGGATTAAGGATTAAGGATTAAGGATTAAG 17560
3426 GGATACGACGATTCGCTTTGAGAGAAATTTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTG 3485
17561 GGATACGACGATTCGCTTTGAGAGAAATTTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTG 17620
3486 GCATACCCGGAAGAAATTTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3545
17621 GCATACCCGGAAGAAATTTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17680
3546 AGTAGTTCATTCATAGTACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3605
17681 AGTAGTTCATTCATAGTACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 17740
3606 TATGCAAAATCTAATTTAATATTTATATTTATATTTATATTTATATTTATATTTATATTT 3665
17741 TATGCAAAATCTAATTTAATATTTATATTTATATTTATATTTATATTTATATTTATATTT 17800
3666 TTTTGTACAAACTTG-----TCTAGAGT 3688
17801 TTTTGTACAAAGTTGGCATTTAAAAAGCATTTGCTCATCAATTTGTTGCAACGAACAGG 17860
3681 -----TCTAGAGT 3688
17861 TCATATCAGTCAAAATAAATCAATTTTGGGCGCGAGATCCATGCTAGCTTAGAGT 17920
3689 CTTGCTTTAATGAGATATGCGAGACGCTATGATCGCATGATATTTGCTTTCAATTTCTGT 3748
17921 CTTGCTTTAATGAGATATGCGAGACGCTATGATCGCATGATATTTGCTTTCAATTTCTGT 17980

QY 506 CTAAACGTGATTAAGTTCTCTTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGATA 565
DB 13601 CTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGATA 13660
QY 566 AGGAGCGCTGACATTTATATATCCCCAGAACATCAAGTTTAATGGCGTTTTTTCATGTCATTT 625
DB 13661 AGGAGCGCTGACATTTATATATCCCCAGAACATCAAGTTTAATGGCGTTTTTTCATGTCATTT 13720
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATA 685
DB 13721 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACTGGCCATA 13780
QY 686 TCGGTGGCTCATCATCGCCAGCTTTTCATCCCGGATATGCACACCGGGTAAAGTTTCACGG 745
DB 13781 TCGGTGGCTCATCATCGCCAGCTTTTCATCCCGGATATGCACACCGGGTAAAGTTTCACGG 13840
QY 746 GAGACTTTATCTGACAGACAGCTGCATGCGCCAGGGGATCAACATCGGTGCGCCGGGC 805
DB 13841 GAGACTTTATCTGACAGACAGCTGCATGCGCCAGGGGATCAACATCGGTGCGCCGGGC 13900
QY 806 GTGTCAATTAATCACTCTGTACATCCCAAAACAGACGATACGGCTCTCTCTTTTATAG 865
DB 13901 GTGTCAATTAATCACTCTGTACATCCCAAAACAGACGATACGGCTCTCTCTTTTATAG 13960
QY 866 GTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGACCGCTTCAT 925
DB 13961 GTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGACCGCTTCAT 14020
QY 926 TTCAATAAACCAGGGGACCTGACGCAATCCCTCTCTGATTTTCGGCTTTCACGGTTCCGC 985
DB 14021 TTCAATAAACCAGGGGACCTGACGCAATCCCTCTCTGATTTTCGGCTTTCACGGTTCCGC 14080
QY 986 AGCAGACACCGCGCTTCACTCTGATGTTGTGCTTACAGACCGAGATATTGACATC 1045
DB 14081 AGCAGACACCGCGCTTCACTCTGATGTTGTGCTTACAGACCGAGATATTGACATC 14140
QY 1046 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTC 1105
DB 14141 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTC 14200
QY 1106 ATAGCACACTCTTTTGTGACATCTTGGGTAGTGGCGATCAACGTCTCATTTTCGCCAA 1165
DB 14201 ATAGCACACTCTTTTGTGACATCTTGGGTAGTGGCGATCAACGTCTCATTTTCGCCAA 14260
QY 1166 AAGTTGGCCACAGGCTTCCCGGTATCAACAGGACACCAAGATTTTATTTCTGCGAAG 1225
DB 14261 AAGTTGGCCACAGGCTTCCCGGTATCAACAGGACACCAAGATTTTATTTCTGCGAAG 14320
QY 1226 TGATCTTCGCTCACAGTATTTATTCGGCGCAAGTGGTGGGTGATGCTGCCAATTA 1285
DB 14321 TGATCTTCGCTCACAGTATTTATTCGGCGCAAGTGGTGGGTGATGCTGCCAATTA 14380
QY 1286 GTGACTTACAGCTCACTAATACCATCTAAGTGTGATTCATAGTGCATGATGTTGT 1345
DB 14381 GTGACTTACAGCTCACTAATACCATCTAAGTGTGATTCATAGTGCATGATGTTGT 14440
QY 1346 GTTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTTGATTTT 1405
DB 14441 GTTTTACAGTATTATGATGCTGTTTTTATGCAAAATCTAAATTTAATATATTTGATTTT 14500
QY 1406 ATATCAATTTACGTTTCTGTTTCAGTTCTTCTGTGACAAAGTGG----- 1448
DB 14501 ATATCAATTTACGTTTCTGTTTCAGTTCTTCTGTGACAAAGTGGCATTTAAGAAAGCAT 14560
QY 1449 ----- 1448
DB 14561 TGCTTATCAATTTGTGCAACGAAACAGTCACTATCAGTCAAAATAAATCAATTTTGC 14620
QY 1449 -----TCTCGAGGAATTCGGTACC---AAGTGAAGGAATAATTTATTTT 1490
DB 14621 CATCCAGCTGCGCTCCTCGAGGAATTCGGTACCCCAATTTGGTGAAGGAATAATTTATTTT 14680

QY 1491 CTTTTTCCCTTTAGTATATAAATAAGTTAAGTGTATTAATAGTATGATTTATTAATATAT 1550
DB 14681 CTTTTTCCCTTTAGTATATAAATAAGTTAAGTGTATTAATAGTATGATTTATTAATATAT 14740
QY 1551 AGTTGTTATTAATTTGTGAARAAATAAATTTATAAATATATTTCTTTACATAAAACAACATAGTA 1610
DB 14741 AGTTGTTATTAATTTGTGAARAAATAAATTTATAAATATATTTCTTTACATAAAACAACATAGTA 14800
QY 1611 ATGTAAAAAATAATGACAGTGTATGTAAGACGAAGAAGATAAAAAGTTGAGAGTAAGTA 1670
DB 14801 ATGTAAAAAATAATGACAGTGTATGTAAGACGAAGAAGATAAAAAGTTGAGAGTAAGTA 14860
QY 1671 TATTATTTTAAATGAAATTTGATCGAACATGTAAGATATATACTAGCAITAA----- 1722
DB 14861 TATTATTTTAAATGAAATTTGATCGAACATGTAAGATATATACCGCGTAAAGAGGTTC 14920
QY 1723 ----- 1722
DB 14921 AACTTTCACCATTAATGAATAAGATCACTACCGGCGTATTTTTTGTAGTTATCGAGATTT 14980
QY 1723 ----- 1722
DB 14981 TCAGGAGCTAAGGAAGCTTAAATTCGAGAAAAAATCACTGGATATACACCGTTGATATA 15040
QY 1723 ----- 1722
DB 15041 TCCCAATGGCATGTAAGAACAATTTTGAGGCATTTGAGTCAGTTGCTCAATGTACCTAT 15100
QY 1723 ----- 1722
DB 15101 AACAGACCGTTTCAGCTGGATATTACGGCCCTTTTTTAAAGACCGTAAAGAAAAATAAGCAC 15160
QY 1723 ----- 1722
DB 15161 AAGTTTATTCGGCGCTTTATTCACATTTCTGCCCGCTGATGAATGCTCATCCGGAATTC 15220
QY 1723 ----- 1722
DB 15221 CGTATGGCAATGAAGAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCTTGTACACC 15280
QY 1723 ----- 1722
DB 15281 GTTTTCCATGAGCAAACTGAACCGTTTTTCATCGCTCTCGAGTGAATACCAACGAGATTC 15340
QY 1723 ----- 1722
DB 15341 CGGCAGTTTCTACACATATATTTCGCAAGATGTGGCGTGTACGGTGAATAAACTGGCCCTAT 15400
QY 1723 ----- 1722
DB 15401 TTCCCTAAAGGGTTATTGAGAAATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTTTC 15460
QY 1723 ----- 1722
DB 15461 ACCAGTTTTTGATTTAAACGTGGCCAATATGGACAACATTTCTTCCGCCCGCTTTTCACCATG 15520
QY 1723 ----- 1722
DB 15521 GGCAAATATTATACGCAAGCGCAAGGTGCTGATGCGCGCTGGCGATTCAGGTTCTCAT 15580
QY 1723 ----- 1722
DB 15581 GCGGTCTGTATGGCTTCCATGTCCGCAGAAATGCTTAAATGAATTAACAACAGTACTGCGAT 15640
QY 1723 ----- 1722
DB 15641 GAGTGGCAGCGCGGCGGTAATCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGTAT 15700
QY 1723 -----TATTGTTTTTAATCATAA 1740
DB 15701 GCGTATTTGCGCGCTGATTTTTTTCGGGTATAAGAAATATACTGATATGCGGGCCCATAA 15760
QY 1741 TAGTAATTTCTAGCTGTTTTGATGAATTAATATCAATGATAAATACTATAGTAAAAATA 1800

Db	14800	AATAAGAAATAAATAAAATTAATAATATTTTTTTATGATTAATAAGTTTATATATATAATTA	14859
Qy	1957	AATATCTATACCATTAATAATATTTTGTAGTTTAAAGTTAATAAATAATTTTGTAGAAAT	1916
Db	14860	AATATCTATACCATTAATAATATTTTGTAGTTTAAAGTTAATAAATAATTTTGTAGAAAT	14919
Qy	1917	TCCAATCTGCTGTGAATTTATCAATAAACAATAATTTAAATPAACAAGCTAAAGTAAACAA	1976
Db	14920	TCCAATCTGCTGTGAATTTATCAATAAACAATAATTTAAATPAACAAGCTAAAGTAAACAA	14979
Qy	1977	TAATATCAAACTAATAGAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATAT	2036
Db	14980	TAATATCAAACTAATAGAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATAT	15039
Qy	2037	BACAAAGCGAAGATCTATCAATTTATATAGTATTTTCAATCAACATTTCTTATTAAT	2096
Db	15040	AACAAAGCGAAGATCTATCAATTTATATAGTATTTTCAATCAACATTTCTTATTAAT	15099
Qy	2097	TTCTAAATAAATACTTGTAGTTTTTATTAATCTCTAAATCGATGTACTTAAATTAATGAA	2156
Db	15100	TTCTAAATAAATACTTGTAGTTTTTATTAATCTCTAAATCGATGTACTTAAATTAATGAA	15159
Qy	2157	TTAGTCGAACATGAATAAACAAGGTAAACATGATAGTATCATGTCTTGTGTATCATTTGAT	2216
Db	15160	TTAGTCGAACATGAATAAACAAGGTAAACATGATAGTATCATGTCTTGTGTATCATTTGAT	15219
Qy	2217	CTTACATTTGGATTCGATTACAGTTACTTACCT-----	2248
Db	15220	CTTACATTTGGATTCGATTACAGTTGGGAGCTGGTTTCGAAATCGATAAGCTTGCGCTGC	15279
Qy	2249	-----	2248
Db	15280	AGTTATCATCATCATCATAGACACAGAAATAAAGTAATCAGATTATCAGTTAAAGCTAT	15339
Qy	2249	-----	2248
Db	15340	GTAATATTTGCGCCATPAACCAATCAATTAATAAATAGATCAGTTTAAAGAAAGATCAAAG	15399
Qy	2249	-----	2248
Db	15400	CTCAAAAAATAAAGAGAAAAGGGTCTTAACCAAGAAAAATGAAGAGAAAACTAGAA	15459
Qy	2249	-----TAAGCTTGGATCCTCTAGACCACTTTGTATCAAGAAAGCTGAACGAGAA	2297
Db	15460	ATTTACCTGCACAAAGCTTGGATCCTCTAGACCACTTTGTATCAAGAAAGCTGAACGAGAA	15519
Qy	2298	CGTAAATAGTATAAATATCAATATATTAATTAGATTTTGGCATAAAAACAGACTACAT	2357
Db	15520	CGTAAATAGTATAAATATCAATATATTAATTAGATTTTGGCATAAAAACAGACTACAT	15579
Qy	2358	AATACTGTAAAAACAAACATATCCAGTCACATGAATCAACTCTTAGATGGTATTAGTG	2417
Db	15580	AATACTGTAAAAACAAACATATCCAGTCACATGAATCAACTCTTAGATGGTATTAGTG	15639
Qy	2418	ACCTGTAGTCGACTAAGTTGGCAGCATCAACCGACGACCTTTGGCCGGAATAATACCTG	2477
Db	15640	ACCTGTAGTCGACTAAGTTGGCAGCATCAACCGACGACCTTTGGCCGGAATAATACCTG	15699
Qy	2478	TGACGGAAGATCACTTCGCGAATAAATAAATCTGCTGTCTGCTGTGTATACCGGGAAGC	2537
Db	15700	TGACGGAAGATCACTTCGCGAATAAATAAATCTGCTGTCTGCTGTGTATACCGGGAAGC	15759
Qy	2538	CCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGATTTCAAACTCTTATCTTTT	2597
Db	15760	CCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGATTTCAAACTCTTATCTTTT	15819
Qy	2598	CTCTTACAAGTCGTTTGGCCTTCACTGGATTTTCHAGCTCTATACTTACTTAAACGTTGATA	2657
Db	15820	CTCTTACAAGTCGTTTGGCCTTCACTGGATTTTCHAGCTCTTATACTTACTTAAACGTTGATA	15879
Qy	2658	AAGTTTCTGTAAATTTCTACTGTATCGACTGCAGACTGCTGTGTATTAAGGAGCCTGCAC	2717
Db	15880	AAGTTTCTGTAAATTTCTACTGTATCGACTGCAGACTGCTGTGTATTAAGGAGCCTGCAC	15939

QY	2718	ATTATATATCCCCAGAACATCAGGTTAAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTG	2777
DB	15940	ATTATATATCCCCAGAACATCAGGTTAAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTG	15999
QY	2778	AGATCAGCCACTTCTTTCCCGGATAACGGAGACGGGACACTGGCCATATCGGTGGTCATC	2837
DB	16000	AGATCAGCCACTTCTTTCCCGGATAACGGAGACGGGACACTGGCCATATCGGTGGTCATC	16059
QY	2838	ATGGCCAGAGCTTTCAATCCCGATATGACACACCGGGTAAAGTTTACCGGAGACTTTATCT	2897
DB	16060	ATGGCCAGAGCTTTCAATCCCGATATGACACACCGGGTAAAGTTTACCGGAGACTTTATCT	16119
QY	2998	GACAGCAGAGCTGCACATGGCCAGGGGATACACATCCGTCCGCCGGGCGTGTCAATAATA	2957
DB	16120	GACAGCAGAGCTGCACATGGCCAGGGGATACACATCCGTCCGCCGGGCGTGTCAATAATA	16179
QY	2958	TCACCTCTGTATCATCCACAAACAGACGATTAACGGGTCTCTCTTTTATAGGTATAACCTTA	3017
DB	16180	TCACCTCTGTATCATCCACAAACAGACGATTAACGGGTCTCTCTTTTATAGGTATAACCTTA	16239
QY	3018	AACATGCAATTCACAGATCCCTGTTCTCGTCAGCAAAAGAGCGGTCATTTCATAAACC	3077
DB	16240	AACATGCAATTCACAGATCCCTGTTCTCGTCAGCAAAAGAGCGGTCATTTCATAAACC	16299
QY	3078	GGGACCTCAGCATCCCTCTCTGATTTTCGGCTTTCAGCGGTTCCGACGCGAGACGAG	3137
DB	16300	GGGACCTCAGCATCCCTCTCTGATTTTCGGCTTTCAGCGGTTCCGACGCGAGACGAG	16359
QY	3138	GGCTTCATTCGATCGGTGGCTTACAGACCGGAGATATTGACATCATATATGCCCTG	3197
DB	16360	GGCTTCATTCGATCGGTGGCTTACAGACCGGAGATATTGACATCATATATGCCCTG	16419
QY	3198	AGCAACTGATAGCTGTCGCTGTCACATGTCATTAACGCTGCTTCATAGCACACCTC	3257
DB	16420	AGCAACTGATAGCTGTCGCTGTCACATGTCATTAACGCTGCTTCATAGCACACCTC	16479
QY	3258	TTTTTGGACATCTCTGTTCTTGATGCGAGATGATTTTCAGGACTATGACACTAGCGTATA	3317
DB	16480	TTTTTGGACATCTCTGTTCTTGATGCGAGATGATTTTCAGGACTATGACACTAGCGTATA	16539
QY	3318	TGAATAGGTAGATGTTTTTATTTTGTCAACAAAAAGAGGCTCGCACCTCTTTTCTTA	3377
DB	16540	TGAATAGGTAGATGTTTTTATTTTGTCAACAAAAAGAGGCTCGCACCTCTTTTCTTA	16599
QY	3378	TTTTCTTTTATGATTTAATACGGCATTGAGGACAAATAGCGATGAGCTGGATACGAGAT	3437
DB	16600	TTTTCTTTTATGATTTAATACGGCATTGAGGACAAATAGCGATGAGCTGGATACGAGAT	16659
QY	3438	TCGGTTTGAGAGAAACATTTGGAAGGCTGTCCGTCCGACTAAGTTGGCGCATCACCCGAA	3497
DB	16660	TCGGTTTGAGAGAAACATTTGGAAGGCTGTCCGTCCGACTAAGTTGGCGCATCACCCGAA	16719
QY	3498	GAACTTTGGAAGGCTGTCCGTCCGACTAAGTTGACATTAATACCATCTAAGTAGTTGATTC	3557
DB	16720	GAACTTTGGAAGGCTGTCCGTCCGACTAAGTTGACATTAATACCATCTAAGTAGTTGATTC	16779
QY	3558	ATAGTGACTGGATATGTTGTTTACAGTATTATGATGTCGTGTTTTTATGCAAAATCT	3617
DB	16780	ATAGTGACTGGATATGTTGTTTACAGTATTATGATGTCGTGTTTTTATGCAAAATCT	16839
QY	3618	AATTTAATATATTGATTTTATATCATTTTACGTTTTCTCGTTCAGCTTTTTTGTAACAAC	3677
DB	16840	AATTTAATATATTGATTTTATATCATTTTACGTTTTCTCGTTCAGCTTTTTTGTAACAAC	16899
QY	3678	TTGTCATAGTCCCTGCTTTTAATGAGATATCGGAGACGCTTATGATCCCATGATTTGCT	3737
DB	16900	TTGTCATAGTCCCTGCTTTTAATGAGATATCGGAGACGCTTATGATCCCATGATTTGCT	16959
QY	3738	TTCAATTTCTGTTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCATTACGC	3797
DB	16960	TTCAATTTCTGTTGCGAGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCATTACGC	17019

region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

Query Match 94.2%; Score 4200; DB 6; Length 17681;
Best Local Similarity 95.0%; Pred No. 0;
Matches 4449; Conservative 0; Mismatches 10; Indels 223; Gaps 2;

QY 1 TTTCATTTTGGAGGACGCTCGAGACAAGTTTCTACAAAAAGCTGAACGAGAAAGCT 60
DB 13000 TTTCATTTTGGAGGACGCTCGAGACAAGTTTCTACAAAAAGCTGAACGAGAAAGCT 13059

QY 61 AAAATGATATAAATATCAATATTAATAGATTTCGATATAAAAAAGACTACATAAT 120
DB 13060 AAAATGATATAAATATCAATATTAATAGATTTCGATATAAAAAAGACTACATAAT 13119

QY 121 ACTGTAACAAACAATATCCAGTCACTATGATCAACTTACATGATGATATAGTGACC 180
DB 13120 ACTGTAACAAACAATATCCAGTCACTATGATCAACTTACATGATGATATAGTGACC 13179

QY 181 TGTAGTCGACGACGACCTTCCAAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACGG 240
DB 13180 TGTAGTCGACGACGACCTTCCAAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACGG 13239

QY 241 ACAGCTTCCAAATGTTCTTCACACGAATCGTGTATCCAGCTACTCGCTATTGTC 300
DB 13240 ACAGCTTCCAAATGTTCTTCACACGAATCGTGTATCCAGCTACTCGCTATTGTC 13299

QY 301 CTCATGCGGTATTAATCATAAAAAGAAATGAAGAAAGAGGTGCGAGCTCTTTTGG 360
DB 13300 CTCATGCGGTATTAATCATAAAAAGAAATGAAGAAAGAGGTGCGAGCTCTTTTGG 13359

QY 361 TGTGACAAATATAAACAATCTACCTATTTCATATAGCTAGTGTCAATGTCCTGAAATCA 420
DB 13360 TGTGACAAATATAAACAATCTACCTATTTCATATAGCTAGTGTCAATGTCCTGAAATCA 13419

QY 421 TCTGATCAAGAACAAATTTCAACCTCTTATCTTTCTTACAGTCTGTTCCGGCTTCA 480
DB 13420 TCTGATCAAGAACAAATTTCAACCTCTTATCTTTCTTACAGTCTGTTCCGGCTTCA 13479

QY 481 TCTGGATTTTCAGCTCTTACTTACTAAACGATGATAAGTTTCTGTAAATTTCTACTGTA 540
DB 13480 TCTGGATTTTCAGCTCTTACTTACTAAACGATGATAAGTTTCTGTAAATTTCTACTGTA 13539

QY 541 TCGACTCGAGACTGGCTGTATATAGGAGGCTTGACATTTATTTCCCCAGAACATCAG 600
DB 13540 TCGACTCGAGACTGGCTGTATATAGGAGGCTTGACATTTATTTCCCCAGAACATCAG 13599

QY 601 GTTAATGGGTTTTTCATGTCATTTTTCGGGTGCTGAGATCAGGCACCTTCTTCCCGGAT 660
DB 13600 GTTAATGGGTTTTTCATGTCATTTTTCGGGTGCTGAGATCAGGCACCTTCTTCCCGGAT 13659

QY 661 AACGGAGACCGGACACTGCGCCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGGAT 720
DB 13660 AACGGAGACCGGACACTGCGCCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGGAT 13719

QY 721 ATGCACACCGGGTAAAGTTTCACGGGAGACTTTTATCTGACAGCAGAGCTGCGCCAG 780

DB 13720 ATGCACACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAG 13779

QY 781 GGGGATCACCATCGCTCGCCCGCGGTGTCATAATATCACTCTGTATCATCCACAAACAG 840

DB 13780 GGGGATCACCATCGCTCGCCCGCGGTGTCATAATATCACTCTGTATCATCCACAAACAG 13839

QY 841 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGT 900

DB 13840 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGT 13899

QY 901 TCTCGTCAGCAAAAGACCGCTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCCCT 960

DB 13900 TCTCGTCAGCAAAAGACCGCTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCCCT 13959

QY 961 GATTTTCCGCTTCCACGCTTCGGCACGACGACGCGGGTTCATTTCTGATGTTGTCG 1020

DB 13960 GATTTTCCGCTTCCACGCTTCGGCACGACGACGCGGGTTCATTTCTGATGTTGTCG 14019

QY 1021 TTACCAGACCGGAGATATTGACATCATATATATGCTTTCGAGCAACTGATGTCGCTGTC 1080

DB 14020 TTACCAGACCGGAGATATTGACATCATATATGCTTTCGAGCAACTGATGTCGCTGTC 14079

QY 1081 AACTGTCACTGTATACTGCTCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGTG 1140

DB 14080 AACTGTCACTGTATACTGCTCTTCATAGCACACCTCTTTTGTGACATCTTCGGGTAGTG 14139

QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCCGCAGGGCTTCGCCGTATCAACAGGGAC 1200

DB 14140 CCGATCAACGCTCTCATTTTCGCCAAAAGTTGGCCCGCAGGGCTTCGCCGTATCAACAGGGAC 14199

QY 1201 ACCAGGATTTATTTATTCGCGAAGTGANCTTCGCTCACAGGTATTTATTCGCGGCAAG 1260

DB 14200 ACCAGGATTTATTTATTCGCGAAGTGANCTTCGCTCACAGGTATTTATTCGCGGCAAG 14259

QY 1261 TGCGTCCGGTGCATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGT 1320

DB 14260 TGCGTCCGGTGCATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGT 14319

QY 1321 GATTCATAGTACCTGGATATGTTGTTTACAGTATTTATGATGCTGTGTTTTTATGCAA 1380

DB 14320 GATTCATAGTACCTGGATATGTTGTTTACAGTATTTATGATGCTGTGTTTTTATGCAA 14379

QY 1381 AATCTAATTTAATATTTATGATTTATATCATTTTACGTTTCTCGTTCAGCTTCTTGTA 1440

DB 14380 AATCTAATTTAATATTTATGATTTATATCATTTTACGTTTCTCGTTCAGCTTCTTGTA 14439

QY 1441 CAAAGTGTCTCGAGGAATTCGGTACCAAC---TGTAAAGAAATAATTTATTTCTTTT 1496

DB 14440 CAAAGTGTCTCGAGGAATTCGGTACCAAC---TGTAAAGAAATAATTTATTTCTTTT 14499

QY 1497 TCCTTTTAGTATAAAATAGTTAAGTGTAAATTTAGTATGATTAATAATAATATAGTTGT 1556

DB 14500 TCCTTTTAGTATAAAATAGTTAAGTGTAAATTTAGTATGATTAATAATAATATAGTTGT 14559

QY 1557 TATAATTTGAAAAATAATTTATTAATAATTTGTTTACATAAAACAACATAGTATGTA 1616

DB 14560 TATAATTTGAAAAATAATTTATTAATAATTTGTTTACATAAAACAACATAGTATGTA 14619

QY 1617 AAAAAATATGACAAGTGTGTGAACGAGAAAGATAAAAGTTGAGAGTAAGTATATAT 1676

DB 14620 AAAAAATATGACAAGTGTGTGAACGAGAAAGATAAAAGTTGAGAGTAAGTATATAT 14679

QY 1677 TTTTAATGAATTTGATCGAACATGTAAGATGATATATAGCAATTAATTTGTTTAAATC 1736

DB 14680 TTTTAATGAATTTGATCGAACATGTAAGATGATATATAGCAATTAATTTGTTTAAATC 14739

QY 1737 ATAAATGTAATTTCTAGCTGGTTTGTGAATTTAAATATCAATGATAAATATCTATAGTAA 1796

DB 14740 ATAAATGTAATTTCTAGCTGGTTTGTGAATTTAAATATCAATGATAAATATCTATAGTAA 14799

QY 1797 AATAAGATAAATAAATAAATAATATTTTATGATTAATAGTTTATATAATAATTA 1856

Db 15940 GGATCACCATCGTCCGCGCGGTGTCATTAATATCACTCTGTACATCCCAACAGAC 15999
QY 2983 GATACGGCTCTCTCTTTATAGGTGTAACCTTAACTGATTTCCAGTCCCGTGTTC 3042
Db 16000 GATAACGGCTCTCTCTTTATAGGTGTAACCTTAACTGATTTCCAGTCCCGTGTTC 16059
QY 3043 TCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGGGCGACCTCAGCCATCCCTTCCTGA 3102
Db 16060 TCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGGGCGACCTCAGCCATCCCTTCCTGA 16119
QY 3103 TTTTCGGCTTTCAGGTTTCGCGACGACGACGGGCTTCACTTCGATGGTGTGCTT 3162
Db 16120 TTTTCGGCTTTCAGGTTTCGCGACGACGACGGGCTTCACTTCGATGGTGTGCTT 16179
QY 3163 ACCAGACCGGAGATTTGACATCATATATGCTTCGAGCAACTGATAGCTGTCGCTGTCAA 3222
Db 16180 ACCAGACCGGAGATTTGACATCATATATGCTTCGAGCAACTGATAGCTGTCGCTGTCAA 16239
QY 3223 CTGTCACTGTAATACGCTCTTCATAGCACACCTCTTTTGTGACATCTCTCTCTCTGAT 3282
Db 16240 CTGTCACTGTAATACGCTCTTCATAGCACACCTCTTTTGTGACATCTCTCTCTCTGAT 16299
QY 3283 GCAGATGATTTTCAGGACTATGACACTAGCTATGATAGTATGATGATGATGATGATGAT 3342
Db 16300 GCAGATGATTTTCAGGACTATGACACTAGCTATGATAGTATGATGATGATGATGATGAT 16359
QY 3343 TCACACAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATTTTAAACGGCA 3402
Db 16360 TCACACAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATTTTAAACGGCA 16419
QY 3403 TTGAGGACAAATAGCGAGTGGGTAACGACGATTCGCTTTGAGAGAACATTTGGGAAG 3462
Db 16420 TTGAGGACAAATAGCGAGTGGGTAACGACGATTCGCTTTGAGAGAACATTTGGGAAG 16479
QY 3463 GCTGTCGTCGACTAAGTTGGGAGCATCACCGAGAACATTTGGAAGGCTGCGGTGCA 3522
Db 16480 GCTGTCGTCGACTAAGTTGGGAGCATCACCGAGAACATTTGGAAGGCTGCGGTGCA 16539
QY 3523 CTACAGGTCACATAACCTCTAAGTAGTGTGATTCATAGTGTGATGATGATGATGATGATGAT 3582
Db 16540 CTACAGGTCACATAACCTCTAAGTAGTGTGATTCATAGTGTGATGATGATGATGATGATGAT 16599
QY 3583 ACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3642
Db 16600 ACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16659
QY 3643 ATTTTACGTTCTCGTTTCAGCTTTTGTACAACTTGTCTAGAGTCTGCTTTTATGAG 3702
Db 16660 ATTTTACGTTCTCGTTTCAGCTTTTGTACAACTTGTCTAGAGTCTGCTTTTATGAG 16719
QY 3703 ATATCGAGACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3762
Db 16720 ATATCGAGACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16779
QY 3763 AAAACCTGACATGCTAGCTAGATGCTTACCGCGGTTTCGGTTCACTTCAATCAATA 3822
Db 16780 AAAACCTGACATGCTAGCTAGATGCTTACCGCGGTTTCGGTTCACTTCAATCAATA 16839
QY 3823 TATCACCGTTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3882
Db 16840 TATCACCGTTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16899
QY 3883 CCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3942
Db 16900 CCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 16959
QY 3943 TAGCGACATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4002
Db 16960 TAGCGACATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 17019
QY 4003 CAATTTTAAAAAGCGGAGACCGGTCAAACCTAAAGACTGATTTACATAAATCTTAT 4062

Db 17020 CAATTTTAAAAAGCGGAGACCGGTCAAACCTAAAGACTGATTTACATAAATCTTAT 17079
QY 4063 TCAAAATTTCAAAAGCGGCCCTAGTATCTACGACACACCGAGCGGCGAACTAATAA 4122
Db 17080 TCAAAATTTCAAAAGCGGCCCTAGTATCTACGACACACCGAGCGGCGAACTAATAA 17139
QY 4123 CGTTCACTGAAGGAACTCCGGTTCCCGGCGGCGGCGATGGGTGAGATTCCTTGAAGTT 4182
Db 17140 CGTTCACTGAAGGAACTCCGGTTCCCGGCGGCGGCGATGGGTGAGATTCCTTGAAGTT 17199
QY 4183 GAGTATTTGGCGCTCCGCTTACCGAAAGTTACGGGACCACTTCAACCGGTCACAGCAGG 4242
Db 17200 GAGTATTTGGCGCTCCGCTTACCGAAAGTTACGGGACCACTTCAACCGGTCACAGCAGG 17259
QY 4243 CGGCGGGTAAACCGACTTGTGCTGCGGAGAAATTAAGCAGCAATTTTGTGTGATGTTGG 4302
Db 17260 CGGCGGGTAAACCGACTTGTGCTGCGGAGAAATTAAGCAGCAATTTTGTGTGATGTTGG 17319
QY 4303 CCCCAATGAAGTCAGGTCAAACTTTGACAGTACGACAAATCGTTGGGCGGTCACAG 4362
Db 17320 CCCCAATGAAGTCAGGTCAAACTTTGACAGTACGACAAATCGTTGGGCGGTCACAG 17379
QY 4363 GCGAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTGAGGATGCAAGCTAGCTTGA 4422
Db 17380 GCGAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTGAGGATGCAAGCTAGCTTGA 17439
QY 4423 CTAGTGTGATGATTTCTATAGTGTCACTAAATCTGC 4459
Db 17440 CTAGTGTGATGATTTCTATAGTGTCACTAAATCTGC 17476

RESULT 3
ABQ82143
ID ABQ82143 standard; DNA; 17681 BP.
XX
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 17; Page 93-102; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter

QY 781 GGGATCACCATCCGTCGCCGGGGGTGTCAATAATATCACTCTGTACATCACAAAAG 840
Db 13780 GGGGATCACCATCCGTCGCCGGGGGTGTCAATAATATCACTCTGTACATCACAAAAG 13839
QY 841 AGGATAAGCGGCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGT 900
Db 13840 AGGATAAGCGGCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGT 13899
QY 901 TCTCGTCAGCAAAAGAGCGGTTCATTTCAATAAAACGGGGGAGCCCTCAGCCATCCCTTCC 960
Db 13900 TCTCGTCAGCAAAAGAGCGGTTCATTTCAATAAAACGGGGGAGCCCTCAGCCATCCCTTCC 13959
QY 961 GATTTTCGCGTTTCAGCGTTCGGCAGCAGCAGCGGGCTTCATTTCTGCATGGTGTGTC 1020
Db 13960 GATTTTCGCGTTTCAGCGTTCGGCAGCAGCAGCGGGCTTCATTTCTGCATGGTGTGTC 14019
QY 1021 TTACAGACCGGAGATATGACATCATATATGCTTGGACCACTGATAGCTGTGCTGTC 1080
Db 14020 TTACAGACCGGAGATATGACATCATATATGCTTGGACCACTGATAGCTGTGCTGTC 14079
QY 1081 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTCATATCTCGGGTAGTG 1140
Db 14080 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTCATATCTCGGGTAGTG 14139
QY 1141 CCGATCAAGCTCTCATTTTTCGCAAAAGTTGGCCCAAGGCTTCCCGGTATCAACAGGAC 1200
Db 14140 CCGATCAAGCTCTCATTTTTCGCAAAAGTTGGCCCAAGGCTTCCCGGTATCAACAGGAC 14199
QY 1201 ACCAGGATTTATTTTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGGCCAAG 1260
Db 14200 ACCAGGATTTATTTTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGGCCAAG 14259
QY 1261 TCGCTCGGGTGATGCTGCCAATTAAGTGCATACAGGTCACTAATACCATCTAAGTAGTT 1320
Db 14260 TCGCTCGGGTGATGCTGCCAATTAAGTGCATACAGGTCACTAATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTACGTGATGTTGTTTACAGTATTAAGTAGTCTGTTTATGCA 1380
Db 14320 GATTCATAGTACGTGATGTTGTTTACAGTATTAAGTAGTCTGTTTATGCA 14379
QY 1381 AATCTAATTTATATATATGATATTTATATCATTTTACGTTCTCGTTCAGCTTCTTGTA 1440
Db 14380 AATCTAATTTATATATGATATTTATATCATTTTACGTTCTCGTTCAGCTTCTTGTA 14439
QY 1441 CAAAGTGTCTCGAGGAATTCGGTACC-----AAGTGTAAAGAAATAATTTATTTTCTTTT 1496
Db 14440 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTATTTTCTTTT 14499
QY 1497 TCGTTTATGATAAATAGTTAAGTGATGTTAATAGTATGATTAATAATATAGTTGT 1556
Db 14500 TCGTTTATGATAAATAGTTAAGTGATGTTAATAGTATGATTAATAATATAGTTGT 14559
QY 1557 TATAATTTGAAAAAATAATTTATAAATAATATTTGTTTACATAAAACACATAGTAATGTA 1616
Db 14560 TATAATTTGAAAAAATAATTTATAAATAATATTTGTTTACATAAAACACATAGTAATGTA 14619
QY 1617 AAAAAATGCAAGTGATGTTAAGCAGGAAGATATAAAGTTGAGGTAAGTATATAT 1676
Db 14620 AAAAAATGCAAGTGATGTTAAGCAGGAAGATATAAAGTTGAGGTAAGTATATAT 14679
QY 1677 TTTTAAATGATTTGATCGAAGATGTAAGATGATATATAGTATTAATAATTTCTTTTATTC 1736
Db 14680 TTTTAAATGATTTGATCGAAGATGTAAGATGATATATAGTATTAATAATTTCTTTTATTC 14739
QY 1737 ATAATAGTAATTTCTAGCTGGTTGATGAATTAATAATATCAATGATAAAATACATAGTAA 1796
Db 14740 ATAATAGTAATTTCTAGCTGGTTGATGAATTAATAATCAATGATAAAATACATAGTAA 14799
QY 1797 ATAAGATAAATAAATTAATAATATTTTATGATAATATAGTTTATTAATAATTA 1856
Db 14800 ATAAGATAAATAAATTAATAATATTTTATGATAATATAGTTTATTAATAATTA 14859

QY 1857 AATATCTATACCAATTTACTAAATATTTTAGTTTAAAAAGTTAATAAATAATTTTGTAGAAAT 1916
Db 14860 AATATCTATACCAATTTACTAAATATTTTAGTTTAAAAAGTTAATAAATAATTTTGTAGAAAT 14919
QY 1917 TCCAAATCTGCTGTAAATTTTCAATAAACAATAATTTAAATAACAAGCTAAAGTAACAA 1976
Db 14920 TCCAAATCTGCTGTAAATTTTCAATAAACAATAATTTAAATAACAAGCTAAAGTAACAA 14979
QY 1977 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATAT 2036
Db 14980 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATAT 15039
QY 2037 AACAAAGCGCAAGATCTATCAATTTATATAGTATTAATTTTCAATCAACATCTTATTAAT 2096
Db 15040 AACAAAGCGCAAGATCTATCAATTTATATAGTATTAATTTTCAATCAACATCTTATTAAT 15099
QY 2097 TTCTAATAATAACTGTGTAGTTTATTAACCTTCAATTCGAATGGATGACTATTAATTAATGAA 2156
Db 15100 TTCTAATAATAACTGTGTAGTTTATTAACCTTCAATTCGAATGGATGACTATTAATTAATGAA 15159
QY 2157 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATTTGTATCATTTGAT 2216
Db 15160 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCATTTGTATCATTTGAT 15219
QY 2217 CTTACATTTGGATGATTTACAGTTACTTACCT-----TAAAGCTTGGATCCT 2262
Db 15220 CTTACATTTGGATGATTTACAGTTGGGAAGCTGGGTTGAAATCGATAAGCTTGGATCCT 15279
QY 2263 CTAGACCACTTTTGTACAGAAGAGCTGAACGAGAAGCTGAAATGATATAAATATCAATAT 2322
Db 15280 CTAGACCACTTTTGTACAGAAGAGCTGAACGAGAAGCTGAAATGATATAAATATCAATAT 15339
QY 2323 ATTAATTTAGATTTTGCATAAAAAACAGACTACATAATATCTGTAAAAACACAACATATCCA 2382
Db 15340 ATTAATTTAGATTTTGCATAAAAAACAGACTACATAATATCTGTAAAAACACAACATATCCA 15399
QY 2383 GTCATATGATCAACTACTTTAGATGGTATTTAGTGACCTGTAGTCGACTAAGTTGGCAGC 2442
Db 15400 GTCATATGATCAACTACTTTAGATGGTATTTAGTGACCTGTAGTCGACTAAGTTGGCAGC 15459
QY 2443 ATCACCCAGCACCTTTTCGCGCGAATAAATACCTGTGACGGAAGATCACTTCGCGAGAATA 2502
Db 15460 ATCACCCAGCACCTTTTCGCGCGAATAAATACCTGTGACGGAAGATCACTTCGCGAGAATA 15519
QY 2503 AATAAATCCTGGTCCCTGTGTGATACCGGAAGCCCTGGGCCAACCTTTTCGCGAAAAATG 2562
Db 15520 AATAAATCCTGGTCCCTGTGTGATACCGGAAGCCCTGGGCCAACCTTTTCGCGAAAAATG 15579
QY 2563 AGACGTTGATCGGATTTTCAACACTTTTATACCTTTCTTACAGTCGCTGGCTTCATC 2622
Db 15580 AGACGTTGATCGGATTTTCAACACTTTTATACCTTTCTTACAGTCGCTGGCTTCATC 15639
QY 2623 TGGATTTTCAGCCTCTATCTACTTAAACGTAATAAGTTTCTGTAAATTTCTACTGTATC 2682
Db 15640 TGGATTTTCAGCCTCTATCTACTTAAACGTAATAAGTTTCTGTAAATTTCTACTGTATC 15699
QY 2683 GACCTGACAGCTGGCTGTGATTAAGGAGCCTGACATTTATTTCCCGAGAACATCAGGT 2742
Db 15700 GACCTGACAGCTGGCTGTGATTAAGGAGCCTGACATTTATTTCCCGAGAACATCAGGT 15759
QY 2743 TAAATGGCGTTTGTGATGTCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAA 2802
Db 15760 TAAATGGCGTTTGTGATGTCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAA 15819
QY 2803 CGGAGACCGGACACCTGGCCCATATCGGTGTCATCATCGCCAGCTTTTCATCCCGATAT 2862
Db 15820 CGGAGACCGGACACCTGGCCCATATCGGTGTCATCATCGCCAGCTTTTCATCCCGATAT 15879
QY 2863 GCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGG 2922
Db 15880 GCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACAGCAGAGCTGCACTGGCCAGG 15939
QY 2923 GGATCACCATCCGTCGCCCGGGCGGTGTCAATAATATCACTCTGTATATCCACACAGAC 2982

QY 4081 CAGGGGCTAGTATCTACGACACACCGAGCGGCACTAATAACGTTCACTGAGGGAAC 4140
DB |||||
QY 17080 CAGGGGCTAGTATCTACGACACACCGAGCGGCACTAATAACGTTCACTGAGGGAAC 17139
DB |||||
QY 4141 CCGGTTCCCGCGCGCGCATGGGTGAGATTCCTTGAAGTTGATTTGGCGGTCGCT 4200
DB |||||
QY 17140 CCGGTTCCCGCGCGCGCATGGGTGAGATTCCTTGAAGTTGATTTGGCGGTCGCT 17199
DB |||||
QY 4201 CTACCGAAGTTACGGGACCAATTCACCCGCTCCAGCACGCGCGCGGTTAACCGACTT 4260
DB |||||
QY 17200 CTACCGAAGTTACGGGACCAATTCACCCGCTCCAGCACGCGCGCGGTTAACCGACTT 17259
DB |||||
QY 4261 GCTGCCCCGAGAAATATGACGCAATTTTGTGTGATGTGGCCCCCAATGAAGTGCAGG 4320
DB |||||
QY 17260 GCTGCCCCGAGAAATATGACGCAATTTTGTGTGATGTGGCCCCCAATGAAGTGCAGG 17319
DB |||||
QY 4321 TCAAACTTGACAGTACGACGACAAATCGTTGGCGGGTCCAGGCGCAATTTGCGACACA 4380
DB |||||
QY 17320 TCAAACTTGACAGTACGACGACAAATCGTTGGCGGGTCCAGGCGCAATTTGCGACACA 17379
DB |||||
QY 4381 TGTGAGGCTCAGCAGGACCTGAGGCATGCAAGCTAGCTTACTAGTGTGATGATTTCTA 4440
DB |||||
QY 17380 TGTGAGGCTCAGCAGGACCTGAGGCATGCAAGCTAGCTTACTAGTGTGATGATTTCTA 17439
DB |||||
QY 4441 TAGTGTACCTAAATCTGC 4459
DB |||||
QY 17440 TAGTGTACCTAAATCTGC 17458
DB |||||

RESULT 2

AB082141
ID AB082141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELSSGATE 8 nucleotide sequence SEQ ID NO:24.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
XX WO200259294-A1.
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU0000073.
XX
PF 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX WPI; 2002-682669/73.
DR
XX
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
XX Claim 15; Page 74-83; 104pp; English.
PS
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in Bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and

CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX

SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 98.8%; Score 4406.6; DB 6; Length 17476;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;

QY 1 TTTCAATTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGT 60
DB |||||
QY 13000 TTTCAATTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGT 13059
DB |||||
QY 61 AAAATGATATAATATCAATATATATAATTTAGATTTTGCATAAAAAACAGACTACATAAT 120
DB |||||
QY 13060 AAAATGATATAATATCAATATATATAATTTAGATTTTGCATAAAAAACAGACTACATAAT 13119
DB |||||
QY 121 ACTGTAAAAACAACATATCCAGTCATATGAATCAACTACTTAGATGGTATTAGTGACC 180
DB |||||
QY 13120 ACTGTAAAAACAACATATCCAGTCATATGAATCAACTACTTAGATGGTATTAGTGACC 13179
DB |||||
QY 181 TGTAGTCGACGACGAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCGACCG 240
DB |||||
QY 13180 TGTAGTCGACGACGAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCGACCG 13239
DB |||||
QY 241 ACAGCCTTCCAAATGTTCTTCAAACGGAATCGTCGCTATCCAGCCTACTCGCTATTGTC 300
DB |||||
QY 13240 ACAGCCTTCCAAATGTTCTTCAAACGGAATCGTCGCTATCCAGCCTACTCGCTATTGTC 13299
DB |||||
QY 301 CTCATGCGGTATTAATCATATAAAGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGG 360
DB |||||
QY 13300 CTCATGCGGTATTAATCATATAAAGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGG 13359
DB |||||
QY 361 TGTGACAAAATAAAAAACATCTACCTATTATATACGCTAGTGTGATAGTCTCTGAAAAATCA 420
DB |||||
QY 13360 TGTGACAAAATAAAAAACATCTACCTATTATATACGCTAGTGTGATAGTCTCTGAAAAATCA 13419
DB |||||
QY 421 TCTGATCAAGAACAAATTCACACTCTTATACCTTTCTTCTTACAGTCGTTTCGGCTTCA 480
DB |||||
QY 13420 TCTGATCAAGAACAAATTCACACTCTTATACCTTTCTTCTTACAGTCGTTTCGGCTTCA 13479
DB |||||
QY 481 TCTGATTTTCAGGCTCTATACCTTACTAAAGCTGATAAAGTTCTGTAATTTCTACTGTA 540
DB |||||
QY 13480 TCTGATTTTCAGGCTCTATACCTTACTAAAGCTGATAAAGTTCTGTAATTTCTACTGTA 13539
DB |||||
QY 541 TCGACCTGCAGACTGGCTGTGTATAAAGGAGCCTGACATTTATATTTCCCAAGAACATCAG 600
DB |||||
QY 13540 TCGACCTGCAGACTGGCTGTGTATAAAGGAGCCTGACATTTATATTTCCCAAGAACATCAG 13599
DB |||||
QY 601 GTTAATGCGTTTTTGTATGTCATTTTTCGGGTGCTGAGATCAGGCACCTTCTTCCCGAT 660
DB |||||
QY 13600 GTTAATGCGTTTTTGTATGTCATTTTTCGGGTGCTGAGATCAGGCACCTTCTTCCCGAT 13659
DB |||||
QY 661 AACGAGACCGGCACTACCTGGCCATATCGTGTGCTCATCATGCGCAGCTTTTCATCCCGAT 720
DB |||||
QY 13660 AACGAGACCGGCACTACCTGGCCATATCGTGTGCTCATCATGCGCAGCTTTTCATCCCGAT 13719
DB |||||
QY 721 ATGCACACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGCTGCACTGGCCAG 780
DB |||||
QY 13720 ATGCACACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGCTGCACTGGCCAG 13779
DB |||||

Db 14860 TCTATACCATTACTAAATATTTTAGTTTAAAGTTTAAATAATATTTTGTAGAAATTCGA 14919
QY 1921 ATCTGCTGTAAATTTATCAATAAACAATAATTAATAACAGCTAAAGTAAACAATAAT 1980
Db 14920 ATCTGCTGTAAATTTATCAATAAACAATAATTAATAACAGCTAAAGTAAACAATAAT 14979
QY 1981 ATCAAACCTAAATAGAAACAGTAAATCTAATGTAACAAAACATAATCTAATGCTAAATATAACA 2040
Db 14980 ATCAAACCTAAATAGAAACAGTAAATCTAATGTAACAAAACATAATCTAATGCTAAATATAACA 15039
QY 2041 AAGCGCAAGATCTATCAATTTTATATAGTATTTTCAATCAACATCTCTATTAATTTCT 2100
Db 15040 AAGCGCAAGATCTATCAATTTTATATAGTATTTTCAATCAACATCTCTATTAATTTCT 15099
QY 2101 AAATAAATCTGTAGTTTATTAATCTCTAAATGGATTGACTATTAATAATAATGAATTAG 2160
Db 15100 AAATAAATCTGTAGTTTATTAATCTCTAAATGGATTGACTATTAATAATAATGAATTAG 15159
QY 2161 TCGAACATGAATAAACAAGGTAAACATAGATGATCATGTGTTGTTATCATGATCTTA 2220
Db 15160 TCGAACATGAATAAACAAGGTAAACATAGATGATCATGTGTTGTTATCATGATCTTA 15219
QY 2221 CATTTGGATTGATACAGTTACTTACCTTAAGCTTGGATCTCTAGACCACTTTGTACAA 2280
Db 15220 CATTTGGATTGATACAGTTACTTACCTTAAGCTTGGATCTCTAGACCACTTTGTACAA 15279
QY 2281 GAAAGCTGAACAGAAACGTAATAATGATATAAATCAATATATAAATTAAGATTGCA 2340
Db 15280 GAAAGCTGAACAGAAACGTAATAATGATATAAATCAATATATAAATTAAGATTGCA 15339
QY 2341 TAAAAACAGACTACATAAATCTGTAAACACACATATCAAGTCACTATGAATCAACTA 2400
Db 15340 TAAAAACAGACTACATAAATCTGTAAACACACATATCAAGTCACTATGAATCAACTA 15399
QY 2401 CTTAGATGGTATTAGTGACCTGTAGTCGACCTAAGTTGCGAGCATCACCGACGCACTTTG 2460
Db 15400 CTTAGATGGTATTAGTGACCTGTAGTCGACCTAAGTTGCGAGCATCACCGACGCACTTTG 15459
QY 2461 CGCCGAATAAATACCTGTGAAGAGATCACTTTCGAGAAATAAATAAATCTGTTGTCCTC 2520
Db 15460 CGCCGAATAAATACCTGTGAAGAGATCACTTTCGAGAAATAAATAAATCTGTTGTCCTC 15519
QY 2521 TGTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTGTGATCGGATTC 2580
Db 15520 TGTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTGTGATCGGATTC 15579
QY 2581 ACAACTCTTATCTTTCTCTTACAAAGTCGTTGCGCTTCATCTGGATTTCAGCCCTCTAT 2640
Db 15580 ACAACTCTTATCTTTCTCTTACAAAGTCGTTGCGCTTCATCTGGATTTCAGCCCTCTAT 15639
QY 2641 ACTTACTAAACGTGATAAAGTTTCTGTAATTTCTATGATCGACCTCGACACTGGCTGT 2700
Db 15640 ACTTACTAAACGTGATAAAGTTTCTGTAATTTCTATGATCGACCTCGACACTGGCTGT 15699
QY 2701 GTATAAGGAGCGCTGACATTTATTTATTTCCAGAACATCAGTTAATCGGTTTGTATGT 2760
Db 15700 GTATAAGGAGCGCTGACATTTATTTATTTCCAGAACATCAGTTAATCGGTTTGTATGT 15759
QY 2761 CATTTTCGCGTGGCTGAGATCAGCACCTTTCTCCCGATTAACGAGACCGGCACACTGG 2820
Db 15760 CATTTTCGCGTGGCTGAGATCAGCACCTTTCTCCCGATTAACGAGACCGGCACACTGG 15819
QY 2821 CCATATCGGTGTGATCATGTCGCCAGCTTTATCCCGATGATGCAACACCGGGTAAAGTT 2880
Db 15820 CCATATCGGTGTGATCATGTCGCCAGCTTTATCCCGATGATGCAACACCGGGTAAAGTT 15879
QY 2881 CACGGAGACTTTATCTGACAGACAGCGTCGACTGGCCAGGGGATCACCATCCGTCGCC 2940
Db 15880 CACGGAGACTTTATCTGACAGACAGCGTCGACTGGCCAGGGGATCACCATCCGTCGCC 15939
QY 2941 CGGGGTGTCAATAATATCACTCTGTACATCCACAAAACAGAGATAACGGCTCTCTCTTT 3000
Db 15940 CGGGGTGTCAATAATATCACTCTGTACATCCACAAAACAGAGATAACGGCTCTCTCTTT 15999

QY 3001 TATAGGTGTAAACCTTTAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGAGCGG 3060
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QY 3061 TTAATTTCAATAAACCAGGCGGAGCTCAGCAATCCCTTCTGATTTTCCGCTTTCCAGCGT 3120
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QY 3121 TCGGCAACGAGACGAGCGGCTTCATCTGATGCTGCTGCTTACCAACCGGAGATATTG 3180
Db 16120 TCGGCAACGAGACGAGCGGCTTCATCTGATGCTGCTGCTTACCAACCGGAGATATTG 16179
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Db 17020 CAGAACCGGTCAAAACCTAAAAAGACTGATTAATAAATCTTATTTCAAAATTTCAAAAGGCC 17079

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;

Query Match 100.0%; Score 4459; DB 6; Length 17458;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 TGTAGTCGACCGACAGCCCTCCAAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACCG 240
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QY 301 CTCATGCGGTATTAATCATATAAAGAAATGAAGAAAGAGGTGGAGCCCTTTTTTG 360
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QY 361 TGTGACAAAATAAAAAATCAATCTACTATTCATATACGCTAGTGTCTAGTCTGAAATCA 420
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QY 481 TCTGGAATTTTACGCTCTATCTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTA 540
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QY 721 ATGCACACACCGGTAAAGTTTACGGGAGACTTTATCTGACAGACAGCTGACCTGGCCAG 780
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QY 841 ACGATAACGCTCTCTCTTTTATAGTGTGTAACCTTAAACCTGCAATTCACAGTCCCTGT 900

Db 13840 ACGATAACGCTCTCTCTTTTATAGTGTGTAACCTTAAACCTGCAATTCACAGTCCCTGT 13899

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Db 14320 GATTCATAGTCACTGGATATGTTCTGTTTACAGTATTTATGCTGCTGTTTTTATGCAA 14379

QY 1381 AATCTAATTTAATATTTATTTATATCAATTTTACGTTTCTCGTTTCAGCTTCTTGTA 1440

Db 14380 AATCTAATTTAATATTTATTTATATATATTTTACGTTTCTCGTTTCAGCTTCTTGTA 14439

QY 1441 CAAGTGTCTCGAGGATTCGGTACCACTGTAAGGAAATTAATTTCTCTTTTCTTCCCT 1500

Db 14440 CAAGTGTCTCGAGGAAATTCGGTACCACTGTAAGGAAATTAATTTCTCTTTTCTTCCCT 14499

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QY 1621 ATATCACAAGTGTGTGTAAGCAGGAAGATAAAGTTGAGAGTAAGTATATATTTT 1680

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QY 1681 AATGAATTTGATCGAACATGTAAAGATGATATACCTAGCATTAATTTGTTTAAATCAATA 1740

Db 14680 AATGAATTTGATCGAACATGTAAAGATGATATACCTAGCATTAATTTGTTTAAATCAATA 14739

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1027.16 Seconds
(without alignments)
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Perfect score: 4459

Sequence: 1 tttcatttggagagacacg.....atagtgtaacataatctgc 4459

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
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- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4459	100.0	17458	6	ABQ82142 Acceptor
2	4406.6	98.8	17476	6	ABQ82141 Acceptor
3	4200	94.2	17681	6	ABQ82143 Acceptor
4	3182.2	71.4	18691	6	ABQ82130 Acceptor
C 5	1305	29.3	17458	6	ABQ82142 Acceptor
C 6	1277.8	28.7	17476	6	ABQ82141 Acceptor
7	1108.8	24.9	4470	3	AAC55521 Donor pla
8	1108.8	24.9	4470	3	AAC55521 Donor pla
9	1108.8	24.9	4892	8	ADA50329 Plasmid v
10	1108.8	24.9	4939	3	AAC55525 Donor pla
C 11	1108.8	24.9	5584	3	AAC55632 Donor pla
C 12	1108.8	24.9	5584	7	ABZ58766 Donor pla
13	1102.4	24.7	4428	7	ABZ58768 Destinati
14	1102.4	24.7	4627	7	ABZ58769 Destinati
15	1102.4	24.7	4627	7	ABZ58770 Destinati
C 16	1072.8	24.1	17681	6	ABQ82143 Acceptor
17	989.6	22.2	4165	3	AAC55524 Donor pla
18	947.8	21.3	4208	3	AAC55523 Donor pla
C 19	827	18.5	4204	3	AAC55522 Donor pla
C 20	823.8	18.5	5156	3	AAC55526 Donor pla
21	769	17.2	786	3	AAC38603 Flavaria
22	769	17.2	786	9	ADD44386 Flavaria
23	747	16.8	7050	2	AAQ40419 Sequence

ALIGNMENTS

RESULT 1

ABQ82142					
ID	ABQ82142	standard; DNA; 17458 BP.			
XX	AC	ABQ82142;			
XX	DT	11-DEC-2002 (first entry)			
XX	DE	Acceptor vector PHELLSGATE 11 nucleotide sequence SEQ ID NO:25.			
XX	KW	Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.			
XX	OS	Synthetic.			
XX	PN	WO200259294-A1.			
XX	PD	01-AUG-2002.			
XX	PF	24-JAN-2002; 2002WO-AU000073.			
XX	PR	26-JAN-2001; 2001US-0264067P.			
XX	PR	29-NOV-2001; 2001US-0333743P.			
XX		(CSIR) COMMONWEALTH SCI & IND RES ORG.			
XX		Wesley S, Waterhouse P, Helliwell C;			
XX		WPI; 2002-682669/73.			
XX		New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.			
XX		Claim 16; Page 83-93; 104pp; English.			
XX		The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and			

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25	728.8	16.3	7639	2	AAQ42159	AAQ42159 Plasmid p
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27	711.4	16.0	3435	8	ACC85049	ACC85049 Nucleotid
C 28	710.2	15.9	7599	4	AAF25320	AAF25320 Nucleotid
29	709.8	15.9	5399	2	AAQ25706	AAQ25706 PDE108. 3
30	709.8	15.9	6555	2	AAQ53874	AAQ53874 Plasmid p
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C 32	707	15.9	24596	1	AAN50182	AAN50182 Complete
C 33	703.8	15.8	24593	1	AAN50226	AAN50226 Sequence
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C 35	621.6	13.9	18691	6	ABQ82130	ABQ82130 Acceptor
C 36	597	13.4	1846	6	AAD44626	AAD44626 Gateway t
C 37	597	13.4	5148	6	AAD27063	AAD27063 Plasmid p
C 38	597	13.4	5957	3	AAC55467	AAC55467 Destinati
C 39	597	13.4	5957	3	AAC55464	AAC55464 Destinati
C 40	597	13.4	6025	3	AAC55469	AAC55469 Destinati
C 41	597	13.4	6264	3	AAC55507	AAC55507 Destinati
C 42	597	13.4	6354	3	AAC55491	AAC55491 Destinati
C 43	597	13.4	6422	3	AAC55483	AAC55483 Destinati
C 44	597	13.4	6464	3	AAC55454	AAC55454 Destinati
C 45	597	13.4	6526	3	AAC55471	AAC55471 Destinati

Db	4292	AGCATTTT	TTTGGTGTATGTGGCCCAATGAAGTCAGGTCAAACCTTGACAGTGACG	4351
Qy	4340	ACAAATCGT	TGGCGGGTCCAGGGCGAAATTTTGCACAAATGTCTGAGGCTCAGCAGGAC	4399
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Qy	4400	CTGCAGGCATGC		4411
Db	4412	CTGCAGGAATTC		4423

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 Job time : 11116.3 secs

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RESULT 13
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DEFINITION A23998
ACCESSION A23998
VERSION A23998.1 GI:833338
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 7049)
AUTHORS Nazarov,V., Botterman,J., Stanssens,P. and Sevcik,J.
TITLE A novel ribonuclease and its inhibitor
JOURNAL Patent: EP 0537399-A 3 21-APR-1993;
PLANT GENETIC SYSTEMS, N.V.
FEATURES
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Best Local Similarity 94.6%; Pred. No. 3.7e-98;
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DEFINITION Activation-tagging vector pSKI015, complete sequence.
ACCESSION AF187951
VERSION AF187951.1 GI:6537289
KEYWORDS
SOURCE Activation-tagging vector pSKI015
ORGANISM Activation-tagging vector pSKI015
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 10138)
AUTHORS Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharavi,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and
Chory,J.
TITLE Activation tagging in Arabidopsis
JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000)
MEDLINE 20223715
PubMed 10759496
REFERENCE 2 (bases 1 to 10138)
AUTHORS Kardailsky,I. and Weigel,D.
TITLE Direct Substitution
JOURNAL Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
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    AUTHORS Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
    Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
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    Construct design for efficient, effective and high-throughput gene
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    JOURNAL Plant J. 27 (6), 581-590 (2001)
    MEDLINE 21461301
    PUBMED 11576441
    REFERENCE 2 (bases 1 to 6063)
    AUTHORS Waterhouse,P.M.
    TITLE Direct Submission
    JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
    C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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SOURCE
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artificial sequences.
REFERENCE
1 (bases 1 to 5156)
AUTHORS
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITL
Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL
PAT 17-JUL-2003
COMMENT
OS Artificial Sequence
PN JP 2002537790-A/160
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
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DEFINITION
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ACCESSION
AJ311872
VERSION
AJ311872.1 GI:15982214
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AMP gene; ampicillin resistance protein; pdk gene; promoter.
SOURCE
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ORGANISM
artificial sequences; vectors.
REFERENCE
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AUTHORS
Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
Gleave,A.P., Green,A.G. and Waterhouse,P.M.
TITL
Construct design for efficient, effective and high-throughput gene
silencing in plants
JOURNAL
Plant J. 27 (6), 581-590 (2001)
MEDLINE
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PUBMED
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REFERENCE
2 (bases 1 to 5824)
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Waterhouse,P.M.
TITL
Direct Submission
JOURNAL
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry.

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LOCUS BD263378
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263378
VERSION BD263378.1 GI:33073146
KEYWORDS JP 2002537790-A/156.
SOURCE synthetic construct
ORGANISM Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
REFERENCE 1 (bases 1 to 4204)
AUTHORS Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
TITLE Compositions and methods for use in recombinational cloning of

nucleic acids
JOURNAL Patent: JP 2002537790-A 156 12-NOV-2002;
COMMENT INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/156
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
PI -JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC
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FH Key Location/Qualifiers
FT gene (127).. (269)
FT gene (486).. (1059)
FT gene (1228).. (2107)
FT gene (2140).. (2381)
FT gene (2629).. (3288)
FT gene (3408).. (3492)
FT gene (3630).. (3935).
FEATURES
source 1..4204
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 18.5%; Score 827; DB 6; Length 4204;
Best Local Similarity 100.0%; Pred. No. 1.2e-109; Indels 0; Gaps 0;
Matches 827; Conservative 0; Mismatches 0;
QY 311 TATTAAATCATAAAAAGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAA 370
Db 4204 TATTAAATCATAAAAAGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAA 4145
QY 371 TAAAAACATCTACCTATTTCATATACGTAGTGTCTATAGTCTCTGAAATCATCTGATCAA 430
Db 4144 TAAAAACATCTACCTATTTCATATACGTAGTGTCTATAGTCTCTGAAATCATCTGATCAA 4085
QY 431 GAACAAATTTCAACCTCTTACTTTCTTCTTACAAGTCGTTTCGCTTCTCATCTGATTTT 490
Db 4084 GAACAAATTTCAACCTCTTACTTTCTTCTTACAAGTCGTTTCGCTTCTCATCTGATTTT 4025
QY 491 CAGCCTCTATACTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGATCGACCTGCA 550
Db 4024 CAGCCTCTATACTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGATCGACCTGCA 3965
QY 551 GACTGGCTGTATTAAGGAGCCTGACATTTATATATCCCGACAGACATCAGGTTAATGGC 610
Db 3964 GACTGGCTGTATTAAGGAGCCTGACATTTATATATCCCGACAGACATCAGGTTAATGGC 3905
QY 611 TTTTGTATGTCTATTTTCGCGTGGCTGAGATCAGCACTTCTCCCGATAAACGAGACC 670
Db 3904 TTTTGTATGTCTATTTTCGCGTGGCTGAGATCAGCACTTCTTCCCGATAAACGAGACC 3845
QY 671 GGCACTGTGGCCATATCGGTGTCTATCATGCGCCAGCTTTTCATCCCGATATGACCAACC 730
Db 3844 GGCACTGTGGCCATATCGGTGTCTATCATGCGCCAGCTTTTCATCCCGATATGACCAACC 3785
QY 731 GGGTAAAGTTTCAAGGAGACTTTTATCTGACAGCAGACGCTGCACTGGCCAGGGGATCACC 790
Db 3784 GGGTAAAGTTTCAAGGAGACTTTTATCTGACAGCAGACGCTGCACTGGCCAGGGGATCACC 3725
QY 791 ATCCGTCCCGCGGCGTCTCAATATATCACTCTGTATATCAACAAACAGACGATACGG 850

PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N5/00

CC pDONR204

CC n is any nucleotide

FT Key Location/Qualifiers

FT misc feature (1326).. (1326).

Location/Qualifiers

1..4165

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

FEATURES

source

ORIGIN

Query Match 22.2%; Score 989.6; DB 6; Length 4165;
Best Local Similarity 98.8%; Pred. No. 5e-133; 9; Indels 3; Gaps 1;
Matches 1008; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 2184 GCGCACTTTGTACAAAGAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 2243
QY 2326 AAATTAGATTTGCATAAAGACAGCTACATAACTGTAAACACACATATCCAGTC 2385
DB 2244 AAATTAGATTTGCATAAAGACAGCTACATAACTGTAAACACACATATCCAGTC 2303
QY 2386 ACTATGAATCAACTACTTAGATGGTATTAGTCACCTGTAGTCGACTTAAGTTGGCGAGCATC 2445
DB 2304 ACTATGAATCAACTACTTAGATGGTATTAGTCGACTTAAGTTGGCGAGCATC 2363
QY 2446 ACCGACGACCTTTGGCGGAGTAATAATACCTGTGACGGAAGATCACTTCGCGAGATAAAT 2505
DB 2364 ACCGACGACCTTTGGCGGAGTAATAATACCTGTGACGGAAGATCACTTCGCGAGATAAAT 2423
QY 2506 AAATCTGTGTGCTCTGTATACCGGAGCCCTGGCGCAACTTTTGGCGAAATGAGA 2565
DB 2424 AAATCTGTGTGCTCTGTATACCGGAGCCCTGGCGCAACTTTTGGCGAAATGAGA 2483
QY 2566 CGTTGATCGG---ATTTCACAACTCTTATACCTTTTCTTACAAAGTCGTCGGCTTCATC 2622
DB 2484 CGTTGATCGGCACTTTCACAACTCTTATACCTTTTCTTACAAAGTCGTCGGCTTCATC 2543
QY 2623 TGGATTTTCAGGCTCTATACCTTAAACGTAAGTTTCTGTAAATTTCTACTGTATC 2682
DB 2544 TGGATTTTCAGGCTCTATACCTTAAACGTAAGTTTCTGTAAATTTCTACTGTATC 2603
QY 2683 GACCTGCAGACTGGCTGTGTATAAGGAGCGCTGACATTTATATCCCGAGACATCAGGT 2742
DB 2604 GACCTGCAGACTGGCTGTGTATAAGGAGCGCTGACATTTATATCCCGAGACATCAGGT 2663
QY 2743 TAATGGCGTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAA 2802
DB 2664 TAATGGCGTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAA 2723
QY 2803 CGGAGACCGGACACCTGCGGCATATCGGTGTATATGCGGAGCTTTTCATCCCGATAT 2862
DB 2724 CGGAGACCGGACACCTGCGGCATATCGGTGTATATGCGGAGCTTTTCATCCCGATAT 2783
QY 2863 GCACCAACCGGTAAGTTTCACGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGG 2922
DB 2784 GCACCAACCGGTAAGTTTCACGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGG 2843
QY 2923 GGTACACCATCGTCCGCGGGGTGTCAATATATCATCTGTATCATCCACAAACAGAC 2982
DB 2844 GGTACACCATCGTCCGCGGGGTGTCAATATATCATCTGTATCATCCACAAACAGAC 2903
QY 2983 GATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTTCACTTCAACAGTCCCTGTTC 3042
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QY 3043 TCGTCAGCAAAAGAGCGGTTTCATTTCAATAAAGCGGGCGACCTTCAGCCATCCCTTCCTGA 3102
DB 2964 TCGTCAGCAAAAGAGCGGTTTCATTTCAATAAAGCGGGCGACCTTCAGCCATCCCTTCCTGA 3023

QY 3103 TTTTCCGCTTTCCAGGCTTCCGACGAGACGAGCGGCTTCATTCTGCATGTTGTGCTT 3162
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QY 3163 ACCAGACCGGAGATATTGACATCATATATGCTTGTAGCAACTGATAGCTGTCGCTGCAA 3222
DB 3084 ACCAGACCGGAGATATTGACATCATATATGCTTGTAGCAACTGATAGCTGTCGCTGCAA 3143
QY 3223 CTGTCACTGTATAGCTGCTTCTATAGCACACCTCTTTTGGACATATCTCTGTTCTTCAT 3282
DB 3144 CTGTCACTGTATAGCTGCTTCTATAGCACACCTCTTTTGGACATATCTCTGTTCTTCAT 3203

RESULT 6

BD263379

LOCUS

DEFINITION

BD263379

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

INVITROGEN CORP

OS Artificial Sequence

PN JP 2002537790-A/157

PD 12-NOV-2002

PF 02-MAR-2000 JP 2000602252

PR 02-MAR-1999 US 60/122389; 23-MAR-1999 US 60/126049 PR

PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N5/00

CC pDONR203

CC inactivated ccdA

CC Cmr

CC attP2

CC ori

CC KmR

CC attP1

CC ccdB

PH Key

FT gene

FT gene

FT gene

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FT gene

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RESULT 4
BD263402/c
LOCUS
DEFINITION
  BD263402 5584 bp DNA linear PAT 17-JUL-2003
  Compositions and methods for use in recombinational cloning of
  nucleic acids.
ACCESSION
  BD263402.1 GI:33073170
VERSION
  JP 2002537790-A/180.
KEYWORDS
  synthetic construct
SOURCE
  ORGANISM
    artificial sequences.
REFERENCE
  1 (bases 1 to 5584)
  Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
  Compositions and methods for use in recombinational cloning of
  nucleic acids
  Patent: JP 2002537790-A 180 12-NOV-2002;
  INVITROGEN CORP
COMMENT
  OS Artificial Sequence
  PN JP 2002537790-A/180
  PD 12-NOV-2002
  PF 02-MAR-2000 JP 2000602252
  PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
  28-MAY-1999 US 60/136744
  PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
  C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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  FH Key
  FT source
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FEATURES
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ORIGIN
  Query Match 24.9%; Score 1108.8; DB 6; Length 5584;
  Best Local Similarity 99.8%; Pred. No. 3.3e-150;
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Db 5423 AAATTAGATTTTGCATAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 5364

QY 146 ACTATCAATCAACTACTAGATGGTATAGTGACCTGTAGTCACCGAGAGCCTTCCAA 205
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QY 206 TGTCTTCGGGTGATCGTCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAA 265
Db 5303 TGTCTTCGGGTGATCGTCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAA 5244

QY 266 ACGGAATCGTGTATCGAGCTACTCGCTATTTGCTTCAATGCGGTATTAATCATATAA 325
Db 5243 ACGGAATCGTGTATCGAGCTACTCGCTATTTGCTTCAATGCGGTATTAATCATATAA 5184

QY 326 AGAAATAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAATAAAACATCTACCT 385
Db 5183 AGAAATAAGAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAATAAAACATCTACCT 5124

QY 386 ATTATATATAGCTAGTGTATATAGTCTGAAATCATCTGCATCAAGAAACAATTTTCAAC 445
Db 5123 ATTATATAGCTAGTGTATATAGTCTGAAATCATCTGCATCAAGAAACAATTTTCAAC 5064

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Db 5003 CTAACCGTGATAAAAGCTTTTCTGTAAATTTCTACTGTATGCACTGCAGAGCTGGCTGTGTATA 4944

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QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAAAGGAGACCGGCACACTGGCCATA 685
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QY 686 TCGGTGGTCATCATCGCCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG 745
Db 4823 TCGGTGGTCATCATCGCCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG 4764

QY 746 GAGACTTTTATCTGACAGCAGAGCTGCTGCTGGCCAGGGGATCACCATCGTCGCCGGGC 805
Db 4763 GAGACTTTTATCTGACAGCAGAGCTGCTGCTGGCCAGGGGATCACCATCGTCGCCGGGC 4704

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Db 4703 GTGTCAATATATATCTCTGTACATCCAAACAGACAGATTAACGGCTCTCTCTTTTATAG 4644

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QY 1106 ATAGCACACCTCTTTTGGACATACCTTCGGGTA 1137
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RESULT 5
BD263380
LOCUS
DEFINITION
  BD263380 4165 bp DNA linear PAT 17-JUL-2003
  Compositions and methods for use in recombinational cloning of
  nucleic acids.
ACCESSION
  BD263380
VERSION
  JP 2002537790-A/158.
KEYWORDS
  synthetic construct
SOURCE
  ORGANISM
    artificial sequences.
REFERENCE
  1 (bases 1 to 4165)
  Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
  Compositions and methods for use in recombinational cloning of
  nucleic acids
  Patent: JP 2002537790-A 158 12-NOV-2002;
  INVITROGEN CORP
COMMENT
  OS Artificial Sequence
  PN JP 2002537790-A/158
  PD 12-NOV-2002
  PF 02-MAR-2000 JP 2000602252
  PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
  28-MAY-1999 US 60/136744

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686 TCAGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG 745
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762 TCAGTGGTCAATCATGCGCCAGCTTTTCATCCCGATATGACACACCGGGTAAAGTTCAAGG 821
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RESULT 3

BD263381 4939 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions and methods for use in recombinational cloning of
DEFINITION nucleic acids.
ACCESSION BD263381
VERSION BD263381.1 GI:33073149
KEYWORDS JP 2002537790-A/159.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 4939)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 159 12-NOV-2002;

INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
FI JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
C0, C12N5/00
CC pDONR205
FH Key Location/Qualifiers
FT source 1..4939
FT Location/Qualifiers
FT /organism='Artificial Sequence'.
1..4939
/organism='synthetic construct'
/mol_type='genomic DNA'
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FEATURES
source

Query Match 24.9%; Score 1108.8; DB 6; Length 4939;
Best Local Similarity 99.8%; Pred. No. 3 4e-150;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 3696 AAATTAGATTTTGTACAAAAAGCTGAACGAGAAACGTTAAATCATATATATATATATAT 3755
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Db 3996 ATTATATACGCTAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4055
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Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
JOURNAL MEDLINE 21461301
PUBMED 11576441
REFERENCE 2 (bases 1 to 18691)
AUTHORS Waterhouse, P.M.
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
JOURNAL Location/Qualifiers
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Matches 4406; Conservative 0; Mismatches 28; Indels 1137; Gaps 7;
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 11095.3 Seconds
(without alignments)
17418.703 Million cell updates/sec

Title: US-10-055-001B-25_COPY_13000_17458

Perfect score: 4459

Sequence: 1 tttcatttgaggagacacg.....ataggtcacctaaatctgc 4459

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb.om.*

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6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

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13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

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41: em.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1108.8	24.9	4470	6	BD263377
3	1108.8	24.9	4939	6	BD263381
c	1108.8	24.9	5584	6	BD263402
5	989.6	22.2	4165	6	BD263380
6	947.8	21.3	4208	6	BD263379
c	827	18.5	4204	6	BD263378
c	823.8	18.5	5156	6	BD263382
9	779	17.5	5824	12	CVE311872
10	779	17.5	6063	12	CVE311873
11	769.4	17.3	14645	8	FTPDKG
12	769	17.2	786	6	BD194641
13	747	16.8	7049	6	A23998
c	735	16.5	10138	12	AF187951
15	728.8	16.3	7566	6	A24783
16	728.8	16.3	7566	6	AR074388
17	728.8	16.3	7639	6	A24782
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19	722.8	16.2	11405	12	AY310901
20	719.4	16.1	22574	12	CVE18556
c	713	16.0	4947	6	BD217610
22	710.2	15.9	7599	6	AX063413
23	709.8	15.9	5399	6	AI8050
24	709.8	15.9	5399	6	AR095106
25	709.8	15.9	5399	6	AR098312
26	709.8	15.9	5399	6	I49885
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28	709.8	15.9	5399	6	AX012337
c	709.8	15.9	6428	12	SYN1PSPSS
30	709.8	15.9	6555	6	AR007512
31	709.8	15.9	6555	6	AR084078
32	709.8	15.9	14194	6	AX052541
33	708.8	15.9	10907	12	AY310333
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40	697.2	15.6	6875	12	AF433042
41	697.2	15.6	6928	12	AF433043
c	697.2	15.6	27608	12	AF184978
43	697.2	15.6	28708	12	AY218787
44	695.8	15.6	3669	12	ATU41408
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ALIGNMENTS

RESULT 1
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LOCUS CVE311874 18691 bp DNA circular SYN 09-JUL-2002
DEFINITION Cloning vector pHELLSGATE.
ACCESSION AJ311874
VERSION AJ311874.1 GI:15982218
KEYWORDS kanamycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.
SOURCE Cloning vector pHELLSGATE
ORGANISM Cloning vector pHELLSGATE
REFERENCE 1
AUTHORS Wesley V.S., Helliwell C., Smith N.A., Wang M.B., Rouse D., Liu Q., Gooding P.S., Singh S.R., Abbott D., Stoutjesdijk A., Robinson S.P.,

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 12100.6 Seconds
(without alignments)
17418.703 Million cell updates/sec

Title: US-10-055-001B-23_COPY_13000_17862

Perfect score: 4863

Sequence: 1 ttctattgttgagaggacagc.....atagtgccacataaatctgc 4863

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl:

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	1046.2	21.5	4208	6	BD263379	BD263379 Compositi	
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10	824.2	16.9	6063	12	CVE311873	AJ311873 Cloning v	
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12	780	16.0	786	6	BD194641	BD194641 Method an	
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c	41	697.2	14.3	6875	12	AF433042	AF433042 Cloning v
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c	43	697.2	14.3	27608	12	AF184978	AF184978 Binary ve
44	697.2	14.3	28708	12	AY218787	AY218787 Cloning v	
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ALIGNMENTS

RESULT 1
CVE311874
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

CVE311874
Cloning vector pHELLSGATE.
AJ311874
AJ311874.1 GI:15982218
kanamycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; Spec Gene; spectinomycin resistance protein;
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Cloning vector pHELLSGATE
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Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,

circular SYN 09-JUL-2002

Gleave, A.P., Green, A.G. and Waterhouse, P.M.
 Construct design for efficient, effective and high-throughput gene
 silencing in plants
 Plant J. 27 (6), 581-590 (2001)
 JOURNAL MEDLINE 21461301
 PUBLISHED 11576441
 REFERENCE 2 (bases 1 to 18691)
 Waterhouse, P.M.
 Direct Submission
 TITLE Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
 C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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  Compositions and methods for use in recombinational cloning of
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VERSION
  BD263377.1 GI:33073145
KEYWORDS
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REFERENCE
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  AUTHORS
    Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
  TITLE
    Compositions and methods for use in recombinational cloning of
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  JOURNAL
    Patent: JP 2002537790-A 155 12-NOV-2002;
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PD 12-NOV-2002
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  28-MAY-1999 US 60/136744
PI JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC
  C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N15/10, C12N15/PC
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RESULT 3
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LOCUS BD263381 4939 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263381
VERSION BD263381.1 GI:33073149
KEYWORDS JP 2002537790-A/159.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 4939)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Chao,D.
AUTHORS Compositions and methods for use in recombinational cloning of
TITLE nucleic acids
JOURNAL Patent: JP 2002537790-A 159 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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Best Local Similarity 99.9%; Pred. No. 8.8e-167;
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RESULT 4
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DEFINITION
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JP 2002537790-A/180.
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 5584)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
AUTHORS
TITLE
Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL
Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
OS
Artificial Sequence
PN JP 2002537790-A/180
PD 12-NOV-2002
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/PC
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FT source
FT Location/Qualifiers
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FEATURES
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QY 145 AACGAGAAACGTAAAAATGATATATAATCAATATATTAATTAAGTTTTCATATAAAAC 204
DB 5460 AACGAGAAACGTAAAAATGATATATAATCAATATATTAATTAAGTTTTCATATAAAAC 5401
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Db	2583	TTCTGTAAATTTCTACTGTATCGACCTCGACACTGGCTGTCTATAAAGGAGGACCTGACATTT	2642
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Db	2703	CAGCCACTTCTTCCCGGATTAACCGAGACCCGGGCACATGGCCCATATCCGTTGGTCTCATGTC	2762
QY	3149	GCAGAGTTTCATCCCGGATATGACACACCGGGTAAAGTTTCACGGGAGACTTTATCTGACA	3208
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LOCUS			
DEFINITION	Compositions and methods for use in recombinational cloning of nucleic acids.		
ACCESSION	BD263379		
VERSION	BD263379.1	GI:33073147	
KEYWORDS	JP 2002537790-A/157.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 4208)		
AUTHORS	Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.		
TITLE	Compositions and methods for use in recombinational cloning of nucleic acids		
JOURNAL	Patent: JP 2002537790-A 157 12-NOV-2002;		
INVENTOR	INVIROGEN CORP		
COMMENT	OS Artificial Sequence		
	PN JP 2002537790-A/157		


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PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
00, C12N5/00
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DEFINITION AJ311874
VERSION AJ311874.1 GI:15982218
KEYWORDS kanamycin resistance protein; neomycin phosphotransferase II; nptII
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SOURCE Cloning vector pHELLSGATE
ORGANISM Cloning vector pHELLSGATE
          artificial sequences; vectors.
REFERENCE 1
AUTHORS Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
          Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,
          Gleave, A.P., Green, A.G. and Waterhouse, P.M.
          Construct design for efficient, effective and high-throughput gene
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          Plant J. 27 (6), 581-590 (2001)
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          WATERHOUSE, P.M.
          DIRECT SUBMISSION
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Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1127	GGAGATATGACATCATATATGCTTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACT	1186
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QY	1187	GTAATACGCTGCTTATAGCACACCTCTTTTGTGACATCTTCGGGTA	1233
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RESULT	9		
CVE311872			
LOCUS		5824 bp	DNA
DEFINITION			circular SYN 09-JUL-2002
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			

JOURNAL Plant J. 27 (6), 581-590 (2001)

MEDLINE 21461301

PUBMED 11576441

REFERENCE 2 (bases 1 to 5824)

AUTHORS Waterhouse, P.M.

TITLE Direct Submission

JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES

source

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/db_xref="taxon:83333"

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/note="octopine esynthase (ocs) terminator"

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Best Local Similarity 96.7%; Pred. No. 7e-111.

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QY 1660 CTTGTGAAGGAAATAATTAATTTCTTTTTCCTTTTAGTATAAATAGTTAAGTGATGTT 1719

Db 4232 ATTGCTAAGGAAATAATTAATTTCTTTTTCCTTTTAGTATAAATAGTTAAGTGATGTT 4291

RESULT 9				
CVE311872		DNA	5824 bp	circular SYN 09-JUL-2002
LOCUS				
DEFINITION				
ACCESSION	AJ311872			
VERSION	AJ311872.1			
KEYWORDS	AMP gene; ampicillin resistance protein; pdk gene; promoter.			
SOURCE	Cloning vector PHANNIBAL			
ORGANISM	Cloning vector PHANNIBAL			
	artificial sequences; vectors.			
REFERENCE	1			
AUTHORS	Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q., Gooding,ps., Singh,S.R., Abbott.D., Scoutjesdijk,A., Robinson,S.P., Glave,A.P., Green,A.G. and Waterhouse,P.M.			
TITLE	Construct design for efficient, effective and high-throughput gene silencing in plants			

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QY 1900 ATATACAGCATTAATATTTGTTTAAATCAATATAGTAATCTAGCTGGTTGATGAAT 1959
Db 4711 ATATACAGCATTAATATTTGTTTAAATCAATATAGTAATCTAGCTGGTTGATGAAT 4770
QY 1960 AATATCAATGATAAATATCTAGTAATAAATAGTAATAAATTAATTAATTAATTAATTT 2019
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QY 2440 TGGGTTTCAATCATAGCTTGGATCTCTAGAGAGCTGC 2480
Db 5251 TGGGTTTCAATCATAGCTTGGATCTCTAGAGAGCTGC 5291

RESULT 11
LOCUS BD263382/6
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263382
VERSION BD263382.1 GI:33073150
KEYWORDS JP 2002537790-A/160.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 5156)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL Patent: JP 2002537790-A 160 12-NOV-2002;
COMMENT INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/160
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/136744

PI JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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CC May be any nucleotide
CC May be any nucleotide
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FT misc feature (3080) . (3080) .
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Best Local Similarity 99.8%; Pred. No. 8.2e-111;
Matches 825; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 5156 TATTAAATCATAAAGAAATTAAGAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAA 5097
QY 467 TAAAAACATCTACCTATTATCATATAGCTAGTGTCTAGTAAATCATCTGCATCA 526
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QY 647 GACTGCTGTGTATAAGGAGGCTGATATTAATTTCCCGAAGCATAGGTTAATGGCG 706
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LOCUS	BD194641	Method and means of obtaining improved phenotype.	
DEFINITION	BD194641		
ACCESSION	BD194641.1	GI:330043386	
VERSION	JP 2002511258-A/7.		
KEYWORDS	synthetic construct		
SOURCE	artificial construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 786)		
AUTHORS	Waterhouse,P.M., Wang,M.B. and Graham,M.W.		
TITLE	Method and means of obtaining improved phenotype		
JOURNAL	Patent: JP 2002511258-A 7 16-APR-2002;		
COMMENT	COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION		
	OS Artificial Sequence		
	PN JP 2002511258-A/7		
	PD 16-APR-2002		
	PF 07-APR-1999 JP 2000543598		
	PR 08-APR-1998 US 09/056767,03-AUG-1998 US 09/127735 PI		
	PETER MICHAEL WATERHOUSE,MIN BO WANG,MICHAEL WAIN GRAHAM PC		
	C12N15/09,A01H5/00,C12N15/00,C12N5/00 CC Description of		
	Artificial Sequence: intron 2 of the Flaveria CC		
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Dd	182	AGAAGATAAAGTTGAGAGTAAGTATATTTTAAATGCATTCGAAATCGAACATCTAGA 241	
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Dd	242	TGATATACTAGCATTAATATTTCTTTTAAATCAATAATAGTAATTCAGCTGGTTTATGAA 301	
Qy	1958	TTAAATATCAATGATAAAATCTATAGTAAAAATAGAAATAAATAAATAAATAATTT 2017	
Dd	302	TTAAATATCAATGATAAAATCTATAGTAAAAATAGAAATAAATAAATAAATAAATAATTT 361	
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RESULT 12	BD194641	786 bp DNA linear	PAT 17-JUL-2003
LOCUS	BD194641	Method and means of obtaining improved phenotype.	
DEFINITION	BD194641		
ACCESSION	BD194641.1	GI:330043386	
VERSION	JP 2002511258-A/7.		
KEYWORDS	synthetic construct		
SOURCE	artificial construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 786)		
AUTHORS	Waterhouse,P.M., Wang,M.B. and Graham,M.W.		
TITLE	Method and means of obtaining improved phenotype		
JOURNAL	Patent: JP 2002511258-A 7 16-APR-2002;		
COMMENT	COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION		
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	PF 07-APR-1999 JP 2000543598		
	PR 08-APR-1998 US 09/056767,03-AUG-1998 US 09/127735 PI		
	PETER MICHAEL WATERHOUSE,MIN BO WANG,MICHAEL WAIN GRAHAM PC		
	C12N15/09,A01H5/00,C12N15/00,C12N5/00 CC Description of		
	Artificial Sequence: intron 2 of the Flaveria CC		
	trinervia		
	CC purvate orthophosphate dikinase		
	FH Key Location/Qualifiers		
	FT source 1..786		
FEATURES	Location/Qualifiers		
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	Query Match 16.0%; Score 780; DB 6; Length 786;		
	Best Local Similarity 100.0%; Pred. No. 2.7e-104;		
	Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1658	AGCTTGTGTAAGGAAATAAATTATTTCTTTTTCTTTTAGTATAAAAATAGTTAAGTATG 1717	
Dd	2	AGCTTGTGTAAGGAAATAAATTATTTCTTTTCTTTTAGTATAAAAATAGTTAAGTATG 61	
Qy	1718	TTAATTAGTATGATTATAAATAATAGTTGTTTATAATTCGAAAAATAAATTATAAATA 1777	
Dd	62	TTAATTAGTATGATTATAAATAATAGTTGTTTATAATTCGAAAAATAAATTATAAATA 121	
Qy	1778	TATTGTTTATCAAAACAACATAGTAATGTAAAAAATAATGACAAGTGATGTGTAAGACGA 1837	
Dd	122	TATTGTTTATCAAAACAACATAGTAATGTAAAAAATAATGACAAGTGATGTGTAAGACGA 181	
Qy	1838	AGAAGATAAAGTTGAGAGTAAGTATATTTTAAATGCATTCGAAATCGAACATCTAGA 1897	
Dd	182	AGAAGATAAAGTTGAGAGTAAGTATATTTTAAATGCATTCGAAATCGAACATCTAGA 241	
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LOCUS          Activation-tagging vector pSKI015, complete sequence.
DEFINITION
ACCESSION     AF187951
VERSION       AF187951.1 GI:6537289
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10138)
Weigel, D., Ahn, J.H., Blazquez, M.A., Borevitz, J.O.,
Christensen, S.K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharuk, E.J., Neff, M.M., Nguyen, J.T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R.A., Harrison, M.J., Lamb, C.J., Yanofsky, M.F. and
Chory, J.
TITLE
Activation tagging in Arabidopsis
JOURNAL
Plant Physiol. 122 (4), 1003-1013 (2000)
MEDLINE
20223715
PUBMED
10759496
REFERENCE
2 (bases 1 to 10138)
Kardailsky, I. and Weigel, D.
AUTHORS
Direct Submission
TITLE
Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
JOURNAL
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
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1. 10138
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/db_xref="taxon:109189"
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36. .2204
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2205. 2662
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2663. 2829
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2830. 2849
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2894. 4178
/note="cauliflower mosaic virus 35S gene promoter enhancer
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7690. 7713
/note="T-DNA left border"
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/note="3' end"
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/note="5' end and promoter"

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ORIGIN

Query Match 15.1%; Score 735; DB 12; Length 10138;
 Best Local Similarity 100.0%; Pred. No. 6.7e-98;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Job time : 12136.6 secs

OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

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8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4112.4	84.6	17476	6	ABQ82141	Abq82141 Acceptor
2	4077.2	83.8	17681	6	ABQ82143	Abq82143 Acceptor
3	4042	83.1	17458	6	ABQ82142	Abq82142 Acceptor
4	3985.4	82.0	18691	6	ABQ82130	Abq82130 Acceptor
5	1207.4	24.8	4470	3	AAC55521	Aac55521 Donor pla
6	1207.4	24.8	4470	7	ABZ58767	Abz58767 Destinati
7	1207.4	24.8	4892	8	ADA50329	Ada50329 Plasmid v
8	1207.4	24.8	4939	3	AAC55525	Aac55525 Donor pla
9	1207.4	24.8	5584	3	AAC55632	Aac55632 Donor pla
10	1207.4	24.8	5584	7	ABZ58766	Abz58766 Donor pla
11	1201	24.7	4428	7	ABZ58768	Abz58768 Destinati
12	1194.6	24.6	4627	7	ABZ58769	Abz58769 Destinati
13	1194.6	24.6	4627	7	ABZ58770	Abz58770 Destinati
14	1174.2	24.1	17681	6	ABQ82143	Abq82143 Acceptor
15	1089.4	22.4	17476	6	ABQ82141	Abq82141 Acceptor
16	1079.4	22.2	17458	6	ABQ82142	Abq82142 Acceptor
17	1068.2	22.0	4165	3	AAC55524	Aac55524 Donor pla
18	1046.2	21.5	4208	3	AAC55523	Aac55523 Donor pla
19	842	17.3	18691	6	ABQ82130	Abq82130 Acceptor
20	827	17.0	4204	3	AAC55522	Aac55522 Donor pla
21	823.8	16.9	5156	3	AAC55526	Aac55526 Donor pla
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28	711.8	14.6	3435	8	ACC85049	Nucleotid
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33	707	14.5	24596	1	AAAN50182	Complete
34	703.8	14.5	24593	1	AAAN50226	Sequence
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37	597	12.3	5148	6	ABD27063	Plasmid p
38	597	12.3	5957	3	AAC55467	Destinati
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ALIGNMENTS

RESULT 1
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ID ABQ82141 standard; DNA; 17476 BP.
XX
AC ABQ82141;
XX
DT 11-DEC-2002 (first entry)
XX
DE DE
XX
DE DE
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Wesley S, Waterhouse P, Helliwell C;
XX
DR WPI; 2002-682669/73.
XX
PT New vectors comprising operably linked DNA fragments having an origin of
FT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
XX stranded RNA.
XX
PS Claim 15; Page 74-83; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence	17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
Query Match	84.6%; Score 4112.4; DB 6; Length 17476;
Best Local Similarity	93.8%; Pred. No. 0;
Matches 4446; Conservative	0; Mismatches 6; Indels 290; Gaps 4;
QY	122 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATT 181
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Db	13085 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAACATATCCAGTC 13144
QY	242 ACTATGAATCAACTACTTAGATGGTATTAGTAGACCTGTAGTCGACCGACAGCCTTCAAA 301
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QY	482 ATTCAATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCATCAAGAACAAATTCACAAC 541
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QY	602 CTAACCGTGATAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGATA 661
Db	13505 CTAACCGTGATAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTGATA 13564
QY	662 AGGAGCGCTGACATTTATATCCCGAAGACATCAGGTTAATGGCGTTTTTGATGTCATTT 721
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3190 CGGGAGACTTTATCTGACAGAGAGCTGCACATCGGCGGAGGATCACCATCGTCGCCG 3249
16105 CGGGAGACTTTATCTGACAGAGAGCTGCACATCGGCGGAGGATCACCATCGTCGCCG 16164
3250 GCGGTGTCATAATATCACTCTGTACATCCAAACAGACGATAGCGGCTCTCTCTTTTA 3309
16165 GCGGTGTCATAATATCACTCTGTACATCCAAACAGACGATAGCGGCTCTCTCTTTTA 16224
3310 TAGGTGTAAACCTTAAAGTCACTTACAGTCCCTGTTCTGTCAGAAAAGAGCGGTT 3369
16225 TAGGTGTAAACCTTAAAGTCACTTACAGTCCCTGTTCTGTCAGAAAAGAGCGGTT 16284
3370 CATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTC 3429
16285 CATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTC 16344
3430 GGCACGACAGACGGGCTTCACTTCGATGTTGCTTACAGACCGGAGATATGAC 3489
16345 GGCACGACAGACGGGCTTCACTTCGATGTTGCTTACAGACCGGAGATATGAC 16404
3490 ATCATATGCTTGGAGCACTGATAGTGTGCTGCTCAACTGCTCACTGCTAATACGCTCG 3549
16405 ATCATATGCTTGGAGCACTGATAGTGTGCTGCTCAACTGCTCACTGCTAATACGCTCG 16464
3550 TTCTATGACACACCTCTTTTGAATATCTCTGTTCTTGTATGACAGATGATTTTCAGGACTA 3609
16465 TTCTATGACACACCTCTTTTGAATATCTCTGTTCTTGTATGACAGATGATTTTCAGGACTA 16524
3610 TGACACTAGGATATGATAGTATGATGTTTTTATTTTGTGTCACAAAAAGAGGCTCG 3669
16525 TGACACTAGGATATGATAGTATGATGTTTTTATTTTGTGTCACAAAAAGAGGCTCG 16584
3670 CACCTCTTTTCTATTTCTTTTATTTATGATTTTATGAGCAATGAGCAATAGCGAGTAG 3729
16585 CACCTCTTTTCTATTTCTTTTATTTATGATTTTATGAGCAATGAGCAATAGCGAGTAG 16644
3730 GCTGGATACGACGATTCGGTTTGAGAGAAACATTTGGAAGGCTGTCCGGTCCGATAGTTG 3789

16645 GCTGGATACGACGATTCGGTTTGAGAGAAACATTTGGAAGGCTGTCCGTCGACTAAGTTG 16704
3790 GCAGCATCACCGGAAGAACATTTTGGAAAGGCTGTCCGTCGACTACAGGTCACATAACCAT 3849
16705 GCAGCATCACCGGAAGAACATTTTGGAAAGGCTGTCCGTCGACTACAGGTCACATAACCAT 16764
3850 CTAAGTAGTTGATTCATCAGTAGTACCTGGATATGTTGTTTACAGTATATAGTAGTCTGTT 3909
16765 CTAAGTAGTTGATTCATCAGTAGTACCTGGATATGTTGTTTACAGTATATAGTAGTCTGTT 16824
3910 TTTTATGCAAAATCTAAATTTAAATATATGATATATATATATATATATATATATATATATAT 3969
16825 TTTTATGCAAAATCTAAATTTAAATATATGATATATATATATATATATATATATATATATAT 16884
3970 CTTTATTTGTACAAAGTTGGCAATTAATAAAAGACATTCCTCATCAATTTGTTTGCAACGAC 4029
16885 CTTTATTTGTACAAACTTG----- 16902
4030 AGGTCATCATCAGTCAAAATAAAATCAATATTCTGGGCCCCGAGATCCATGCTAGCTCAG 4089
16903 -----TCTAG 16907
4090 AGTCTCTGCTTTAATAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTC 4149
16908 AGTCTCTGCTTTAATAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTC 16967
4150 TGTGTGTCACGCTGTGTAATAAACCTGAGCATGTGTAGTCTCAGATCCTTACCGCGGTTTCG 4209
16968 TGTGTGTCACGCTGTGTAATAAACCTGAGCATGTGTAGTCTCAGATCCTTACCGCGGTTTCG 17027
4210 GTTCATTTCTAATGAATATATACCGGTTACTATCGTATTTTATGATATATTTCTCGGT 4269
17028 GTTCATTTCTAATGAATATATACCGGTTACTATCGTATTTTATGATATATTTCTCGGT 17087
4270 TCAATTTACTGATTTGATCCCTACTACTATATATGATACAAATATAAAATGAAAAACAATATAT 4329
17088 TCAATTTACTGATTTGATCCCTACTACTATATATGATACAAATATAAAATGAAAAACAATATAT 17147
4330 TGTGCTGAATAGTTTATAGCGACATCTATGATAGAGCGGCACAAATAACAAACAATTCGG 4389
17148 TGTGCTGAATAGTTTATAGCGACATCTATGATAGAGCGGCACAAATAACAAACAATTCGG 17207
4390 TTTTATTTATTAACAATCCAAATTTTAAABAAAGCGGAGAACCGGTCACAACTTAAAGACT 4449
17208 TTTTATTTATTAACAATCCAAATTTTAAABAAAGCGGAGAACCGGTCACAACTTAAAGACT 17267
4450 GATTACATAAATCTTTATTTCAAAATTTCAAAAGCGCCCGAGGGCTAGTATCTACGACACACC 4509
17268 GATTACATAAATCTTTATTTCAAAATTTCAAAAGCGCCCGAGGGCTAGTATCTACGACACACC 17327
4510 GAGCGGGAACATAATAGGTTCACTGAAAGGAACTCCGGTTCCCGGCGGCGCGCATGGG 4569
17328 GAGCGGGAACATAATAGGTTCACTGAAAGGAACTCCGGTTCCCGGCGGCGCGCATGGG 17387
4570 TGAGATTCTCTTGAAGTTTCAGATTGCGCGTCTACCGAAAGTTACGGGCGACCAATTC 4629
17388 TGAGATTCTCTTGAAGTTTCAGATTGCGCGTCTACCGAAAGTTACGGGCGACCAATTC 17447
4630 AACCCGGTCCAGACCGGCGCGGCTTAAACCGACTTGTCTGCCCCGAGAAATATGACAGACT 4689
17448 AACCCGGTCCAGACCGGCGCGGCTTAAACCGACTTGTCTGCCCCGAGAAATATGACAGACT 17507
4690 TTTTGTGTTATGTTGGGCGCCCAATGAGTGCAGGTCAAACTGACGATGACGACCAAT 4749
17508 TTTTGTGTTATGTTGGGCGCCCAATGAGTGCAGGTCAAACTGACGATGACGACCAAT 17567
4750 CTTTGGGCGGTTCCAGGCGCAATTTTGGCAAAATGTCGAGGCTCAGCAGGACTCGGAG 4809
17568 CTTTGGGCGGTTCCAGGCGCAATTTTGGCAAAATGTCGAGGCTCAGCAGGACTCGGAG 17627
4810 GCATCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTCACTAAATCTGC 4863
17628 GCATCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTCACTAAATCTGC 17681

RESULT 3
ABQ82142
ID ABQ82142 standard; DNA; 17458 BP.
XX
AC ABQ82142;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
XX
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
PA Wesley S, Waterhouse P, Helliwell C;
PI WPI; 2002-682669/73.
XX
DR New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
PS Claim 16; Page 83-93; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, or the third and
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 83.1%; Score 4042; DB 6; Length 17458;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 4419; Conservative 0; Mismatches 15; Indels 308; Gaps 6;
QY 122 GCCAATCTGTACAAAAGAGCTCAACGAGAAAGCTAAATGATATATAATCAATATATT 181
DB 13025 GACAAAGTTTGTACAAAAGAGCTCAACGAGAAAGCTAAATGATATATAATCAATATATT 13084
QY 182 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACCAACATATCCAGTC 241

Db 13085 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACCAACATATCCAGTC 13144
QY 242 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA 301
Db 13145 ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCGACCGACAGCCTTCCAAA 13204
QY 302 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 361
Db 13205 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 13264
QY 362 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 421
Db 13265 ACGGAATCGTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 13324
QY 422 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAATAATCATCTACCT 481
Db 13325 AGAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAATAAATAATCATCTACCT 13384
QY 482 ATTCATATACGCTAGTGTATAGTCCCTGAAATCATCTGCAATCAAGAACAAATTTTCAAC 541
Db 13385 ATTCATATACGCTAGTGTATAGTCCCTGAAATCATCTGCAATCAAGAACAAATTTTCAAC 13444
QY 542 TCTTATATCTTTTCTTTTCAAAAGTCTGTCGGCTTCATCTGGATTTTTCAGCCTCTTACTT 601
Db 13445 TCTTATATCTTTTCTTTTCAAAAGTCTGTCGGCTTCATCTGGATTTTTCAGCCTCTTACTT 13504
QY 602 CTAACCGTGATAAAAGTTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTA 661
Db 13505 CTAACCGTGATAAAAGTTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTA 13564
QY 662 AGGAGCGCTGACATTTATATCCAGAAATCATCAGTTTAATGGCGTTTTCATGTCATTT 721
Db 13565 AGGAGCGCTGACATTTATATTTCCCGAGAAATCATCAGTTTAATGGCGTTTTCATGTCATTT 13624
QY 722 TCGCGGTGGCTGAGATCAGCCACTTTCTCCCGATTAACGGAGACCGGACATCTGCCCAT 781
Db 13625 TCGCGGTGGCTGAGATCAGCCACTTTCTCCCGATTAACGGAGACCGGACATCTGCCCAT 13684
QY 782 TCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATTAACGGAGACCGGAGTAAAGTTCAGG 841
Db 13685 TCGGTGGTCATCATGCGCCAGCTTTTCATCCCGATTAACGGAGACCGGAGTAAAGTTCAGG 13744
QY 842 GAGACTTTTATCTGACAGCAGACGTGCTGCTGCGAGGGGATCAACATCCGTCGCCCGGGC 901
Db 13745 GAGACTTTTATCTGACAGCAGACGTGCTGCTGCGAGGGGATCAACATCCGTCGCCCGGGC 13804
QY 902 GTGTCAATAATATCACTCTGTACATCCAAACAGACGATTAACGGCTCTCTCTTTTATAG 961
Db 13805 GTGTCAATAATATCACTCTGTACATCCAAACAGACGATTAACGGCTCTCTCTTTTATAG 13864
QY 962 GTGTAAACCTTAACTGCAATTTCAACGCTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCA 1021
Db 13865 GTGTAAACCTTAACTGCAATTTCAACGCTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCA 13924
QY 1022 TTCAATAAACCGGGGAGCCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTCCGC 1081
Db 13925 TTCAATAAACCGGGGAGCCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTCCGC 13984
QY 1082 ACGCAGACGCGGGCTTCATTTCTGATGCTTGTGCTTACAGACCGGAGATTTGACATC 1141
Db 13985 ACGCAGACGCGGGCTTCATTTCTGATGCTTGTGCTTACAGACCGGAGATTTGACATC 14044
QY 1142 ATATATGCTTTCAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTAAATACGCTGCTTC 1201
Db 14045 ATATATGCTTTCAGCAACTGATAGTGTGCTGCTCAACTGTCACTGTAAATACGCTGCTTC 14104
QY 1202 ATAGCACACCTCTTTTTCACATCTTCGGGTAGTGCCTCAACGCTCTCATTTTCGCCAA 1261
Db 14105 ATAGCACACCTCTTTTTCACATCTTCGGGTAGTGCCTCAACGCTCTCATTTTCGCCAA 14164
QY 1262 AAGTTGGCCCGGGCTTCCCGGTATCAACAGGGACCCAGGATTTATTTATTTCTCGGAG 1321

14165	AGATTGGCCCGCAGGGCTTCCGGGTATCAACAGGGAACACAGGAGTTATTATTATTCCTGCGAAG	14222
1322	TGATCTTCCGTCACAGGATTTATTTCGGCGCAAGATGGCTCGGGGTAGCTGCGCAACTTA	1381
14225	TGATCTCCGTCACAGGATTTATTTCGGCGCAAGATGGCTCGGGGTAGCTGCGCAACTTA	14284
1382	GTGCACTACAGGTCACCTAATACCATCTAAGTAGTATTGATTCATAGTGACTGAGATATGTGT	1441
14285	GTGCACTACAGGTCACCTAATACCATCTAAGTAGTATTGATTCATAGTGACTGAGATATGTGT	14344
1442	GTTTTACAGTATTATAGTCTGTGTTTTTATGCCAAATCTAATTTAAATATATTCGATATTT	1501
14345	GTTTTACAGTATTATAGTCTGTGTTTTTATGCCAAATCTAATTTAAATATATTCGATATTT	14404
1502	ATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTTGCAAAAGTTGGCAATATTAAGAAAGCAT	1561
14405	ATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTTGCAAAAGTTGT-----	14448
1562	TGCTTATCAATTTGTTGCAACGAAAGGTCACCTATCAGTCAAAATAAAATCATTTATTGC	1621
14449	-----	14448
1622	CATCCAGCTGCAGTCTCTCGAGGAATTCGGTACCCAGGCTTGGTAAGGAAATAATTATTT	1681
14449	-----CTCGAGGAATTCGGTACC-----	14488
1682	TCTTTTTCCTTTTACGTATAAATAGTTAAAGTGATGTTAAATAGTAGTATGATTTATAATATA	1741
14489	TCTTTTTTCCTTTTACGTATAAATAGTTAAAGTGATGTTAAATAGTAGTATGATTTATAATATA	14548
1742	TAGTTGTTATAATTTGCGAAAAATAATTTATAAATATATTTGTTACATAAAACAACATAGT	1801
14549	TAGTTGTTATAATTTGCGAAAAATAATTTATAAATATATTTGTTACATAAAACAACATAGT	14608
1802	AATGTAAAAAATAATGACAAGTGATGTGTAAGCAGAGNAGATAAAAGTTGAGAGTAGT	1861
14609	AATGTAAAAAATAATGACAAGTGATGTGTAAGCAGAGNAGATAAAAGTTGAGAGTAGT	14668
1862	ATATTATTTTAAATGAATTTGATCGAAATGTAAGATGATATACATAGCATTTAAATATTTGT	1921
14669	ATATTATTTTAAATGAATTTGATCGAAATGTAAGATGATATACATAGCATTTAAATATTTGT	14728
1922	TTTAAATCAATTAATTTCTAGCTGGTTGGATGAAATTAATAATCAATGATAAAATACATA	1981
14729	TTTAAATCAATTAATTTCTAGCTGGTTGGATGAAATTAATAATCAATGATAAAATACATA	14788
1982	TAGTAAAAATTAAGAAATAATAAATAAATAATTTTTTTTATGATTAATAGTTATTAT	2041
14789	TAGTAAAAATTAAGAAATAATAAATAAATAATTTTTTTTATGATTAATAGTTATTAT	14848
2042	ATAATTAAATCTATACCAATTAATAATTTTTTGTTTTAAAGTTAAATAATTTTTGT	2101
14849	ATAATTAAATCTATACCAATTAATAATTTTTTGTTTTAAAGTTAAATAATTTTTGT	14908
2102	TAGAAATTCCAATCTGCTGTATTTTATCAATAACAAATAATTAATAACAGCTAAAG	2161
14909	TAGAAATTCCAATCTGCTGTATTTATCAATAACAAATAATTAATAACAGCTAAAG	14968
2162	TAACAATAATATCAAACTAATAGAAACAGTATCTAATGTAAACAAACAATAATCTAATG	2221
14969	TAACAATAATATCAAACTAATAGAAACAGTATCTAATGTAAACAAACAATAATCTAATG	15028
2222	CTAATATAACAAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTTCAATCAAGTTCT	2281
15029	CTAATATAACAAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTTCAATCAAGTTCT	15088
2282	TATTAATTTCTAAATAATCTCTGATGTTTTTATTTAACTTCTAAATGATTTACTTAAT	2341
15089	TATTAATTTCTAAATAATCTCTGATGTTTTTATTTAACTTCTAAATGATTTACTTAAT	15148
2342	AAATGAATTAGTCGAACATGAATTAACAGGTAACATGATAGTATGTCATTGTGTTAT	2401
15149	AAATGAATTAGTCGAACATGAATTAACAGGTAACATGATAGTATGTCATTGTGTTAT	15208

Qy	2402	CATTGATCTTTACATTTGGATTCGATTACAGTTGGGAAGCTGGGTTCGAAATCGATRAGCTT	2461
Db	15209	CATTGATCTTTACATTTGGATTCGATTACAGTTACTTTACCTT	15254
Qy	2462	GGATCTCTAGAGAGCTGCAGCTGGATGGCAAAATAATGATTTTATTTTTGACTGATAGTGA	2521
Db	15255	GGATCTCTTAGA	15266
Qy	2522	CTGTGTTCTGTGCAACAAATTGATAAGCAATGCTTCTTTATATGCAACTTTGTACAAGA	2581
Db	15267	-	15281
Qy	2582	AAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATTAATTTAGATTTTGGCATA	2641
Db	15282	AAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATTAATTTAGATTTTGGCATA	15341
Qy	2642	AAAAACAGACTACATAAATACTCTAAAAACAACATATCCAGTCACATATGAATCAACTACT	2701
Db	15342	AAAAACAGACTACATAAATACTCTAAAAACAACATATCCAGTCACATATGAATCAACTACT	15401
Qy	2702	TAGATGGTATTAGTGACCTGTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGC	2761
Db	15402	TAGATGGTATTAGTGACCTGTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGC	15461
Qy	2762	CCGAATAAATACCTGTGACGGAAGATCACTTCGCGAGAATAAATAAATCTCGGTGTCCTGTG	2821
Db	15462	CCGNAATAATACCTGTGACGGAAGATCACTTCGCGAGAATAAATAAATCTCGGTGTCCTGTG	15521
Qy	2822	TTGATACCGGGAAGCCTCGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGCACACTACC	2881
Db	15522	TTGATACCGGGAAGCCTCGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGG	15574
Qy	2882	CANTTCAACAACCTCTATACCTTTCTCTTCAAGTGGTTGGCGTTTCATCTGGATTTTCAGC	2941
Db	15575	-ATTTCAACAACCTCTATACCTTTCTCTTCAAGTGGTTGGCGTTTCATCTGGATTTTCAGC	15633
Qy	2942	CTCTATACCTTATAAACGTAAGAATTTCTGTAAATTTCTACTGTATCGAATCGAGACT	3001
Db	15634	CTCTATACCTTATAAACGTAAGAATTTCTGTAAATTTCTACTGTATCGAATCGAGACT	15693
Qy	3002	GGCTGTGTATAACGGAGCCTGCATTTATATTTCCCGAGAACATCAGGTTAATGGGCTTTT	3061
Db	15694	GGCTGTGTATAACGGAGCCTGCATTTATATTTCCCGAGAACATCAGGTTAATGGGCTTTT	15753
Qy	3062	TGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTTCTCCCGATAACGAGACCGGCA	3121
Db	15754	TGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTTCTCCCGATAACGAGACCGGCA	15813
Qy	3122	CATCGGCCATATCGTGTGTTCATCATCGGCCAGCTTTTCATCCCGGATATGCACCCGGGT	3181
Db	15814	CATCGGCCATATCGTGTGTTCATCATCGGCCAGCTTTTCATCCCGGATATGCACCCGGGT	15873
Qy	3182	AAAGTTTCACGGAGACTTTTATCTGACAGCAGACGTGTCACTGCCAGGGGGATCACAATCC	3241
Db	15874	AAAGTTTCACGGAGACTTTTATCTGACAGCAGACGTGTCACTGCCAGGGGGATCACAATCC	15933
Qy	3242	GTGCCCGGCGGTGCAATAATATCACTCTGTACATCCAAACAGACGATTAACGGCTCT	3301
Db	15934	GTGCCCGGCGGTGCAATAATATCACTCTGTACATCCAAACAGACGATTAACGGCTCT	15993
Qy	3302	CTCTTTTATAGGTGAACCTTTAAACCTGATTTTCAACGATTTTCACGTCCTGTCTCGTCAGCAAAA	3361
Db	15994	CTCTTTTATAGGTGAACCTTTAAACCTGATTTTCAACGATTTTCAACGATTTTTCCTGTCAGCAAAA	16053
Qy	3362	GAGCCGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGTATTTTCCGCTTTC	3421
Db	16054	GAGCCGTTCAATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGTATTTTCCGCTTTC	16113
Qy	3422	CAGCGTTCGGCAGCAGACGACGGCTTCATCTCTGATCGTTGTGCTTACAGACCGGAG	3481
Db	16114	CAGCGTTCGGCAGCAGACGACGGCTTCATCTCTGATCGTTGTGCTTACAGACCGGAG	16173

QY 3482 ATATTGACATCATATATATGCTTGTAGGCAACTGATAGCTGTGCTGTCAACTGTCTACTGTAA 3541
DB 16174 ATATTGACATCATATATATGCTTGTAGGCAACTGATAGCTGTGCTGTCAACTGTCTACTGTAA 16233
QY 3542 TACGCTGCTTCCATAGCACACCTCTTTTGGACATATCTTCTGTCTTGTATGATGAGATGATTTT 3601
DB 16234 TACGCTGCTTCCATAGCACACCTCTTTTGGACATATCTTCTGTCTTGTATGATGAGATGATTTT 16293
QY 3602 CAGGACTATGACACTAGCGTATATGAATPAGTAGATGTTTTTATTTTGTGCACACAAAAA 3661
DB 16294 CAGGACTATGACACTAGCGTATATGAATPAGTAGATGTTTTTATTTTGTGCACACAAAAA 16353
QY 3662 GAGGCTGACACTCTTTTCTTATTTCTTTTATGATTTAATACGGCATGAGGACAATA 3721
DB 16354 GAGGCTGACACTCTTTTCTTATTTCTTTTATGATTTAATACGGCATGAGGACAATA 16413
QY 3722 GCGAGTAGGCTGGATACGACGATTCGGTTTGGAGAACATTTTGGAGGCTGTGCGTCTGA 3781
DB 16414 GCGAGTAGGCTGGATACGACGATTCGGTTTGGAGAACATTTTGGAGGCTGTGCGTCTGA 16473
QY 3782 CTAAGTTGGAGCATCACCCGAGAACATTTTGGAGGCTGTGCGTCTGACATACAGTCACT 3841
DB 16474 CTAAGTTGGAGCATCACCCGAGAACATTTTGGAGGCTGTGCGTCTGACATACAGTCACT 16533
QY 3842 AATACCATCTAAGTAGTTGATTCATGCTAGTCACTGATATGTTGTTTACAGTATATGT 3901
DB 16534 AATACCATCTAAGTAGTTGATTCATGCTAGTCACTGATATGTTGTTTACAGTATATGT 16593
QY 3902 AGTCTGTTTTTATGCAAAATCTAATTTAATATATTTATATATTTATCATTTTACGTTTC 3961
DB 16594 AGTCTGTTTTTATGCAAAATCTAATTTAATATATTTATATATTTATCATTTTACGTTTC 16653
QY 3962 TCGTTACGTTTTTGTGTAAGAGTTGGCATTTAATAAAGCATTTGCTCATCAATTTGTTG 4021
DB 16654 TCGTTACGTTTTTGTGTAAGAGTTGGCATTTAATAAAGCATTTGCTCATCAATTTGTTG 16679
QY 4022 CAACGACAGGTCATCATCAGTCACAAATPAAATCATTATTTGGGGCCCGAGATCATGCT 4081
DB 16680 ----- 16679
QY 4082 AGCTCTAGAGTCCTGCTTTAATAGATATGCGAGACGCTATGATCGCATGATATTTGCT 4141
DB 16680 ---TCTAGAGTCCTGCTTTAATAGATATGCGAGACGCTATGATCGCATGATATTTGCT 16736
QY 4142 TTCATTTCTGTTGCGACGTTGTAAACACCTGACATGTTGATGCTGAGTCCCTTACCGC 4201
DB 16737 TTCATTTCTGTTGCGACGTTGTAAACACCTGACATGTTGATGCTGAGTCCCTTACCGC 16796
QY 4202 CGGTTTCGTTTCATTTCAATGAATATATCACCCGTTACTATCTATTTTATGAATAATA 4261
DB 16797 CGGTTTCGTTTCATTTCAATGAATATATCACCCGTTACTATCTATTTTATGAATAATA 16856
QY 4262 TTCCTCGTTTCAATTTACTGATTTACCTTACTTATGATGATGATGATGATGATGATGATGAT 4321
DB 16857 TTCCTCGTTTCAATTTACTGATTTACCTTACTTATGATGATGATGATGATGATGATGATGAT 16916
QY 4322 CAATATATGCTGCTGATAGGTTTATAGCGATCTATGATGATGATGATGATGATGATGATGAT 4381
DB 16917 CAATATATGCTGCTGATAGGTTTATAGCGATCTATGATGATGATGATGATGATGATGATGAT 16976
QY 4382 CAATTGCGTTTTTATTTATCAAAATCAATTTTAAAAAAGCGGACGCGTCAAACT 4441
DB 16977 CAATTGCGTTTTTATTTATCAAAATCAATTTTAAAAAAGCGGACGCGTCAAACT 17036
QY 4442 AAAAGACTGATTTACATAAATCTTTTCAAAATTTCAAAAGCCGCGGCGCTAGTATCTTAC 4501
DB 17037 AAAAGACTGATTTACATAAATCTTTTCAAAATTTCAAAAGCCGCGGCGCTAGTATCTTAC 17096
QY 4502 GACACACCGCGGCGGAACTAATACGTTTCACTGAGGAACTCCGGTTCCCGCGCGGCG 4561
DB 17097 GACACACCGCGGCGGAACTAATACGTTTCACTGAGGAACTCCGGTTCCCGCGCGGCG 17156
QY 4562 CGCATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCGGTCCGCTCTACCGAAAGTTACGGG 4621

DB 17157 CGCATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCGGTCCGCTCTACCGAAAGTTACGG 17216
QY 4622 CACCATTTCAACCCGGTCCAGCACGGCGGCGGTAACCGACTTTGCTGCCCGGAAATAT 4681
DB 17217 CACCATTTCAACCCGGTCCAGCACGGCGGCGGTAACCGACTTTGCTGCCCGGAAATAT 17276
QY 4682 GCGACATTTTTTTGGTGTATGTTGGGCCCCAAATGAAGTGCAGGTCAACCTTGACAGTGA 4741
DB 17277 GCGACATTTTTTTGGTGTATGTTGGGCCCCAAATGAAGTGCAGGTCAACCTTGACAGTGA 17336
QY 4742 CGCAAAATCTTGGGCGGTCAGGGCGAATTTTGGACAAACATGTCGAGGCTCAGCAGG 4801
DB 17337 CGCAAAATCTTGGGCGGTCAGGGCGAATTTTGGACAAACATGTCGAGGCTCAGCAGG 17396
QY 4802 ACCTGCAGGCATCAAGCTAGCTTACTAGTGCATATTTCTATAGTGTCACTAAATCT 4861
DB 17397 ACCTGCAGGCATCAAGCTAGCTTACTAGTGCATATTTCTATAGTGTCACTAAATCT 17456
QY 4862 GC 4863
DB 17457 GC 17458
RESULT 4
ABQ82130
ID ABQ82130 standard; DNA; 18691 BP.
XX ABQ82130;
XX AC
XX AC
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
FN WO200259294-A1.
XX
PD
XX
XX 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
XX 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
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XX WPI; 2002-682669/73.
XX
PT New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
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PS Claim 13; Page 62-72; 104pp; English.
XX
XX The present invention describes a vector (i) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and

CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ

Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

Query Match 82.0%; Score 3985.4; DB 6; Length 18691;
Best Local Similarity 85.1%; Prid. No. 0;
Matches 4846; Conservative 0; Mismatches 16; Indels 831; Gaps 2;

QY 1 TTTCAATTTGGAGAGACACGCTCGAGGCTAGCATGATCTCGGGCCCAATAATGATTT 60
Db 13000 TTTCAATTTGGAGAGACACGCTCGAGGCTAGCATGATCTCGGGCCCAATAATGATTT 13059
QY 61 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 13060 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13119
QY 121 TGCCAACTTTGACAAAAGCTGAAACGAGAAACGTAATAATGATGATGATGATGAT 180
Db 13120 TGCCAACTTTGACAAAAGCTGAAACGAGAAACGTAATAATGATGATGATGATGAT 13179
QY 181 TAAATTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 13180 TAAATTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13239
QY 241 CACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 13240 CACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13299
QY 301 ATGTTCTTTCGGGTGATGCTGCCAATAGTACGACGAGCCCTCCAAATGTTCTTCFCA 360
Db 13300 ATGTTCTTTCGGGTGATGCTGCCAATAGTACGACGAGCCCTCCAAATGTTCTTCFCA 13359
QY 361 AACGGAATCGTGTATCAGACGCTACTCGCTATGTCCTCAATGCGGTATTAATCATAAA 420
Db 13360 AACGGAATCGTGTATCAGACGCTACTCGCTATGTCCTCAATGCGGTATTAATCATAAA 13419
QY 421 AAGAAATAGAAAGAGGTGCGGCTCTTTTGTGACAAAATGATGATGATGATGATGATGAT 480
Db 13420 AAGAAATAGAAAGAGGTGCGGCTCTTTTGTGACAAAATGATGATGATGATGATGATGAT 13479
QY 481 TATTCATATACGCTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 13480 TATTCATATACGCTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13539
QY 541 CTCCTATATCTTTCTTCAAGTGTGCTCGGCTCATCTGGATTTTTCAGCCTCTATACCT 600
Db 13540 CTCCTATATCTTTCTTCAAGTGTGCTCGGCTCATCTGGATTTTTCAGCCTCTATACCT 13599
QY 601 ACTAAGCGTGAATAAGTTTCTGTAATTTCTACTGTATGACCTGACGAGCTGGCTGTAT 660
Db 13600 ACTAAGCGTGAATAAGTTTCTGTAATTTCTACTGTATGACCTGACGAGCTGGCTGTAT 13659
QY 661 AAGGGAGCCTGACATTTATATTTCCCGAAGACATCAGGTTAATGGGCTTTTGTATGTCATT 720
Db 13660 AAGGGAGCCTGACATTTATATTTCCCGAAGACATCAGGTTAATGGGCTTTTGTATGTCATT 13719
QY 721 TTGCGGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGAGACCGGACACTGGCCAT 780
Db 13720 TTGCGGGTGGCTGAGATCAGCCACTTCTTCCCGATTAACGAGACCGGACACTGGCCAT 13779
QY 781 ATCGGTGGTATCATCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTTCAGG 840
Db 13780 ATCGGTGGTATCATCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTTCAGG 13839

QY 841 GGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCGTCGCCGGG 900
Db 13840 GGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGATCACCATCGTCGCCGGG 13899
QY 901 CGTGTCAATAATATCACTCTGTACATCCACAAACAGACAGATACGGCTCTCTTTTATA 960
Db 13900 CGTGTCAATAATATCACTCTGTACATCCACAAACAGACAGATACGGCTCTCTTTTATA 13959
QY 961 GGTGTAACCTTAAACTGATTTTACAGTCCCTGTCTCTGTCAGCAAAAGACCGCTTCA 1020
Db 13960 GGTGTAACCTTAAACTGATTTTACAGTCCCTGTCTCTGTCAGCAAAAGACCGCTTCA 14019
QY 1021 TTTCAATAPACCGGGGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTCCAGGTCGG 1080
Db 14020 TTTCAATAPACCGGGGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTCCAGGTCGG 14079
QY 1081 CACGACAGACCGGGCTTCATTCTGCATGTTGTGCTTACAGACCGGATATTGACAT 1140
Db 14080 CACGACAGACCGGGCTTCATTCTGCATGTTGTGCTTACAGACCGGATATTGACAT 14139
QY 1141 CATATATGCTTGGACAACTGATGCTGCTGCACTGCTGCACTGCTGATATACGTCGTT 1200
Db 14140 CATATATGCTTGGACAACTGATGCTGCTGCACTGCTGCACTGCTGATATACGTCGTT 14199
QY 1201 CATAGCACACCTCTTTTGGACATCTTTCCGGGTAGTCCGATCAACGCTCTCATTTCCGCA 1260
Db 14200 CATAGCACACCTCTTTTGGACATCTTTCCGGGTAGTCCGATCAACGCTCTCATTTCCGCA 14259
QY 1261 AAGTTGGCCGAGGCTTCCGGGTATCAACAGGACACCGAGGATTTATTTTCTGCGAA 1320
Db 14260 AAGTTGGCCGAGGCTTCCGGGTATCAACAGGACACCGAGGATTTATTTTCTGCGAA 14319
QY 1321 GTGATCTTCGCTGACAGGATTTTATTCGGCGCAAGTCCGCTGATGCTGCAACTT 1380
Db 14320 GTGATCTTCGCTGACAGGATTTTATTCGGCGCAAGTCCGCTGATGCTGCAACTT 14379
QY 1381 AGTCGACTACAGGTCACATATACCATCTAAGTAGTTCATGATGATGATGATGATGAT 1440
Db 14380 AGTCGACTACAGGTCACATATACCATCTAAGTAGTTCATGATGATGATGATGATGAT 14439
QY 1441 TGTTTTACAGTATTTATGATGCTGTTTTTATGCAAAATCTAATTTTATATATGATGAT 1500
Db 14440 TGTTTTACAGTATTTATGATGCTGTTTTTATGCAAAATCTAATTTTATATATGATGAT 14499
QY 1501 TATATCAATTTTACGTTTCTGCTCAGCTTTCTGTACAAAAGTGGCATTTAAGAAAGCA 1560
Db 14500 TATATCAATTTTACGTTTCTGCTCAGCTTTCTGTACAAAAGTGGCATTTAAGAAAGCA 14559
QY 1561 TTGCTTATCAATTTGTTGCAACGAGGTCATCATGCTCAAAATATAATCATTTATTG 1620
Db 14560 TTGCTTATCAATTTGTTGCAACGAGGTCATCATGCTCAAAATATAATCATTTATTG 14619
QY 1621 CCATCCAGCTGAGCTCCGAGGAATTCGTTACCCAGCTTGTGTAAGGAATTAATTTAT 1680
Db 14620 CCATCCAGCTGAGCTCCGAGGAATTCGTTACCCAGCTTGTGTAAGGAATTAATTTAT 14678
QY 1681 TTTCTTTTCTTTTGTATATAAATAGTAAAGTATGATGATGATGATGATGATGATGATGAT 1740
Db 14679 TTTCTTTTCTTTTGTATATAAATAGTAAAGTATGATGATGATGATGATGATGATGATGAT 14738
QY 1741 ATAGTGTATATAATGTAAGGAATTAATTAATAATATTTTACATAAACAACATAG 1800
Db 14739 ATAGTGTATATAATGTAAGGAATTAATTAATAATATTTTACATAAACAACATAG 14798
QY 1801 TAACTAAAAAATATGACAAAGTGTGTAAGCAAGAAAGATAAAGTTGAGAGTAAG 1860
Db 14799 TAACTAAAAAATATGACAAAGTGTGTAAGCAAGAAAGATAAAGTTGAGAGTAAG 14858
QY 1861 TATATTTATTTTAAATGAAATTTGATGCAACATGTAAGATGATATATAGCATTTAA 1914
Db 14859 TATATTTATTTTAAATGAAATTTGATGCAACATGTAAGATGATATACGGCGGTAGAGGTT 14918
QY 1915 ----- 1914

Db	14919	CCACCTTCCACATAATGAATAAGATCACTACCGGCGTATTTTTTGAGTTATCGAGAT	14978
QY	1915	-----	1914
Db	14979	TTTCAGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATA	15038
QY	1915	-----	1914
Db	15039	TATCCCAATGGATCGTAAAGAACATTTTGGAGCATTTTCAGTCACTGCTCAATGTACCT	15098
QY	1915	-----	1914
Db	15099	ATAACAGACCGTTTCAGCTGGATATTACGGCCTTTTAAAGACCGTAAGAAAAATAAGC	15158
QY	1915	-----	1914
Db	15159	ACAACTTTTATCCGGCCTTTTATTCACATTTCTTCCCGCCTGATGAATGCTCATCCGGAAT	15218
QY	1915	-----	1914
Db	15219	TCCGTATGGCAATGAAGACGGTGAGTGGTGATATGGATAGTGTTCACCTTGTTTACA	15278
QY	1915	-----	1914
Db	15279	CGCTTTCATGAGCAAACTGAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATT	15338
QY	1915	-----	1914
Db	15339	TCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCT	15398
QY	1915	-----	1914
Db	15399	ATTTCCCTAAAGGTTTATTGAGATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTT	15458
QY	1915	-----	1914
Db	15459	TCACCACTTTTGATTTAAACGTTGGCCAAATATGGACAACTTCTTCGCCCCGTTTTTCACCA	15518
QY	1915	-----	1914
Db	15519	TGGCAAAATATTATACGCAAGCGCAAGGTGCTGATCCCGTGGCGAATCAGGTTCATC	15578
QY	1915	-----	1914
Db	15579	ATGCGTCTGTGATGGCTTCCATGTCCGCGAAGTCTTAATGAATTACACAGTACTCGG	15638
QY	1915	-----	1914
Db	15639	ATGAGTGGCAGGGCGGGCGTAATCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGT	15698
QY	1915	-----TATTTGTTTTTAATCAT	1930
Db	15699	ATGCGTATTTGGCGCTGATTTTTCGGGTATTAAGAAATATATCTGATATGTCGGGCCCAT	15758
QY	1931	AATAGTAATCTAGCTGGTTTGATGAATTAATATCAATGATAAAATACTAGTAAATA	1990
Db	15759	AATAGTAATCTAGCTGGTTTGATGAATTAATATCAATGATAAAATACTAGTAAATA	15818
QY	1991	TAAAGATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	2050
Db	15819	TAAAGATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	15878
QY	2051	TATCTATACCACTTACTAAATATTTTGTATTAAGTTTAAATAATTTTGTAGAAATTC	2110
Db	15879	TATCTATACCACTTACTAAATATTTTGTATTAAGTTTAAATAATTTTGTAGAAATTC	15938
QY	2111	CAATCTGCTTGTAAATTTATCAATAACAAATAATTTAAATAACAAAGCTAAAGTAAATA	2170
Db	15939	CAATCTGCTTGTAAATTTATCAATAACAAATAATTTAAATAACAAAGCTAAAGTAAATA	15998
QY	2171	ATATCAAACTATAGAAACAGTAACTTAATGTAACAAACAACTAATCTAATCTAATATA	2230

Db	15999	ATATCAAACTATAGAAACAGTAACTTAATGTAACAAACAACTAATCTAATCTAATATA	16058
QY	2231	CAAAAGCGCAAGATCATCATTTTATATAGTATATTTTCAATCAACATTTCTTATTAATTT	2290
Db	16059	CAAAAGCGCAAGATCATCATTTTATATAGTATATTTTCAATCAACATTTCTTATTAATTT	16118
QY	2291	CTAATTAATATCTGCTGCTTTTATTAACCTTCTAATAGATTTGACTATTAATTAATGAAT	2350
Db	16119	CTAATTAATATCTGCTGCTTTTATTAACCTTCTAATAGATTTGACTATTAATTAATGAAT	16178
QY	2351	AGTCGAAACATGAATAAAACAGGTAAATGATAGATCATGTCAATGTGTATCATTTGATCT	2410
Db	16179	AGTCGAAACATGAATAAAACAGGTAAATGATAGATCATGTCAATGTGTATCATTTGATCT	16238
QY	2411	TACATTTGGATGTATTAACAGTTGGGAAGCTGGGTTCGAAATCGAATAAGCTTTGGATCTCT	2470
Db	16239	TACATTTGGATGTATTAACAGTTGGGAAGCTGGGTTCGAAATCGAATAAGCTTTGGATCTCT	16298
QY	2471	AGAGAGCTGCAGCTGGATGGCAATATGATTTTATTTGACTGATAGTGCCTGTTGCT	2530
Db	16299	AGAGAGCTGCAGCTGGATGGCAATATGATTTTATTTGACTGATAGTGCCTGTTGCT	16358
QY	2531	TGCAACAAATTTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGAAC	2590
Db	16359	TGCAACAAATTTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGAAC	16418
QY	2591	GAGAAACGTAATATGATATTAATTAATCAATATTAATTAATTAATTAATTAATTAATTAAT	2650
Db	16419	GAGAAACGTAATATGATATTAATTAATCAATATTAATTAATTAATTAATTAATTAATTAAT	16478
QY	2651	CTACATAATCTGTAAACAAACACATATCCAGTCACTATGAATCACTACTTACATCGTA	2710
Db	16479	CTACATAATCTGTAAACAAACACATATCCAGTCACTATGAATCACTACTTACATCGTA	16538
QY	2711	TTAGTACCTGTAGTTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGCCGAATAAA	2770
Db	16539	TTAGTACCTGTAGTTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGCCGAATAAA	16598
QY	2771	TACCTGTGACGGAAGATCACTTTCGCAATAAATAAATTAATTAATTAATTAATTAATTAAT	2830
Db	16599	TACCTGTGACGGAAGATCACTTTCGCAATAAATAAATTAATTAATTAATTAATTAATTAAT	16658
QY	2831	GGAAAGCCTTGGCCCAACTTTTGGCAAAATGAGACGTTGATCGGCACTACCCATTTTCA	2890
Db	16659	GGAAAGCCTTGGCCCAACTTTTGGCAAAATGAGACGTTGATCGGCACTACCCATTTTCA	16718
QY	2891	ACTCTTATATCTTTCTCTTCAAGTCTGCTCGGCTTCACTGGATTTTTCAGCTCTACT	2950
Db	16719	ACTCTTATATCTTTCTCTTCAAGTCTGCTCGGCTTCACTGGATTTTTCAGCTCTACT	16778
QY	2951	TACTAAACGTTGATAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGA	3010
Db	16779	TACTAAACGTTGATAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGA	16838
QY	3011	TAAGGAGCCTGACATTTATATTTCCCGCAACATCAGGTTAAATGGCGTTTTCATGTCAT	3070
Db	16839	TAAGGAGCCTGACATTTATTTATTTCCCGCAACATCAGGTTAAATGGCGTTTTCATGTCAT	16898
QY	3071	TTTCGCGGTGGCTGAGATCAGCACTTTCTTCCCGATTAACGAGACCCGCACTTGCCCA	3130
Db	16899	TTTCGCGGTGGCTGAGATCAGCACTTTCTTCCCGATTAACGAGACCCGCACTTGCCCA	16958
QY	3131	TATCGGTGGTCATATGCGCCAGCTTTTCATCCCGATATGACCAACCGGTTAAGTTCAC	3190
Db	16959	TATCGGTGGTCATATGCGCCAGCTTTTCATCCCGATATGACCAACCGGTTAAGTTCAC	17018
QY	3191	GGGAGACTTTTATCTGACAGCAGCTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGG	3250
Db	17019	GGGAGACTTTTATCTGACAGCAGCTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGG	17078
QY	3251	CGGTCTCAATTAATATCTCTGTATACCAAAACAGACGATTAACGGCTCTCTCTTTTAT	3310
Db	17079	CGGTCTCAATTAATATCTCTGTATACCAAAACAGACGATTAACGGCTCTCTCTTTTAT	17138

QY 3311 AGTGCTAAACCTTAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTTC 3370
Db 17139 AGGTGTAACCTTAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTTC 17198
QY 3371 ATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCG 3430
Db 17199 ATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGGTTTCG 17258
QY 3431 GCACGACAGACGGGCTTCATCTTGCATGTTGCTTTACAGACCGGAGATATTGACA 3490
Db 17259 GCACGACAGACGGGCTTCATCTTGCATGTTGCTTTACAGACCGGAGATATTGACA 17318
QY 3491 TCATATATGCTTTGACACCTGATAGCTGTCGCTGCTCACTGCTCACTGCTATATAGCTGCT 3550
Db 17319 TCATATATGCTTTGACACCTGATAGCTGTCGCTGCTCACTGCTCACTGCTATATAGCTGCT 17378
QY 3551 TCATAGCACACCTCTTTTGTGACATACCTTCTGTTCTTGATGACGATGATTTTTCAGGACTAT 3610
Db 17379 TCATAGCACACCTCTTTTGTGACATACCTTCTGTTCTTGATGACGATGATTTTTCAGGACTAT 17438
QY 3611 GACACTAGGATATGATAGTAGTATGTTTATTTTATTTTGTGCACAAAAAGAGCTCGC 3670
Db 17439 GACACTAGGATATGATAGTAGTATGTTTATTTTGTGCACAAAAAGAGCTCGC 17498
QY 3671 ACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTGAGGACAAATAGCGAGTAGG 3730
Db 17499 ACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCATTGAGGACAAATAGCGAGTAGG 17558
QY 3731 CTGGATACGAGGATTCGGTTTGGAGAAACATTTGGAGGGCTGTCGGTCGACTAAGTTGG 3790
Db 17559 CTGGATACGAGGATTCGGTTTGGAGAAACATTTGGAGGGCTGTCGGTCGACTAAGTTGG 17618
QY 3791 CAGCATACCCGAGAAACATTTGGAGGGCTGTCGGTCGACTACAGGTCACTAATACCATC 3850
Db 17619 CAGCATACCCGAGAAACATTTGGAGGGCTGTCGGTCGACTACAGGTCACTAATACCATC 17678
QY 3851 TAAAGTAGTTGATTCATAGTACTGATATGTTGTTTACAGTATTAATGATGTCGTTT 3910
Db 17679 TAAAGTAGTTGATTCATAGTACTGATATGTTGTTTACAGTATTAATGATGTCGTTT 17738
QY 3911 TTTATGCAAAATCTAATTTATATATGATATTTATATATATTTTACGTTTTCGTTTCAGC 3970
Db 17739 TTTATGCAAAATCTAATTTATATATGATATTTATATATATTTTACGTTTTCGTTTCAGC 17798
QY 3971 TTTTGTGACAAAGTTGCAATATAAAGAGCATTTGCTCAATCAATTTGCTGCAAGACACA 4030
Db 17799 TTTTGTGACAAAGTTGCAATATAAAGAGCATTTGCTCAATCAATTTGCTGCAAGACACA 17858
QY 4031 GGTCACTATCAGTCAAAATAAAATCAATTTTGGGGCCCGAGATCCATGCTAGCTCTAGA 4090
Db 17859 GGTCACTATCAGTCAAAATAAAATCAATTTTGGGGCCCGAGATCCATGCTAGCTCTAGA 17918
QY 4091 GTCCCTGCTTTAATGATATGCGAGACGCTATGATGCGATGATATTTGCTTCAATTTCT 4150
Db 17919 GTCCCTGCTTTAATGATATGCGAGACGCTATGATGCGATGATATTTGCTTCAATTTCT 17978
QY 4151 GTTGTGCAAGTTGTAATAAAACCTGAGCATGCTAGCTCAGATCCCTTACGCGGTTTCGG 4210
Db 17979 GTTGTGCAAGTTGTAATAAAACCTGAGCATGCTAGCTCAGATCCCTTACGCGGTTTCGG 18038
QY 4211 TTCATCTTAATGAATATATACCCGTTACTATCGTATTTTATGAATAATATTTCTCCGTT 4270
Db 18039 TTCATCTTAATGAATATATACCCGTTACTATCGTATTTTATGAATAATATTTCTCCGTT 18098
QY 4271 CAATTTACTGATGTTACCTACTACTATATGTAATATTAATTAATGAATAATATTT 4330
Db 18099 CAATTTACTGATGTTACCTACTACTATATGTAATATTAATTAATGAATAATATTT 18158
QY 4331 GTGCTGAATAGGTTTATAGCGCATCTATGATAGAGCGCCACAATAACAAACAATTCGTT 4390
Db 18159 GTGCTGAATAGGTTTATAGCGCATCTATGATAGAGCGCCACAATAACAAACAATTCGTT 18218

QY 4391 TTTATTTTACAAATCAATTTTAAAAAGCGGAGAACCGGTCAAAACCTAAAAAGCTG 4450
Db 18219 TTTATTTTACAAATCAATTTTAAAAAGCGGAGAACCGGTCAAAACCTAAAAAGCTG 18278
QY 4451 ATTACATAAATCTTATTTCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGACACACCG 4510
Db 18279 ATTACATAAATCTTATTTCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGACACACCG 18338
QY 4511 AGCGGCAACTAATAACAGTTTCACTGAAAGGAACTCCGTTTCCCGCGCGCGCATGGGT 4570
Db 18339 AGCGGCAACTAATAACAGTTTCACTGAAAGGAACTCCGTTTCCCGCGCGCGCATGGGT 18398
QY 4571 GAGATTCCTTTGAAATTTGAGTATTTGGCGTTCGCTTACCCAAAAGTTACGGGACCATTTCA 4630
Db 18399 GAGATTCCTTTGAAATTTGAGTATTTGGCGTTCGCTTACCCAAAAGTTACGGGACCATTTCA 18458
QY 4631 ACCCGGTCCAGCAGCGGCGGGGTAAACGACTTGTCTGCCCGGAGAAATTTATGAGCAATTT 4690
Db 18459 ACCCGGTCCAGCAGCGGCGGGGTAAACGACTTGTCTGCCCGGAGAAATTTATGAGCAATTT 18518
QY 4691 TTTTGGTGTATGTGGGCCCCCAAAATGAAAGTGCAGGTCAAACTTGACAGTGAOCGAAATC 4750
Db 18519 TTTTGGTGTATGTGGGCCCCCAAAATGAAAGTGCAGGTCAAACTTGACAGTGAOCGAAATC 18578
QY 4751 GTTGGCGGGTCCAGGGCGGAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTGCAGG 4810
Db 18579 GTTGGCGGGTCCAGGGCGGAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCTGCAGG 18638
QY 4811 CATGCAAGCTAGCTTACTAGTATGATGATATTTCTATAGTGTCACTAAATCTGC 4863
Db 18639 CATGCAAGCTAGCTTACTAGTATGATGATATTTCTATAGTGTCACTAAATCTGC 18691
RESULT 5
AAC5521
ID AAC5521 standard; DNA; 4470 BP.
XX AAC5521;
AC AAC5521;
XX
DT 11-JAN-2001 (first entry)
XX
DE Donor plasmid pDONR201 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL; attL1;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.
XX WO200052027-A1.
PN
PD 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
PF
PR 02-MAR-1999; 99US-01222389P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
PI
PI Hartley JH, Brasch MA, Temple GF, Cheo D;
XX
XX WPI; 2000-543948/49.
DR
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
PS Example 9; Fig 49; 459pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (1)

CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX

SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.8%; Score 1207.4; DB 3; Length 4470;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGGCTAGCATGATCTCGGGCCCCAAATAAGATTTTATTGATGATGATGACCTGTT 84
DB 5 AGGCTAGCATGATCTCGGGCCCCAAATAAGATTTTATTGATGATGATGACCTGTT 64
QY 85 CTTTCAACAAATTGATGAGCAATCTTTTATATATGCAATTTTGACAAAAAAGCTG 144
DB 65 CTTTCAACAAATTGATGAGCAATCTTTTATATATGCAATTTTGACAAAAAAGCTG 124
QY 145 AACGAGAAACGTAATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAC 204
DB 125 AACGAGAAACGTAATGATATAAATATCAATATATTAATTTAGATTTTGCATAAAAAC 184
QY 205 AGACTACATATCTGTAACACACACATATCCAGTCACTATGATCACTACTTAGATG 264
DB 185 AGACTACATATCTGTAACACACACATATCCAGTCACTATGATCACTACTTAGATG 244
QY 265 GTATTAGTGACCTGTAGTCGACCGACGACCTTCCAAATGTTCTCGGGTGATGCTGCCAA 324
DB 245 GTATTAGTGACCTGTAGTCGACCGACGACCTTCCAAATGTTCTCGGGTGATGCTGCCAA 304
QY 325 CTTAGTCGACGACGACCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCCTA 384
DB 305 CTTAGTCGACGACGACCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCCTA 364
QY 385 CTCGCTATTGCTCAATGCGGTATTAATATCAATAAAGAAATAGAAAGAGGTGCGA 444
DB 365 CTCGCTATTGCTCAATGCGGTATTAATATCAATAAAGAAATAGAAAGAGGTGCGA 424
QY 445 GCCTCTTTTGTGACAAAAATAAAACATCTACTATTTCATATACGCTAGTGTCTATAG 504
DB 425 GCCTCTTTTGTGACAAAAATAAAACATCTACTATTTCATATACGCTAGTGTCTATAG 484
QY 505 TCCTGAATATCATCTGCATCAAGACAATTTACACACTCTTATACCTTTCTCTTCAAGT 564
DB 485 TCCTGAATATCATCTGCATCAAGACAATTTACACACTCTTATACCTTTCTCTTCAAGT 544
QY 565 CGTTGGCTTCTATCGGATTTTCAGCTCTATCTACTTAAACGTCATAAAGTTTCTGTA 624
DB 545 CGTTGGCTTCTATCGGATTTTCAGCTCTATCTACTTAAACGTCATAAAGTTTCTGTA 604
QY 625 ATTCTACTGTATCGACCTGCAGCTGGCTGTATAGGGAGCCTGACATTTATATTC 684
DB 605 ATTCTACTGTATCGACCTGCAGCTGGCTGTATAGGGAGCCTGACATTTATATTC 664
QY 685 CCAGAACATCAGGTTAATGGCTTTTGTGATGATCAATTTTCGGGGTGGCTGAGATCAGCCAC 744

DB 665 CCAGAACATCAGGTTAATGGCTTTTGTGATGATCAATTTTCGGGGTGGCTGAGATCAGCCAC 724
QY 745 TTCTTCCCGGATAAACGAGACCGGCAACACTGGCCATATCGGTGTCTATCGGCCAGCT 804
DB 725 TTCTTCCCGGATAAACGAGACCGGCAACACTGGCCATATCGGTGTCTATCGGCCAGCT 784
QY 805 TTCTATCCCGGATAGCACCCCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGC 864
DB 785 TTCTATCCCGGATAGCACCCCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGC 844
QY 865 TGCACTGGCCAGGGGGATCAACATCCCTCGCCGGGGGTGTCAATAATATCACTCTGTAC 924
DB 845 TGCACTGGCCAGGGGGATCAACATCCCTCGCCGGGGGTGTCAATAATATCACTCTGTAC 904
QY 925 ATCCACAAAACAGACGATAAAGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCATTC 984
DB 905 ATCCACAAAACAGACGATAAAGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCATTC 964
QY 985 ACCAGTCCCTGTTCTCGTCAAGCAAAAGAGCGGTTCAATTTCAATAAACCGGGCGACCTCAG 1044
DB 965 ACCAGTCCCTGTTCTCGTCAAGCAAAAGAGCGGTTCAATTTCAATAAACCGGGCGACCTCAG 1024
QY 1045 CCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGCAACGACGACGCGCTTCATCT 1104
DB 1025 CCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCGGCAACGACGACGCGCTTCATCT 1084
QY 1105 GCATGGTGTGCTTACCAGACCGGAGATATGACATCATATATGCTTGAGCAACTGATA 1164
DB 1085 GCATGGTGTGCTTACCAGACCGGAGATATGACATCATATATGCTTGAGCAACTGATA 1144
QY 1165 GCTGTGCTGTCAACTGTCACTGTAAATACGCTGTTCATAGCACACCTCTTTTGGACATA 1224
DB 1145 GCTGTGCTGTCAACTGTCACTGTAAATACGCTGTTCATAGCACACCTCTTTTGGACATA 1204
QY 1225 CTTCCGGTA 1233
DB 1205 CTTCCGGTA 1213
RESULT 6
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
AC ABZ58767;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR201 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
FN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX

BS Disclosure; Fig 26B-C; 273pp; English.

XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
XX represents the destination plasmid pDONR201 nucleotide sequence
SQ

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.8%; Score 1207.4; DB 7; Length 4470;

Best Local Similarity 99.9%; Pred. No. 1.6e-164;

Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	25	AGCTAGCATGATCTCGGCGCCCAAAATGATTTTATTTGACATGATGACCTGTT	84
DB	5	ACGCTAGCATGATCTCGGCGCCCAAAATGATTTTATTTGACATGATGACCTGTT	64
QY	85	CGTTGCAACAAATGATGAGCAATGCTTTTATATGACCACTTTGTACAAAAGCTG	144
DB	65	CGTTGCAACAAATGATGAGCAATGCTTTTATATGACCACTTTGTACAAAAGCTG	124
QY	145	AACGAGAAACGTAATGATATATAATATCAATATATTAATTTAGATTTTGCATAAAAAC	204
DB	125	AACGAGAAACGTAATGATATATAATATCAATATATTAATTTAGATTTTGCATAAAAAC	184
QY	205	AGACTACATTAATCTGTAACACACACATATCCAGTCACTATGAATCACTATTAGTG	264
DB	185	AGACTACATTAATCTGTAACACACACATATCCAGTCACTATGAATCACTATTAGTG	244
QY	265	GTATTAGTGACCTGTAGTCGACGAGCCTTCCAAATGCTTCGGGTGATGCTGCCAA	324
DB	245	GTATTAGTGACCTGTAGTCGACGAGCCTTCCAAATGCTTCGGGTGATGCTGCCAA	304
QY	325	CTTAGTGACGACGAGCCTTCCAAATGCTTCGTAACGGAATCGTGTATCCAGCCTA	384
DB	305	CTTAGTGACGACGAGCCTTCCAAATGCTTCGTAACGGAATCGTGTATCCAGCCTA	364
QY	385	CTCGCTATTGCTCAATCGCTATTATATATCAATATTAATTAAGAAAGAGGTGCGA	444
DB	365	CTCGCTATTGCTCAATCGCTATTATATATCAATATTAATTAAGAAAGAGGTGCGA	424
QY	445	GCCTCTTTTGTGTGACAAATAAAACATCTACCTATTTCATATACGCTAGTGCATAG	504
DB	425	GCCTCTTTTGTGTGACAAATAAAACATCTACCTATTTCATATACGCTAGTGCATAG	484
QY	505	TGCTGAATCATCTGCATCAAGACAAATTCAGAACCTTTATCTTTCTCTTCAAGT	564
DB	485	TCCTGAAATCATCTGCATCAAGACAAATTCAGAACCTTTATCTTTCTCTTCAAGT	544
QY	565	CGTTGGCTTCACTGGATTTTTCAGCTCTATCTACTTACCAAGTATAGAGTCTCTGTA	624
DB	545	CGTTGGCTTCACTGGATTTTTCAGCTCTATCTACTTACCAAGTATAGAGTCTCTGTA	604
QY	625	ATTCTACTGTATCGACCTGAGCTGGCTGTGTATAGGGAGCCTGACATTTATATCC	684
DB	605	ATTCTACTGTATCGACCTGAGCTGGCTGTGTATAGGGAGCCTGACATTTATATCC	664
QY	685	CCAGAACATCAGTTAATCGGCTTTTGTATGATCAATTTCCGGGTGCTAGATCAGCCAC	744
DB	665	CCAGAACATCAGTTAATCGGCTTTTGTATGATCAATTTCCGGGTGCTAGATCAGCCAC	724
QY	745	TTCTTCCCGATAACGAGACCGGACACTGGCCATATCGGTGGTCAATCGGCCAGCT	804
DB	725	TTCTTCCCGATAACGAGACCGGACACTGGCCATATCGGTGGTCAATCGGCCAGCT	784

QY	805	TTATCCCGGATATGACACCAACCGGGTAAAGTTCAAGGAGACTTTATCTGACAGCAGC	864
DB	785	TTATCCCGGATATGACACCAACCGGGTAAAGTTCAAGGAGACTTTATCTGACAGCAGC	844
QY	865	TGCACTGCGCAGGGGATCAACATCCGTCGCGCGGGGTGTCATAATATCACTCTGTAC	924
DB	845	TGCACTGCGCAGGGGATCAACATCCGTCGCGCGGGGTGTCATAATATCACTCTGTAC	904
QY	925	ATCCACAAACAGAGATAAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTC	984
DB	905	ATCCACAAACAGAGATAAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTC	964
QY	985	ACAGTCCCTCTCTCTGTCAGCAAAAGAGCGTTTCATTTCAATAACCGGCGACCTCAG	1044
DB	965	ACAGTCCCTCTCTCTGTCAGCAAAAGAGCGTTTCATTTCAATAACCGGCGACCTCAG	1024
QY	1045	CCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGGCAGCAGCAGCGGCTTCATCT	1104
DB	1025	CCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGGCAGCAGCAGCGGCTTCATCT	1084
QY	1105	GCATGGTTGCTTACACAGACCGGAGATATGACATATATATGCTTTGAGCAACTGATA	1164
DB	1085	GCATGGTTGCTTACACAGACCGGAGATATGACATATATATGCTTTGAGCAACTGATA	1144
QY	1165	GCTGTCGCTGTCACACTGTCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA	1224
DB	1145	GCTGTCGCTGTCACACTGTCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA	1204
QY	1225	CTTCGGGTA 1233	
DB	1205	CTTCGGGTA 1213	

RESULT 7
ADA50329
ID ADA50329 standard; DNA; 4892 BP.
XX
AC ADA50329;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid vector pMK2010 DNA sequence.
XX
KW site-specific recombination; array construction; reporter gene fusion;
KW mutagenesis; protein production; protein characterisation;
KW plasmid pMK2010; ds.
XX
OS Synthetic.
XX
PN WO2003064623-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003176.
XX
PR 31-JAN-2002; 2002US-0354063P.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Kahn ML, House BL, Mortimer MW;
XX
DR WPI; 2003-679497/64.
XX
PT Moving an insert nucleic acid between vectors using site-specific
PT recombination in vivo, useful for studying the biology of the organism,
PT including array construction, reporter gene fusions, mutagenesis and
PT protein production.
XX
PS Claim 41; Page 47-51; 52pp; English.
XX
CC The invention comprises a method for moving an insert nucleic acid
CC molecule between vectors, the method involves moving an insert nucleic
CC acid from one vector to another using site-specific recombination. The

CC method of the invention is useful for studying the biology of an
CC organism, including array construction, reporter gene fusions,
CC mutagenesis, protein production and characterisation. The present DNA
CC sequence represents the plasmid vector pMK2010 of the invention.

XX SQ Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;

Query Match 24.8%; Score 1207.4; DB 8; Length 4892;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 25 AGCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACATGATGACTGTT 84
DB 5 AGCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACATGATGACTGTT 64
QY 85 CGTTGCAACAAATGATGAGCAATGCTTTTATATGCAACTTTGTCACAAAAGCTG 144
DB 65 CGTTGCAACAAATGATGAGCAATGCTTTTATATGCAACTTTGTCACAAAAGCTG 124
QY 145 AAGCGAAACGTAATAATGATATATAATATCAATATATAATAGATTTTGCATAAAAAC 204
DB 125 AAGCGAAACGTAATAATGATATATAATATCAATATATAATAGATTTTGCATAAAAAC 184
QY 205 AGACTACATAATGATGTAATAACACACATATCCGTCACATGATCACTACTTAGATG 264
DB 185 AGACTACATAATGATGTAATAACACACATATCCGTCACATGATCACTACTTAGATG 244
QY 265 GTATTAGTGAACCTGTAGTCGACCGCAGCCTTCCAAATGTTCTCGGGTGATGTCGCAA 324
DB 245 GTATTAGTGAACCTGTAGTCGACCGCAGCCTTCCAAATGTTCTCGGGTGATGTCGCAA 304
QY 325 CTTAGTCGACCGCAGCCTTCCAAATGTTCTCGGGTGATGTCGCAA 384
DB 305 CTTAGTCGACCGCAGCCTTCCAAATGTTCTCGGGTGATGTCGCAA 364
QY 385 CTCGCTATTGCTCAATGCGCTTAAATATATAAAGCAATATAGAAAGAGTGCGA 444
DB 365 CTCGCTATTGCTCAATGCGCTTAAATATATAAAGCAATATAGAAAGAGTGCGA 424
QY 445 GCCTCTTTTGTGTGACAAAATAAAACATCTACTTATATACGCTAGTGTCAATAG 504
DB 425 GCCTCTTTTGTGTGACAAAATAAAACATCTACTTATATACGCTAGTGTCAATAG 484
QY 505 TCCTGAAATCATCTGCAATCAAGACAATTCACAACTCTTATCTTTCTCTTACAAGT 564
DB 485 TCCTGAAATCATCTGCAATCAAGACAATTCACAACTCTTATCTTTCTCTTACAAGT 544
QY 565 CGTTCGGCTTCACTCTGGATTTTCAGCCTCTACTTACTTAACGTCATAGTATCTGTA 624
DB 545 CGTTCGGCTTCACTCTGGATTTTCAGCCTCTACTTACTTAACGTCATAGTATCTGTA 604
QY 625 ATTCTACTGTATCGACCTGACACTGGCTGTGTATAGGGAGCCTGACATTTATTTCC 684
DB 605 ATTCTACTGTATCGACCTGACACTGGCTGTGTATAGGGAGCCTGACATTTATTTCC 664
QY 685 CCAGACATCAGTTTAAAGCGCTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCAC 744
DB 665 CCAGAACATCAGTTTAAAGCGCTTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCAC 724
QY 745 TTCTTCCCGGATPACCGGAGACCGGACACTGCGCCATATCGGTGTCATCATGCGCCAGCT 804
DB 725 TTCTTCCCGGATPACCGGAGACCGGACACTGCGCCATATCGGTGTCATCATGCGCCAGCT 784
QY 805 TTCATCCCGGATPACCGACCGGTCAGGTCAGGAGACTTTTATCTGACAGCAGACG 864
DB 785 TTCATCCCGGATPACCGACCGGTCAGGTCAGGAGACTTTTATCTGACAGCAGACG 844
QY 865 TGCATGCGCGGAGATCACCATCGTCGCGCGCGGTGTCAATAATATCACTCTGTAC 924
DB 845 TGCATGCGCGGAGATCACCATCGTCGCGCGCGGTGTCAATAATATCACTCTGTAC 904
QY 925 ATCCACAAACAGACGATACGCTCTCTTTTATAGGTGTAACCTTAAACGTCATTTC 984
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RESULT 8

AAC55525

ID AAC55525 standard; DNA; 4939 BP.

XX AC AAC55525;

XX DT 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR205 nucleotide sequence.

XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

XX KW mutant; recombinational cloning; entry vector; destination vector;

XX KW gene product targeting; fusion tag cleavage; ds.

XX OS Bacteriophage lambda.

XX OS Synthetic.

XX FN WO2000052027-A1.

XX XX 08-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US005432.

XX PR 02-MAR-1999; 99US-0122389P.

XX PR 23-MAR-1999; 99US-0126049P.

XX PR 28-MAY-1999; 99US-0136744P.

XX XX (LIFE-) LIFE TECHNOLOGIES INC.

XX PA Hartley JL, Brasch MA, Temple GF, Chao D;

XX PI WPI; 2000-543948/49.

XX DR WPI; 2000-543948/49.

XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides.

XX PS Example 10; Fig 53; 459pp; English.

XX CC The present invention describes isolated nucleic acid molecules (I)
encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
nucleotide sequence. Also described are: (1) an isolated nucleic acid
molecule (II) comprising one or more att recombination sites comprising
at least one mutation in its core region that increases the specificity
of interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule

at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

Query Match 24.8%; Score 1207.4; DB 3; Length 5584;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGCTAGCATGATCTCGGGCCCAAAATGAATTTATTTGACTGATAGTGAAGCTGT 84
DB 5580 AGCTAGCATGATCTCGGGCCCAAAATGAATTTATTTGACTGATAGTGAAGCTGT 5521

QY 85 CGTTGCAACAATGATGAGCAATGCTTTTATATGCGCACTTTGTAACAAAAAGCTG 144
DB 5520 CGTTGCAACAATGATGAGCAATGCTTTTATATGCGCACTTTGTAACAAAAAGCTG 5461

QY 145 AACGAGAAACGTAATAATGATATATCAATATATTAATTTAGATTTTGCATATAAAAC 204
DB 5460 AACGAGAAACGTAATAATGATATATCAATATATTAATTTAGATTTTGCATATAAAAC 5401

QY 205 AGACTACATATCTGTAATAACACACATATCCAGTCACTATGAATCACTACTTAGATG 264
DB 5400 AGACTACATATCTGTAATAACACACATATCCAGTCACTATGAATCACTACTTAGATG 5341

QY 265 GTATTAGTACCTGTAGTCGACGAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 324
DB 5340 GTATTAGTACCTGTAGTCGACGAGCGCTTCCAAATGTTCTCGGGTGATGCTGCCAA 5281

QY 325 CTATTGCGACGACAGCGCTTCCAAATGTTCTTCAACGGAATCGTGTATCCAGCCTA 384
DB 5280 CTATTGCGACGACAGCGCTTCCAAATGTTCTTCAACGGAATCGTGTATCCAGCCTA 5221

QY 385 CTCGCTATTGCTCAATGCGGTATTTAAATCATATAAAGAAATAAGAAAGAGGTGCGA 444
DB 5220 CTCGCTATTGCTCAATGCGGTATTTAAATCATATAAAGAAATAAGAAAGAGGTGCGA 5161

QY 445 GCCTCTTTTGTGTCACAAATAAACAATCTACTATTATATACGCTAGTGTATAG 504
DB 5160 GCCTCTTTTGTGTCACAAATAAACAATCTACTATTATATACGCTAGTGTATAG 5101

QY 505 TCCTGAAATCATCTGCATCAAGAACAAATTCACAACTCTTATATCTTTCTCTTCAAGT 564
DB 5100 TCCTGAAATCATCTGCATCAAGAACAAATTCACAACTCTTATATCTTTCTCTTCAAGT 5041

QY 565 CGTTGCGCTTCACTGGATTTTACGCTCTATCTACTTACTTAAACGTTAATAAGTTCTGTG 624
DB 5040 CGTTGCGCTTCACTGGATTTTACGCTCTATCTACTTACTTAAACGTTAATAAGTTCTGTG 4981

QY 625 ATTTCTACTGTATCGACCTGACGCTGCTGTGTATAGGGAGCTGACATTTATATCC 684
DB 4980 ATTTCTACTGTATCGACCTGACGCTGCTGTGTATAGGGAGCTGACATTTATATCC 4921

QY 685 CCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGCGTGTGCTGAGATCAGCCAC 744
DB 4920 CCAGAACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGCGTGTGCTGAGATCAGCCAC 4861

QY 745 TTCTTCCCGATACGAGACGCGCACACTGCGCATATCGGTGTCATCATCGCCAGCT 804
DB 4860 TTCTTCCCGATACGAGACGCGCACACTGCGCATATCGGTGTCATCATCGCCAGCT 4801

QY 805 TTCACTCCCGATATGACACACCGGTAAGTTTACGGGAGACTTTTATCTGACAGCAGCG 864
DB 4800 TTCACTCCCGATATGACACACCGGTAAGTTTACGGGAGACTTTTATCTGACAGCAGCG 4741

QY 865 TGCATCGCGAGGGGATACCATCCGTCGCCCGGCGGTGTCATAATATCACTCTGTAC 924
DB 4740 TGCATCGCGAGGGGATACCATCCGTCGCCCGGCGGTGTCATAATATCACTCTGTAC 4681

QY 925 ATCCAAACAGACGATTAACGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTC 984
DB 4680 ATCCAAACAGACGATTAACGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTC 4621

QY 985 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCGCTTCATTTCAATAAACCGGGCGACCTCAG 1044
DB 4620 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCGCTTCATTTCAATAAACCGGGCGACCTCAG 4561

QY 1045 CCATCCCTTCTGATTTTCCGCTTTCAGCGTTCCGACGAGCAGCAGCGGCTTCATTTCT 1104
DB 4560 CCATCCCTTCTGATTTTCCGCTTTCAGCGTTCCGACGAGCAGCAGCGGCTTCATTTCT 4501

QY 1105 GCATGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCTTGTGACCACTGATA 1164
DB 4500 GCATGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCTTGTGACCACTGATA 4441

QY 1165 GCTGTCGTGTCACCTGTCATCTGTAATACGCTGTCTTATAGCACAACCTCTTTTGTGACATA 1224
DB 4440 GCTGTCGTGTCACCTGTCATCTGTAATACGCTGTCTTATAGCACAACCTCTTTTGTGACATA 4381

QY 1225 CTTGCGGTA 1233
DB 4380 CTTGCGGTA 4372

RESULT 10
ABZ58766/c
ID ABZ58766 standard; DNA; 5584 BP.

XX AC ABZ58766;
DT 01-MAY-2003 (first entry)
XX DE Donor plasmid pDONR207 nucleotide sequence.
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX OS Nucleic acid isolation; ds.
XX OS Synthetic.
XX PN WO200295055-A2.
XX XX 28-NOV-2002.
XX PD 21-MAY-2002; 2002WO-US015947.
XX PF 21-MAY-2001; 2001US-0291973P.
XX PR (INVI-) INVITROGEN CORP.
XX PA Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX PI WPI; 2003-129436/12.
XX DR Inserting a population of nucleic acids into a second target molecule for
XX PT selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid.
XX PS Disclosure; Fig 18B-C; 273pp; English.
XX CC The invention relates to inserting a population of nucleic acids into a

CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the donor plasmid pDONR207 nucleotide sequence
XX
SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.8%; Score 1207.4; DB 7; Length 5584;
Best Local Similarity 99.9%; Pred. No. 1.6e-164;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGCTAGCATGATCTCGGCCCCCAATAATGATTTTATTTTACATGATGACCTGTT 84
DB 5580 ACCTAGCATGATCTCGGCCCCCAATAATGATTTTATTTTACATGATGACCTGTT 5521

QY 85 CGTTGCAACAAATGATGACGAATGCTTTTATATAATGCCAACTTTGTACAAAAAGCTG 144
DB 5520 CGTTGCAACAAATGATGACGAATGCTTTTATATAATGCCAACTTTGTACAAAAAGCTG 5461

QY 145 AACGGAACCGTAAATGATATAATATCAATATATTAATTAATGATTTTGCATAAAAAC 204
DB 5460 AACGGAACCGTAAATGATATAATATCAATATATTAATTAATGATTTTGCATAAAAAC 5401

QY 205 AGACTACATAATCTCTAAAAACACACATATCCAGTCACATGAATCAACTACTTAGATG 264
DB 5400 AGACTACATAATCTCTAAAAACACACATATCCAGTCACATGAATCAACTACTTAGATG 5341

QY 265 GTATTAGTACCTGTAGTCAGCGACAGCGCTCCAAATGTTCTCGGGTGATGCTGCCAA 324
DB 5340 GTATTAGTACCTGTAGTCAGCGACAGCGCTCCAAATGTTCTCGGGTGATGCTGCCAA 5281

QY 325 CTTAGTCGACGACGCTTCCAAATGTTCTCTCAAAACGGAATCGTGTATCCAGCCTA 384
DB 5280 CTTAGTCGACGACGCTTCCAAATGTTCTCTCAAAACGGAATCGTGTATCCAGCCTA 5221

QY 385 CTGCTATTGTTCTCAATCGGTATTAAATCATATAAAGAAATAAGAAAAAGAGGTGCGA 444
DB 5220 CTGCTATTGTTCTCAATCGGTATTAAATCATATAAAGAAATAAGAAAAAGAGGTGCGA 5161

QY 445 GCCTCTTTTGTGACAAATATAAACAATCTACCTATTATATACGCTAGTGATAG 504
DB 5160 GCCTCTTTTGTGACAAATATAAACAATCTACCTATTATATACGCTAGTGATAG 5101

QY 505 TCTGAAAAATCATCTGCATCAAGAACAAATTTCAAACTCTTATACATTTTCTCTTACAAGT 564
DB 5100 TCTGAAAAATCATCTGCATCAAGAACAAATTTCAAACTCTTATACATTTTCTCTTACAAGT 5041

QY 565 CGTTCCGCTTCATCTGGATTTTCAGCTCTATCTTACTTAACGATGATAAGTTTCTGTA 624
DB 5040 CGTTCCGCTTCATCTGGATTTTTCAGCTCTATCTTACTTAACGATGATAAGTTTCTGTA 4981

QY 625 ATTCTTACTGTATCGACCTGACAGCTGGCTGTGTATAGGAGCGCTGACATTTATATCC 684
DB 4980 ATTCTTACTGTATCGACCTGACAGCTGGCTGTGTATAGGAGCGCTGACATTTATATCC 4921

QY 685 CCAGAACATCAGGTTAATGCGGTTTTTGTATGTCATTTTTCGCGTGGCTGAGATCAGCCAC 744
DB 4920 CCAGAACATCAGGTTAATGCGGTTTTTGTATGTCATTTTTCGCGTGGCTGAGATCAGCCAC 4861

QY 745 TTCTTCCCGATACCGGACCGGACACTGGCCATATCGTGGTCAATCATGCGCCAGCT 804
DB 4860 TTCTTCCCGATACCGGACCGGACACTGGCCATATCGTGGTCAATCATGCGCCAGCT 4801

QY 805 TTCTTCCCGATATGCACCAACCGGTTAAAGTTTCCAGCGGACGCTTTATCTGACAGACG 864
DB 4800 TTCTTCCCGATATGCACCAACCGGTTAAAGTTTCCAGCGGACGCTTTATCTGACAGACG 4741

QY 865 TGCATCGCCAGGGGGATATCAATCGTCGCCCGGGCGTGTCAATAATATCACTCTGTAC 924
DB 4740 TGCATCGCCAGGGGGATATCAATCGTCGCCCGGGCGTGTCAATAATATCACTCTGTAC 4681

QY 925 ATCCCAAAACAGACATAAAGCGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTTC 984
DB 4680 ATCCCAAAACAGACATAAAGCGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTTC 4621

QY 985 ACCAGTCCCTGTTCGTCAGCAAAAGACCGCTTCATTTCAATTAACCGGGCGACCTCAG 1044
DB 4620 ACCAGTCCCTGTTCGTCAGCAAAAGACCGCTTCATTTCAATTAACCGGGCGACCTCAG 4561

QY 1045 CCATCCCTCTCTGATTTTCCGCTTTCAGCGTTCGGCAGCAGCAGCGGCTTCATTTCT 1104
DB 4560 CCATCCCTCTCTGATTTTCCGCTTTCAGCGTTCGGCAGCAGCAGCGGCTTCATTTCT 4501

QY 1105 GCATGTTGTGCTTACCAGACCGGAGATTTGACATCATATATATGCTTTGAGCACTGATA 1164
DB 4500 GCATGTTGTGCTTACCAGACCGGAGATTTGACATCATATATATGCTTTGAGCACTGATA 4441

QY 1165 GCTGTCGTGTCAACTGTCACGTGAATACGCTTTCATAGCACACACCTCTTTTGTGACATA 1224
DB 4440 GCTGTCGTGTCAACTGTCACGTGAATACGCTTTCATAGCACACACCTCTTTTGTGACATA 4381

QY 1225 CTTCCGGTA 1233
DB 4380 CTTCCGGTA 4372

RESULT 11
ABZ58768
ID ABZ58768 standard; DNA; 4428 BP.
XX
AC ABZ58768;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 27B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to

CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212 nucleotide sequence
XX
SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 24.7%; Score 1201; DB 7; Length 4428;
Best Local Similarity 99.6%; Pred. No. 1.3e-163;
Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 25 AGGCTAGCATGATCTCGGGCCCCCAATAATGATTTTATTTGACGTAGTGCACCTGTT 84
DB 842 ACGCTAGCATGATCTCGGGCCCCCAATAATGATTTTATTTGACGTAGTGCACCTGTT 901
QY 85 CGTTGCAACAATGATGAGCAATGCTTTTATATGCAACTTTTGTACAAAAAGCTG 144
DB 902 CGTTGCAACAATGATGAGCAATGCTTTTATATGCAACTTTTGTACAAAAAGCTG 961
QY 145 AAGCGAAGACGTAAATGATATATAATATCAATATATTAATAGATTTTGCATAAAAAC 204
DB 962 ATATCGAAGACGTAAATGATATATAATATCAATATATTAATAGATTTTGCATAAAAAC 1021
QY 205 AGACTACATAATCTGTAAACAACAATATCCAGTCACTATGAAATCAACTACTTAGATG 264
DB 1022 AGACTACATAATCTGTAAACAACAATATCCAGTCACTATGAAATCAACTACTTAGATG 1081
QY 265 GTATTAGTACCTGTAGTGCACCGACAGCGTCCCAATGTTCTTCGGGTGATGTCGCAA 324
DB 1082 GTATTAGTACCTGTAGTGCACCGACAGCGTCCCAATGTTCTTCGGGTGATGTCGCAA 1141
QY 325 CTTAGTGCACCGACAGCGTCCCAATGTTCTTCCAAGGAATCGTGTATCCAGCCCTA 384
DB 1142 CTTAGTGCACCGACAGCGTCCCAATGTTCTTCCAAGGAATCGTGTATCCAGCCCTA 1201
QY 385 CTGCTATTGTTCTCAATCGGTATTAAATCATPAAAAAGAAATPAGAAAAAGAGGTGCGA 444
DB 1202 CTGCTATTGTTCTCAATCGGTATTAAATCATPAAAAAGAAATPAGAAAAAGAGGTGCGA 1261
QY 445 GCTCTTTTGTGTCAGAAAAATAAACAATCTACCTATTTCATATACGTGTGTCATAG 504
DB 1262 GCTCTTTTGTGTCAGAAAAATAAACAATCTACCTATTTCATATACGTGTGTCATAG 1321
QY 505 TCCTGAAATCATCTGCATCAAGAAACAATTTTCAAACTCTTTATCTTTCTTTTCAAGT 564
DB 1322 TCCTGAAATCATCTGCATCAAGAAACAATTTTCAAACTCTTTATCTTTCTTTCAAGT 1381
QY 565 CGTTCCGCTTCATCTGGATTTTTCAGCCTCTATCTTACTTAACGCGATAAAGTTTCTGTA 624
DB 1382 CGTTCCGCTTCATCTGGATTTTTCAGCCTCTATCTTACTTAACGCGATAAAGTTTCTGTA 1441
QY 625 ATTCTACTGTATCGACCTGCAGACTGGCTGTGTATAGGAGGCGCTGACATTATATTC 684
DB 1442 ATTCTACTGTATCGACCTGCAGACTGGCTGTGTATAGGAGGCGCTGACATTATATTC 1501
QY 685 CCAGAACATCAGGTTAATGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCAC 744
DB 1502 CCAGAACATCAGGTTAATGCGTTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCAC 1561
QY 745 TTCTTCCCGATACCGAGACCGGCACTGGCCATATCGTGGTGTATATGCGCCAGCT 804
DB 1562 TTCTTCCCGATACCGAGACCGGCACTGGCCATATCGTGGTGTATATGCGCCAGCT 1621
QY 805 TTCTTCCCGATATGCACACCGGGTAAAGTTTCCAGGAGACTTTTCTGACAGCAGCG 864
DB 1622 TTCTTCCCGATATGCACACCGGGTAAAGTTTCCAGGAGACTTTTCTGACAGCAGCG 1681
QY 865 TGCACTGGCCAGGGGATACCATCCGTCGTCGCGGGCGTGTCAATATATCACTCTGTAC 924
DB 1682 TGCACTGGCCAGGGGATACCATCCGTCGTCGCGGGCGTGTCAATATATCACTCTGTAC 1741
QY 925 ATCCAAAAACAGAGTAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTC 984

DB 1742 ATCCAAACACAGACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCATTTC 1801
QY 985 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCGGGGAGCTCAG 1044
DB 1802 ACCAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCATTTCAATAAACCGGGGAGCTCAG 1861
QY 1045 CCATCCCTTCCGTGATTTTCCGCTTTCCAGCGTTCCGACGACGAGCGGGCTTCAATCT 1104
DB 1862 CCATCCCTTCCGTGATTTTCCGCTTTCCAGCGTTCCGACGACGAGCGGGCTTCAATCT 1921
QY 1105 GCATGTTGTGTTTACCAGACCGGAGATATTGACATCATATATATGCTTTGAGCAACTGATA 1164
DB 1922 GCATGTTGTGTTTACCAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATA 1981
QY 1165 GCTGTCGTGTCACCTGTCACCTGTAATAGCTGCTTCATAGCACACCTCTTTTGCACATA 1224
DB 1982 GCTGTCGTGTCACCTGTCACCTGTAATAGCTGCTTCATAGCACACCTCTTTTGCACATA 2041
QY 1225 CTTCGGGTA 1233
DB 2042 CTTCGGGTA 2050

RESULT 12
ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.
XX
AC ABZ58769;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212(F) nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 28B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence
XX
SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match		24.6%;	Score 1194.6;	DB 7;	Length 4627;	
Best Local Similarity		99.7%;	Pred. No. 1.1e-162;			
Matches 1197;		Conservative	0;	Mismatches	4;	Indels
					0;	Gaps
					0;	
QY	33	ATGGATCTCGGGCCCAAAATATGATTTTATTTTGAATGATAGTACCTGTTGCGTTCGAA	92			
Db	1	AUGGATCTCGGGCCCAAAATATGATTTTATTTTGAATGATAGTACCTGTTGCGTTCGAA	60			
QY	93	CAAAATGATGAGCAATGCTTTTATTAATGCGCAATTTGTACAAAAAAGCTGAACAGAA	152			
Db	61	CAAAATGATGAGCAATGCTTTTATTAATGCGCAATTTGTACAAAAAAGCTGATATCGAA	120			
QY	153	ACGTAAATGATATTAATATCAATATATTAATATGATTTTGCATAAAAACAGACTACA	212			
Db	121	ACGTAAATGATATTAATATCAATATATTAATATGATTTTGCATAAAAACAGACTACA	180			
QY	213	TAATACTGTAAAAACACAAATATCCAGTCACTATGAATCAACTACTAGATGGTATTAGT	272			
Db	181	TAATACTGTAAAAACACAAATATCCAGTCACTATGAATCAACTACTAGATGGTATTAGT	240			
QY	273	GACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATTAGTCG	332			
Db	241	GACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATTAGTCG	300			
QY	333	ACCGACAGCCTTCCAAATGTTCTTCAAACGGAATCGTCGATCCAGGCTACTCGCTAT	392			
Db	301	ACCGACAGCCTTCCAAATGTTCTTCAAACGGAATCGTCGATCCAGGCTACTCGCTAT	360			
QY	393	TGTCCTCAATGCGGTATTAATATCAATAAAAAGAAATTAAGAAAAAGAGGTGCGAGCCTCTTT	452			
Db	361	TGTCCTCAATGCGGTATTAATATCAATAAAAAGAAATTAAGAAAAAGAGGTGCGAGCCTCTTT	420			
QY	453	TTTGTGTGACAAATAAAAACATCTACCTATTCATATAGCTAGTGTATAGTCCTGAAA	512			
Db	421	TTTGTGTGACAAATAAAAACATCTACCTATTCATATAGCTAGTGTATAGTCCTGAAA	480			
QY	513	ATCATCTGCATCAAGAACAAATTCACAACTCTTATATCTTTCTTCTTACAAAGTCTGCGC	572			
Db	481	ATCATCTGCATCAAGAACAAATTCACAACTCTTATATCTTTCTTCTTACAAAGTCTGCGC	540			
QY	573	TTCATCTGGATTTTCAGCCTCTATATCTTAAACGTGATAAAGTTTCTGTATTTCTAC	632			
Db	541	TTCATCTGGATTTTCAGCCTCTATATCTTAAACGTGATAAAGTTTCTGTATTTCTAC	600			
QY	633	TGATCTGACCTGCAGCTGCTGTATAGGAGCGCTGACATTTATATCCCAAGAA	692			
Db	601	TGATCTGACCTGCAGCTGCTGTATAGGAGCGCTGACATTTATATCCCAAGAA	660			
QY	693	TCAGGTTAATGCGGTTTTTGAATCTCATTTTCGGCGTGGCTGAGATCAGGCACCTTCTCC	752			
Db	661	TCAGGTTAATGCGGTTTTTGAATCTCATTTTCGGCGTGGCTGAGATCAGGCACCTTCTCC	720			
QY	753	CGATACGGAGACCGGACACTGGCCATATCGGTGTCTATCGTCGCCAGCTTTTCATCC	812			
Db	721	CGATACGGAGACCGGACACTGGCCATATCGGTGTCTATCGTCGCCAGCTTTTCATCC	780			
QY	813	CGATATGCACCCCGGTAAAGTTTCAGGAGACTTTTCTGACAGACAGCGCACTGG	872			
Db	781	CGATATGCACCCCGGTAAAGTTTCAGGAGACTTTTCTGACAGACAGCGCACTGG	840			
QY	873	CCAGGGGGATCACCATCCGTCGCCCGCGGTGTCAATAATATCACTCTGTACATCCACAA	932			
Db	841	CCAGGGGGATCACCATCCGTCGCCCGCGGTGTCAATAATATCACTCTGTACATCCACAA	900			
QY	933	ACAGACGATACGGCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTTACAGTCC	992			
Db	901	ACAGACGATACGGCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTTACAGTCC	960			
QY	993	CTGTTCTGTCGACAAAAGACCGTTCAATTAATAACCGGCGACCTCAGCCATCCCT	1052			
Db	961	CTGTTCTGTCGACAAAAGACCGTTCAATTAATAACCGGCGACCTCAGCCATCCCT	1020			
QY	1053	TCCTGATTTTCCGCTTTCCAGCGTTTCGGCAGCAGACGCGGCTTCATTCTGTCATGGTT	1112			
Query Match		24.6%;	Score 1194.6;	DB 7;	Length 4627;	
Best Local Similarity		99.7%;	Pred. No. 1.1e-162;			
Matches 1197;		Conservative	0;	Mismatches	4;	Indels
					0;	Gaps
					0;	
QY	33	ATGGATCTCGGGCCCAAAATATGATTTTATTTTGAATGATAGTACCTGTTGCGTTCGAA	92			
Db	1	ATGGATCTCGGGCCCAAAATATGATTTTATTTTGAATGATAGTACCTGTTGCGTTCGAA	60			
QY	1021	TCCTGATTTTCCGCTTTCCAGGTTTCGGCACGACGACGCGGCTTCATTTCTGATGGTT	1080			
Db	1113	GTGCTTACAGACCGGAGATATTGACATATATATGCTTGGAGCAACTGATAGCTGTGCG	1172			
QY	1081	GTGCTTACAGACCGGAGATATTGACATATATATGCTTGGAGCAACTGATAGCTGTGCG	1140			
Db	1173	TGTCAACTGTCACTGTAATAGCTCTTTCATAGCAACACTCTTTTGTACATACCTTCGGGT	1232			
QY	1141	TGTCAACTGTCACTGTAATAGCTCTTTCATAGCAACACTCTTTTGTACATACCTTCGGGT	1200			
Db	1233	A 1233				
Db	1201	A 1201				
RESULT 13						
ABZ58770						
ID	ABZ58770	standard; DNA; 4627 BP.				
XX	AC	ABZ58770;				
AC	XX					
DT	01-MAY-2003	(first entry)				
XX	DE	Destination plasmid pDONR212(R) nucleotide sequence.				
XX	XX	Nucleic acid insertion; recombination; nucleic acid selection;				
KW	XX	nucleic acid isolation; ds.				
OS	XX	Synthetic.				
XX	XX	WO200295055-A2.				
PN	XX	28-NOV-2002.				
XX	XX	21-MAY-2002; 2002WO-US015947.				
PF	XX	21-MAY-2001; 2001US-0291973P.				
PR	XX	(INVI-) INVITROGEN CORP.				
PA	XX	Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;				
PI	XX	WPI; 2003-129436/12.				
XX	XX	Inserting a population of nucleic acids into a second target molecule for				
PT	XX	selecting and isolating nucleic acid molecules by mixing the second				
PT	XX	population of nucleic acid with a second target nucleic acid.				
XX	XX	Disclosure; Fig 29B-C; 273pp; English.				
BS	XX	The invention relates to inserting a population of nucleic acids into a				
CC	XX	second target molecule. The method involves (a) mixing a first population				
CC	XX	of nucleic acid comprising one or more recombination sites with a target				
CC	XX	nucleic acid; (b) causing some or all of the nucleic acid molecules of				
CC	XX	the first population to recombine with the first target nucleic acid				
CC	XX	molecules to form a second population; (c) mixing the second population				
CC	XX	of nucleic acid with a second target nucleic acid; and (d) causing some				
CC	XX	or all of the nucleic acid molecules of the second population to				
CC	XX	recombine with some or all of the second target nucleic acid molecules to				
CC	XX	form a third population of nucleic acid. The method is useful for				
CC	XX	selecting and isolating nucleic acid molecules. The present sequence				
CC	XX	represents the destination plasmid pDONR212(R) nucleotide sequence				
XX	XX	Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;				
Query Match		24.6%;	Score 1194.6;	DB 7;	Length 4627;	
Best Local Similarity		99.7%;	Pred. No. 1.1e-162;			
Matches 1197;		Conservative	0;	Mismatches	4;	Indels
					0;	Gaps
					0;	
QY	33	ATGGATCTCGGGCCCAAAATATGATTTTATTTTGAATGATAGTACCTGTTGCGTTCGAA	92			
Db	1	ATGGATCTCGGGCCCAAAATATGATTTTATTTTGAATGATAGTACCTGTTGCGTTCGAA	60			

QY 93 CAAATTGATGAGCAATGCTTTTATTAATGCGCAACTTTGTACAAAAGAGCTGAACGAGAA 152
Db |||||
QY 61 CAAATTGATGAGCAATGCTTTTATTAATGCGCAACTTTGTACAAAAGAGCTGAATCGAA 120
Db |||||
QY 153 ACGTAAATGATATAATATCAATATATTAATTAAGATTGTCATATAAAACAGACTACA 212
Db |||||
QY 121 ACGTAAATGATATAATATCAATATATTAATTAAGATTGTCATATAAAACAGACTACA 180
QY 213 TAATACGTAAACACAAATATCCAGTCACTATGAATCACTACTATAGTATAGT 272
Db |||||
QY 181 TAATACGTAAACACAAATATCCAGTCACTATGAATCACTACTATAGTATAGT 240
Db |||||
QY 273 GACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCG 332
Db |||||
QY 241 GACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCG 300
QY 333 ACCGACAGCCTTCCAAATGTTCTTCCTCAACCGAATCGTCGATATCCAGCTACTCGCTAT 392
Db |||||
QY 301 ACCGACAGCCTTCCAAATGTTCTTCCTCAACCGAATCGTCGATATCCAGCTACTCGCTAT 360
QY 393 TGTCTCAATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGCGAGCCTCTTT 452
Db |||||
QY 361 TGTCTCAATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGCGAGCCTCTTT 420
QY 453 TTTGTGTGACAAATATAAATCTCTACCTATTATATAGCTAGTGTCTATAGTCTGAAA 512
Db |||||
QY 421 TTTGTGTGACAAATATAAATCTCTACCTATTATATAGCTAGTGTCTATAGTCTGAAA 480
QY 513 ATCATCTGATCAAGAACAAATTTCAAACTTTATATCTTTCTTTCAAGTGTCTGCG 572
Db |||||
QY 481 ATCATCTGATCAAGAACAAATTTCAAACTTTATATCTTTCTTTCAAGTGTCTGCG 540
QY 573 TTCATCTGATTTTACGCTCTATATCTTACTAAACGTGATTAAGTTCTGTATTTCTAC 632
Db |||||
QY 541 TTCATCTGATTTTACGCTCTATATCTTACTAAACGTGATTAAGTTCTGTATTTCTAC 600
QY 633 TGTATCGACCTGACAGCTGGCTGTGTATTAAGGAGCTGACATTTATATCCCCAGAA 692
Db |||||
QY 601 TGTATCGACCTGACAGCTGGCTGTGTATTAAGGAGCTGACATTTATATCCCCAGAA 660
QY 693 TCAGTTAATGGGTTTGTATGTCATTTTTCGGGTGGGTGAGATCAGGCACTTTCTCC 752
Db |||||
QY 661 TCAGTTAATGGGTTTGTATGTCATTTTTCGGGTGGGTGAGATCAGGCACTTTCTCC 720
QY 753 CGATAACGGAGACCGGCACACTGGCCATATCGTGTGTCATATGCGCCAGCTTTCTATCC 812
Db |||||
QY 721 CGATAACGGAGACCGGCACACTGGCCATATCGTGTGTCATATGCGCCAGCTTTCTATCC 780
QY 813 CGATATGCAACCGGGTAAAGTTTCAGGAGACTTTATCTGACAGCAGACGTGCACTGG 872
Db |||||
QY 781 CGATATGCAACCGGGTAAAGTTTCAGGAGACTTTATCTGACAGCAGACGTGCACTGG 840
QY 873 CCAGGGGGATCACCTCCCTGCGCGGGGTGTCATATATATCACTCTGTATCATCAAA 932
Db |||||
QY 841 CCAGGGGGATCACCTCCCTGCGCGGGGTGTCATATATATCACTCTGTATCATCAAA 900
QY 933 ACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTTACACAGTCC 992
Db |||||
QY 901 ACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTTACACAGTCC 960
QY 993 CTGTTCTCTGACAAAAGAGCGGTTTCAATTAATAAACCGGCGACCTCAGCCATCCCT 1052
Db |||||
QY 961 CTGTTCTCTGACAAAAGAGCGGTTTCAATTAATAAACCGGCGACCTCAGCCATCCCT 1020
QY 1053 TCTGATTTTCCGCTTCCAGCTTCCGACCGCAGCAGCGGCTTCATCTTCGATGTT 1112
Db |||||
QY 1021 TCTGATTTTCCGCTTCCAGCTTCCGACCGCAGCAGCGGCTTCATCTTCGATGTT 1080
QY 1113 GTGCTTACAGACCGGAGATTTGACATCATATATGCTTGTAGCACTGATAGTGTGCG 1172
Db |||||
QY 1081 GTGCTTACAGACCGGAGATTTGACATCATATATGCTTGTAGCACTGATAGTGTGCG 1140

QY 1173 TGTCAACTGTCACTGTAAATACGCTCTCATAGCACACCTCTTTTGACATACTTCGGGT 1232
Db |||||
QY 1141 TGTCAACTGTCACTGTAAATACGCTCTCATAGCACACCTCTTTTGACATACTTCGGGT 1200
Db |||||
QY 1233 A 1233
Db 1201 A 1201
RESULT 14
ABQ82143/c
ID ABQ82143 standard; DNA; 17681 BP.
XX
AC ABQ82143;
XX
DT 11-DEC-2002 (first entry)
XX
DE Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
XX
DE Chimeric nucleic acid construct; recombinational cloning; silencing;
KW recombination site; double stranded RNA; plant; ds.
XX
OS Synthetic.
XX
PN WO200259294-A1.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-AU0000073.
XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Wesley S, Waterhouse P, Helliwell C;
XX
WPI; 2002-682669/73.
XX
PT New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
PS Claim 17; Page 93-102; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention
SQ Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;
Query Match 24.1%; Score 1174.2; DB 6; Length 17681;
Best Local Similarity 59.5%; Pred. No. 8.5e-160;

Matches 2327; Conservative 0; Mismatches 1508; Indels 78; Gaps 17;

QY	122	GCACCTTTGTACAAAAGCTGAAACGAGAAACGTAAATGATATAAATATCAATATATT	181	1193	CGCTGCTTCATAGCACACCTCTTTTGTGACATACCTTCGGGTAGTG-----CGATCAACGTC	1248	
Db	16904	GACAAGTTTGTACAAAAGAGCTGAAACGAGAAACGTAAATGATATAAATATCAATATATT	16845	Db	15845	AGATGAAGCCGCAACGACTTTGTAAGAGAAAGATATAAGAGTTGTGAAATCCGATCAACGTC	15786
QY	182	AAATTAGATTTTCATATAAAACAGACTACATATCTGTAAACACACATATCCAGTC	241	QY	1249	TCATTTTCGCGAAAAGTTGGCCACGGCTTCGCGGTATCAACAGGAGACACAGGATTTAT	1308
Db	16844	AAATTAGATTTTCATATAAAACAGACTACATATCTGTAAACACACATATCCAGTC	16785	Db	15785	TCATTTTCGCGAAAAGTTGGCCACGGCTTCGCGGTATCAACAGGAGACACAGGATTTAT	15726
QY	242	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCCTCCAAA	301	QY	1309	TTATTTCTCGGAAGTGATCTTCGCTCACAGGTATTATTTCGGCGCAAGTGCGTCCGGTGA	1368
Db	16784	ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCCTCCAAA	16725	Db	15725	TTATTTCTCGGAAGTGATCTTCGCTCACAGGTATTATTTCGGCGCAAGTGCGTCCGGTGA	15666
QY	302	TGTTCTTCGGGTGATGTCGCACTTAGTCGACGAGCGACGCTTCGAAATGTTCTCTCAA	361	QY	1369	TCCTGCCAACCTTAGTCGACTACAGCTCACTAATCACTAAGTAGTAGTCACTAGTGA	1428
Db	16724	TGTTCTTCGGGTGATGTCGCACTTAGTCGACGAGCGACGCTTCGAAATGTTCTCTCAA	16665	Db	15665	TCCTGCCAACCTTAGTCGACTACAGCTCACTAATCACTAAGTAGTAGTCACTAGTGA	15606
QY	362	ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATGCGGTATTAAATCATAAAA	421	QY	1429	CTGGATATGTTGTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAA	1488
Db	16664	ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATGCGGTATTAAATCATAAAA	16605	Db	15605	CTGGATATGTTGTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAA	15546
QY	422	AGAAATAAGAAAAGAGTTCGAGCCCTCTTTTGTGTGACAAAATAAACAATCTACCT	481	QY	1489	TATATTGATATTATATCATTTTACGTTCTCGTTACGTTTCTTGTGACAAAGTTGGCAT	1548
Db	16604	AGAAATAAGAAAAGAGTTCGAGCCCTCTTTTGTGTGACAAAATAAACAATCTACCT	16545	Db	15545	TATATTGATATTATATCATTTTACGTTTCTCGTTACGTTTCTTGTGACAAAGTTGGCAT	15486
QY	482	ATTATATAGCTAGTGTCTATGCTGCTGAAATCATCTGCATCAAGACAAATTTCAAC	541	QY	1549	TATAAGAAAGCATTCGTTATCAATTTGTGTGAAACGACAGGTCACTATCAGTCAAAATA	1608
Db	16544	ATTATATAGCTAGTGTCTATGCTGCTGAAATCATCTGCATCAAGACAAAGTATGTC	16485	Db	15485	GAGGATCCAGCTTGTGAGGTAAATTTCTAGTTTTTCTCTTCAATTTCTTGTGTTAGGA	15426
QY	542	TCTTATATCTTCTCTTACAAAGTCGTTTCGGCTTCATCTGGATTTTCAGCCCTCTATCTTA	601	QY	1609	AATCATATTATTCCTCCATCCAGCTGCAGCT-----CCTCGAGGAATTCGGTACCCGACTGG	1664
Db	16484	AAAAAGAGGTGCTGATGAA--GCAGCGTATTACAGTGACAGTTGACAGCGACGCTAT	16428	Db	15425	CCCTTTCTCTTTTATTTTGTAGCTTTGATCTTTCTTTAACTGATCTATTTTTTAA	15366
QY	602	CTAAACGTGATAAAGTTCTGTGTAATTTCTACTGATACGACCTGCAGCTGGCTGTGATA	661	QY	1665	TAAGGAATAATATTTTCTTTTCTTTAGTATAAAATAGTTAAGTAGTGTAAATTA	1724
Db	16427	CAGTTGCTCAAGCATATATGATGTCAATATCTCCGCTCTGTTAAGCAACAACCATCGA	16368	Db	15365	TTGATTTGTTTATGCGGCAAAATATACATAGCTTTTAACTGATATCTGATTTACTTTTC	15306
QY	662	AGGAGCTCAGATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATCTATTT	721	QY	1725	GTATGATATAATAATATAGTTTGTATTAATCTGTGAAAAATAAATTTATAAATATATTGT	1784
Db	16367	ATGAAGCCCTGCTGTGCGTGCC---GAACGTGGAAGCGGAAATTCAGGAAGGATGG	16311	Db	15305	GTGTGCTATGATGATGATGATGATACTGCAGCGCAAGCTTATCGATTCGACCCAGCTTC	15246
QY	722	TCGCGGTGCTGAGATCAGCACCTTCTTCCCGATACAGGAGACCGGCACACTGGCCATA	781	QY	1785	TACATAAAACAATAGTAAATGTAATAAATAATGCAAGTGATGTGTAAGAGCAAGAAAT	1844
Db	16310	CTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCTTTTGTGACGAGAACAGGG-----	16257	Db	15245	CCAACTGTAATCAATCCAAATGTAAGATCAATGATAACACAAATGACATGATCTATCATG	15186
QY	782	TCGGTGGTATCATGCGCCAGCTTTCAATCCCGATATGCACACCGCGGTAAAGTTCAAG	841	QY	1845	AAAAGTTGAGAGTAACTATATTATTTTAAAGAAATTTGATCGAATGTAAGATGATATA	1904
Db	16256	ACTGGTGAATGCAATTAAGGTTTACACCTATAAAAGAGAGAGCGGTATATCGTCTGTTT	16197	Db	15185	TACCTTGTGTTTATTCATGTTTCGACTAATTCATTTAATTAATAGTCAATCCATTTAGAAGTT	15126
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Db	16196	GTGATGTACAGAGTGATATTATTGACACCGCCGGCGACGGATGTTGATCCCGCTGGCC	16137	Db	15125	AATAAACTACAAGTATTATTAGAAATTAATAAGAAATGTTGATTGAAATAATACTATA	15066
QY	902	GTGCAATAATATCATCTCTGATCATCAACAAACAGAGGATAACGGCTCTCTCTTTTATAG	961	QY	1965	TCATGATATAAA-----TACTATAGTAAAAATAAGATAAATAAATTTAAATAAT	2014
Db	16136	AGTGCACTGTGCTGCAGATAAAGTCTCCCGTGAACTTTACCCGGTGTGCTATATCGGG	16077	Db	15065	TAAAAATGATAGATCTTCGCGCTTGTATATATTAGCATTTAGATTATGTTTTTTTACATTAGA	15006
QY	962	GTGTAACCTTAACCTGCAATTTTCAAC-----AGTCCCTGTTCTCGTCAGCAAAAGGCC	1015	QY	2015	ATTTTTTTATGATTAATAGTCTTTTATTAATAATATCTATACCATTTACTTAAATATT	2074
Db	16076	GATGAAGCTGGCGATGATGACACCGATATGCCAGTGTGCGGGTCTCCGTTATCGGG	16017	Db	15005	TTACTGTTTCTATAGTTTGATATTATTGTTTACTTTTACCTTTAGCTTTTATTAATTTTGT	14946
QY	1016	GTTTATTTCATTAACACCGGCGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCCAGCG	1075	QY	2075	TAGTTTAAAGTTAAATAATTTTTTTTGAATAATTTTCAATCTGCTTGTAAATTTTCAATA	2134
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QY	1076	TTC---GGCAGCAGACGAGCGGGTTCATTTCTGATGATGTTGTGTTTACAGACCGAGAT	1132	QY	2135	ACAAAAATTTAAATAACAGCTAAAGTAAACAAATAA-----TATCAAACTAATAGAAC	2189
Db	15956	TTCTGGGGAATATAAATGTGAGGCTCCCTTTATACAG-----CCAGTCTGCAGGT	15906	Db	14885	AAATATTTAGTAATGGTATAGATATTAAATATAATAAACTATTAAATCAATAAAAAAT	14826
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QY 3877 TATGTTGTTTTACAGTATTATGAGTCTGTTTTTTATGCAAAATCTAATTTAATATAT 3936
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13137 TATGTTGTTTTACAGTATTATGAGTCTGTTTTTTATGCAAAATCTAATTTAATATAT 13078
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Search completed: May 7, 2004, 18:28:01
Job time : 1169.23 secs

ORGANISM: plasmid DNA designated as pps0212
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1785 /note= "Coding region of a
OTHER INFORMATION: truncated modified bt2 (cryIAb) gene, also designated as the
OTHER INFORMATION: cryIAb6 gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA gene 7."
FEATURE:
NAME/KEY: misc feature
LOCATION: 2396..2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
FEATURE:
NAME/KEY: misc feature
LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 3582..4407
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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NAME/KEY: misc feature
LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
US-08-232-016-23
Query Match 15.0%; Score 729.6; DB 2; Length 7566;
Best Local Similarity 98.8%; Pred. No. 5.9e-140;
Matches 735; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 4072 GATCCATGCTAGCTCTAGATCTCTGTTTAAATGAGATATCGGAGCGCCTATGATCGCAT 4131
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QY 3680 GACCCATCGCGCTCTAGATCTCTGTTTAAATGAGATATCGGAGCGCCTATGATCGCAT 3739
Db |
QY 4132 GATATTTGCTTCAATCTGTTGTGACGTTGTAATAAAGCCTGAGCATGTAGCTCAGA 4191
Db |
QY 3740 GATATTTGCTTCAATCTGTTGTGACGTTGTAATAAAGCCTGAGCATGTAGCTCAGA 3799
Db |
QY 4192 TCCTTACCGCGGTTTCGGTTTCTTCTATGAATATATCACCGTTACTATCTATTTT 4251
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QY 3800 TCCTTACCGCGGTTTCGGTTTCTTCTATGAATATATCACCGTTACTATCTATTTT 3859
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QY 3980 CAATAACAACAATATGCTTTTATATACAAATCCAAATTTTAAAAAGCGCAGAACC 4039
Db |
QY 4432 GGTCAAACTTAAAGACTGATTACATAAATCTTATTCAAAATTTTCAAAAGGCCCGGCGC 4491
Db |

Db 4040 GGTCAAACTTAAAGACTGATTACATAAATCTTATTCAAAATTTTCAAAAGGCCCGGCGC 4099
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Db 4340 TTGACAGTGACGACAAATCGTTGGCGGCTCGAGCGCGGTAAACCGACTTGTCTGCC 4399
QY 4792 GCTCAGCAGGACCTGCAGGCAATGC 4815
Db 4400 GCTCAGCAGGACCTGCAGGCAATTC 4423
RESULT 2
US-08-232-016-22
; Sequence 22, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN AARSSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7639 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: plasmid DNA designated as pUD884
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1869
OTHER INFORMATION: /note= "Coding region of a truncated bt2 (cryIab) gene, also designated as the bt884 gene"
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: 1877..2110
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene 7."
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2480..3005
OTHER INFORMATION: /note= "35S promoter sequence derived from Cauliflower mosaic virus."
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: 3006..3665
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 3666..4491
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA octopine synthase gene."
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary to Patent No. 5952547"
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7155..7639
OTHER INFORMATION: /note= "TR1' and TR2' promoter derived from Agrobacterium T-DNA."
OTHER INFORMATION:
US-08-232-016-22
Query Match 15.0%; Score 729.6; DB 2; Length 7639;
Best Local Similarity 98.8%; Pred. No. 6e-140;
Matches 735; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 4072 GATCATGCTAGCTTAGAGTCCCTGTTTAAATGAGATATGCGAGCGCTATGATCGCAT 4131
DB 3764 GACCCATCGCGCTAGAGTCCCTGTTTAAATGAGATATGCGAGCGCTATGATCGCAT 3823
QY 4132 GATATTTCTTTCAATTCCTGTTGTCAGCTGTGTAATAAACCTGAGCATGTAGCTCAGA 4191
DB 3824 GATATTTCTTTCAATTCCTGTTGTCAGCTGTGTAATAAACCTGAGCATGTAGCTCAGA 3883
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DB 4064 CAATAACAAACAAATTCGGTTTATTATTACAAATCCAAATTTAAAAAGCGGCAAGACC 4123

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RESULT 3
US-08-064-121-1
; Sequence 1. Application US/08064121
; Patent No. 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,121
; FILING DATE: 24-MAY-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Peury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; Patent No. 5712135			
; GENERAL INFORMATION:			
; APPLICANT: D'HALLUIN, Kathleen			
; APPLICANT: GOBEL, Elke			
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING			
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Burns, Doane, Swecker & Mathis			
; STREET: P.O. Box 1404			
; CITY: Alexandria			
; STATE: Virginia			
; COUNTRY: United States			
; ZIP: 22313-1404			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
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; APPLICATION NUMBER: US/08/478,015			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 435			
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; APPLICATION NUMBER: EP 90403332.1			
; FILING DATE: 23-NOV-1990			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: EP 91401888.2			
; FILING DATE: 08-JUL-1991			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/064,121			
; FILING DATE: 23-JUN-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: McGowan, Malcolm K.			
; REGISTRATION NUMBER: 39,300			
; REFERENCE/DOCKET NUMBER: 010830-088			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (703) 836-6620			
; TELEFAX: (703) 836-2021			
; INFORMATION FOR SEQ ID NO: 1:			
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; LENGTH: 5399 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: circular			
; MOLECULE TYPE: DNA (genomic)			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; ORIGINAL SOURCE:			
; ORGANISM: plasmid pDEL08			
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FEATURE:
NAME/KEY: -
LOCATION: 2101..3160
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OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from the Agrobacterium T-DNA octopine synthase"
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FEATURE:
NAME/KEY: -
LOCATION: 3161..5399
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US-08-478-015-1
Query Match 14.6%; Score 709.8; DB 1; Length 5399;
Best Local Similarity 99.7%; Pred. No. 6e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4093 CTTGCTTTAATGAGATATCGGAGACGCTATGATCGCATGATTTGCTTCAATTCGT 4152
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QY 4153 TGTGACGTTGTAAATAAAGCTGAGATGTTAGTCTGAGATCCTTACCGCGGTTTGGTT 4212
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QY 4213 CATTCCTAATGAATATATACCCGTTACTATCGTATTTTATGAATATATTCCTCGTTCA 4272
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DB 2753 GATTCCTTGAAGTTGAGTATTTGGCCGTCGGTCTACCGAAGTTACGGGACCACTTCAAC 2812
QY 4633 CCGGTCAGACCGCGCGGTAACCGACTTGTGCGCCGAGATTTATGAGCATTTT 4692
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; Sequence 1, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
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; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
; OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"
; FEATURE:
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; LOCATION: 1285..2100

Wed May 12 08:20:59 2004

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; OTHER INFORMATION: /label= NPTII
; OTHER INFORMATION: /note= "coding sequence of neomycine
; OTHER INFORMATION: phosphotransferase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: 2101...3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
; OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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; LOCATION: 3161...5399
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; US-08-475-975-1
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Best Local Similarity 99.7%; Pred. No. 6e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; US-09-084-889-1
; Sequence 1, Application US/09084889
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; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
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; NAME/KEY: -
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; OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"
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DB 3969 CCGGTCCAGCACGGCGCGGTAACCGACTTGTGTCGCCGAGAAATTATGAGCATTTT 4028
QY 4693 TTGTGTATGTGGGCGGCCCAATTAAGTCCAGTCAACCTTACAGTACGACGAAATCGT 4752
DB 4029 TTGTGTATGTGGGCGGCCCAATTAAGTCCAGTCAACCTTACAGTACGACGAAATCGT 4088
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DB 4089 TGGCGGGTCCAGGCGCAATTTTGGCAACAATGTCGAGGCTCAGCAGGACCT 4141

RESULT 8
US-09-025-583-2
; Sequence 2, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: complement (752..1024)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: -
LOCATION: 1608..2440
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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OTHER INFORMATION: cauliflower mosaic virus isolate Cabb-J1"

FEATURE:
NAME/KEY: 2441..3256
LOCATION: 2441..3256 /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
NAME/KEY: 3257..4315
LOCATION: 3257..4315 /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: 4316..6555
LOCATION: 4316..6555 /label= pUC18
OTHER INFORMATION: /label= "pUC18 derived sequence"
US-09-025-583-2

Query Match 14.6%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 6.4e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	4093	CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT	4152
Db	3429	CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT	3488
QY	4153	TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	4212
Db	3489	TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	3548
QY	4213	CAATTCATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA	4272
Db	3549	CAATTCATGAATATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA	3608
QY	4273	ATTACTGATGTACCTACTACTATATAGTACAAATTAATAATTAATTAATTTCT	4332
Db	3609	ATTACTGATGTACCTACTACTATATAGTACAAATTAATAATTAATTAATTTCT	3668
QY	4333	GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCCAATTAACAAATTTGGGTTT	4392
Db	3669	GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCCAATTAACAAATTTGGGTTT	3728
QY	4393	TATTATTACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	4452
Db	3729	TATTATTACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	3788
QY	4453	TACATAAATCTTATTCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	4512
Db	3789	TACATAAATCTTATTCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	3848
QY	4513	CGGCGAACTAATAACGTTCACTGAAGGAACTCCCGTTCCCGCGCGCGCATGGGTGA	4572
Db	3849	CGGCGAACTAATAACGTTCACTGAAGGAACTCCCGTTCCCGCGCGCGCATGGGTGA	3908
QY	4573	GATTCTTGAAGTTGAGTATTGGCCGTTCCCGTTCCCGCGCGCGCATGGGTGA	4632
Db	3909	GATTCTTGAAGTTGAGTATTGGCCGTTCCCGTTCCCGCGCGCGCATGGGTGA	3968
QY	4633	CCGCTCCAGCACCGCGCGCGGTAAACGACTTGTCTGCCCGAGAAATTATGCAGCATTTT	4692
Db	3969	CCGCTCCAGCACCGCGCGCGGTAAACGACTTGTCTGCCCGAGAAATTATGCAGCATTTT	4028
QY	4693	TTGCTGTATGTGGGCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAAAATCGT	4752
Db	4029	TTGCTGTATGTGGGCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAAAATCGT	4088
QY	4753	TGGCGGGTCCAGGGCGGAATTTTTCGCAACCATGTGAGGCTCAGCAGGACCT	4805
Db	4089	TGGCGGGTCCAGGGCGGAATTTTTCGCAACCATGTGAGGCTCAGCAGGACCT	4141

RESULT 9

US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577.424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 14.6%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 8e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	4093	CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT	4152
Db	9830	CCTGCTTTAATGAGATATCGGAGACGCCCTATGATCGCATGATATTGCTTCAATTCGT	9889
QY	4153	TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	4212
Db	9890	TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCCTTACCGCGGTTTCGGTT	9949
QY	4213	CAATTCATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA	4272
Db	9950	CAATTCATGAATATACCCGTTACTATCGPATTTTATGAATATATTTCTCCGTTCA	10009
QY	4273	ATTACTGATGTACCTACTACTATATAGTACAAATTAATAATTAATTAATTTCT	4332
Db	10010	ATTACTGATGTACCTACTACTATATAGTACAAATTAATAATTAATTAATTTCT	10069
QY	4333	GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCCAATTAACAAATTTGGGTTT	4392
Db	10070	GCTGAATAGTTTATAGGACATCTATGATAGAGCGCCCAATTAACAAATTTGGGTTT	10129
QY	4393	TATTATTACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	4452
Db	10130	TATTATTACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	10189
QY	4453	TACATAAATCTTATTCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	4512
Db	10190	TACATAAATCTTATTCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT	10249
QY	4513	CGGCGAACTAATAACGTTCACTGAAGGAACTCCCGTTCCCGCGCGCGCATGGGTGA	4572
Db	10250	CGGCGAACTAATAACGTTCACTGAAGGAACTCCCGTTCCCGCGCGCGCATGGGTGA	10309
QY	4573	GATTCTTGAAGTTGAGTATTGGCCGTTCCCGTTCCCGCGCGCGCATGGGTGA	4632
Db	10310	GATTCTTGAAGTTGAGTATTGGCCGTTCCCGTTCCCGCGCGCGCATGGGTGA	10369
QY	4633	CCGCTCCAGCACCGCGCGCGGTAAACGACTTGTCTGCCCGAGAAATTATGCAGCATTTT	4692
Db	10370	CCGCTCCAGCACCGCGCGCGGTAAACGACTTGTCTGCCCGAGAAATTATGCAGCATTTT	10429
QY	4693	TTGCTGTATGTGGGCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAAAATCGT	4752
Db	10430	TTGCTGTATGTGGGCCCAATTAAGTGCAGGTCAAACTTGAAGTGCAGCAAAATCGT	10489
QY	4753	TGGCGGGTCCAGGGCGGAATTTTTCGCAACCATGTGAGGCTCAGCAGGACCT	4805
Db	10490	TGGCGGGTCCAGGGCGGAATTTTTCGCAACCATGTGAGGCTCAGCAGGACCT	10542

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RESULT 10
5428147-1/c
;PATENT NO. 5428147
;APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
;TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
;NUMBER OF SEQUENCES: 17
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/91,538
;FILING DATE: 13-JUL-1993
;PRIORITY APPLICATION DATA:
;APPLICATION NUMBER: 869,216
;FILING DATE: 13-APR-1992
;APPLICATION NUMBER: 869,216
;FILING DATE: 13-APR-1992
;APPLICATION NUMBER: 440,432
;FILING DATE: 21-NOV-1989
;APPLICATION NUMBER: 553,786
;FILING DATE: 19-NOV-1983
;APPLICATION NUMBER: 741,034
;FILING DATE: 06-AUG-1991
;APPLICATION NUMBER: 144,775
;FILING DATE: 20-JAN-1988
;APPLICATION NUMBER: 485,614
;FILING DATE: 15-APR-1983
;APPLICATION NUMBER: 713,624
;FILING DATE: 10-JUN-1991
;APPLICATION NUMBER: 260,574
;FILING DATE: 21-OCT-1988
;APPLICATION NUMBER: 848,733
;FILING DATE: 01-APR-1986
;APPLICATION NUMBER: 535,354
;FILING DATE: 26-SEP-1983
;SEQ ID NO: 1
;LENGTH: 24595
5428147-1
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Best Local Similarity 100.0%; Pred. No. 3.5e-135;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4094 CTGCTTTAATGAGATATGGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGTGTT 4153
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QY 4154 GTGACGCTTTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTTACCGCGGTTTCGGTTC 4213
DB 12481 GTGACGCTTTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTTACCGCGGTTTCGGTTC 12422
QY 4214 ATTCTAATGAATATATCACCGGTTACTATCGTATTTTATGAATAATATTTCTCGGTTCAA 4273
DB 12421 ATTCTAATGAATATATCACCGGTTACTATCGTATTTTATGAATAATATTTCTCGGTTCAA 12362
QY 4274 TTTACTGATTTGACCTTACTTATATGATGACATATTTAAATGAAAAACAATATATTTG 4333
DB 12361 TTTACTGATTTGACCTTACTTATATGATGACATATTTAAATGAAAAACAATATATTTG 12302
QY 4334 CTGAATAGTTTATAGGACATCTATGATAGCGGCACAAATACAAACAATTCGGTTT 4393
DB 12301 CTGAATAGTTTATAGGACATCTATGATAGCGGCACAAATACAAACAATTCGGTTT 12242
QY 4394 ATTATTAACAATCAATTTTAAAAAAGCGCAGAACCGGTCAAACTTAAAGACTGATT 4453
DB 12241 ATTATTAACAATCAATTTTAAAAAAGCGCAGAACCGGTCAAACTTAAAGACTGATT 12182
QY 4454 ACATTAATCTTATTAACAATTTTCAAAAGCCCGGCTAGTATCTACGACACACCGGAGC 4513
DB 12181 ACATTAATCTTATTAACAATTTTCAAAAGCCCGGCTAGTATCTACGACACACCGGAGC 12122
QY 4514 GCGCAACTTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCGCGCGCATGGGTGAG 4573
DB 12121 GCGCAACTTAATAACGTTCACTGAAGGGAACCTCCGGTTCCCGCGCGCGCATGGGTGAG 12062
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DB 12061 ATTCTTGAAGTTAGTATTTGGCCGCTCCGCTTACCGAAGTTACGGGACCAATTCACACC 12002
QY 4634 CGGTCCAGCACGCGCGCGGTAACCGACTTGTGCTGCCGAGAAATATATGACGATTTTTT 4693
DB 12001 CGGTCCAGCACGCGCGCGGTAACCGACTTGTGCTGCCGAGAAATATATGACGATTTTTT 11942
QY 4694 TGGTGTATGTGGCCCCCAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAATCGTT 4753
DB 11941 TGGTGTATGTGGCCCCCAATGAAGTGCAGGTCAAACTTGCAGTGCAGCAAAATCGTT 11882
QY 4754 GGGCGGCTCCAGGCGGAATTTTTCGACAAACATGTCGAGGCTCAGCAG 4800
DB 11881 GGGCGGCTCCAGGCGGAATTTTTCGACAAACATGTCGAGGCTCAGCAG 11835

RESULT 11
US-08-673-768-1
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-673-768-1

Query Match 11.6%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.7e-106;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4093 CCTGCTTTAATGAGATATGGAGACGCCCTATGATCGCATGATATTTGCTTTCAATTCGT 4152
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QY 4153 TGTGACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4212

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Db 7170 TGTGACGCTGTAAACACCTGAGCATGTGTAGTCTAGATCCTTACCGCGGTTTCGGTT 7229
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Db 7230 CATTCATATGATATATACCGGTTACTATCTATCTATTTTATGAATATATCTCCGTTCA 7289
QY 4273 ATTACTGATGTCACCTACTACTACTATATGTACATATTAATGAATGAACATATATGT 4332
Db 7290 ATTACTGATGTCACCTACTACTACTATATGTACATATTAATGAATGAACATATATGT 7349
QY 4333 GGTGAATAGGTTTATAGGACATCTATGATAGAGCGCCACAATAACAAACAATTCGGTTT 4392
Db 7350 GGTGAATAGGTTTATAGGACATCTATGATAGAGCGCCACAATAACAAACAATTCGGTTT 7409
QY 4393 TATTATCAAAATCCAAATTTTAAACACCGGAGAACCCGTTCAACCTTAAAGACTGAT 4452
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Db 7470 TACATTAATCTTATCAAAATTTTAAACACCGGAGAACCCGTTCAACCTTAAAGACTGAT 7529
QY 4513 CGGCGAACCTAAATACCGTTCACTGAAGGGAACCTCCGTTTCCCGCGCGCGCATGGTGA 4572
Db 7530 CGGCGAACCTAAATACCGTTCACTGAAGGGAACCTCCGTTTCCCGCGCGCGCATGGTGA 7589
QY 4573 GATTCCTTGAAGTTGAGTATGCGCGTCTTACCGAAAGTTACGGGCAACATTCAC 4632
Db 7590 GATTCCTTGAAGTTGAGTATGCGCGTCTTACCGAAAGTTACGGGCAACATTCAC 7649
QY 4633 CCGGTCACGACGCGCGCGGTTAAACCG 4660
Db 7650 CCGGTCACGACGCGCGCGGTTAAACCG 7677

RESULT 12

US-08-673-768-1/c
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 11.6%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 1.7e-106;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4093 CTTGCTTTTAAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 4152
Db 14394 CTTGCTTTTAAATGAGATATGCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 14335
QY 4153 TGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 4212
Db 14334 TGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 14275
QY 4213 CATTCATATGATATATACCGGTTACTATCTATTTTATGAATATATTTCTCCGTTCA 4272
Db 14274 CATTCATATGATATATACCGGTTACTATCTATTTTATGAATATATTTCTCCGTTCA 14215
QY 4273 ATTTACTGATGTCACCTACTACTTATATGTACATATTTAAATGAAAAATATATTCGT 4332
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QY 4333 GGTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAAACAATTCGGTT 4392
Db 14154 GGTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAAACAATTCGGTT 14095
QY 4393 TATTATCAAAATCCAAATTTTAAACACCGGAGAACCCGTTCAACCTTAAAGACTGAT 4452
Db 14094 TATTATCAAAATCCAAATTTTAAACACCGGAGAACCCGTTCAACCTTAAAGACTGAT 14035
QY 4453 TACATAAATCTTATCAAAATTTCAAAAGCGCCCGGCTAGTATCTACGACACACCGAG 4512
Db 14034 TACATAAATCTTATCAAAATTTCAAAAGCGCCCGGCTAGTATCTACGACACACCGAG 13975
QY 4513 CGGCGAACCTAAATACCGTTCACTGAAGGGAACCTCCGTTTCCCGCGCGCGCATGGTGA 4572
Db 13974 CGGCGAACCTAAATACCGTTCACTGAAGGGAACCTCCGTTTCCCGCGCGCGCATGGTGA 13915
QY 4573 GATTCCTTGAAGTTGAGTATGCGCGTCTTACCGAAAGTTACGGGCAACATTCAC 4632
Db 13914 GATTCCTTGAAGTTGAGTATGCGCGTCTTACCGAAAGTTACGGGCAACATTCAC 13855
QY 4633 CCGGTCACGACGCGCGGTTAAACCG 4660
Db 13854 CCGGTCACGACGCGCGGTTAAACCG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible


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; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of plasmid pK1L 19
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
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; US-08-379-614-3
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; Query Match
; Best Local Similarity 6.6%; Score 323.2; DB 2; Length 416;
; Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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; QY 655 GTGTATAAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGGTTTTTGAT 714
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 402 GTGTATAAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGGTTTTTGAT 343
;
; QY 715 GTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACT 774
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 342 GTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGCACACT 283
;
; QY 775 GGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGGATATCACACCGGGTAAAG 834
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 282 GGCCATATCGGTGGTGCATCATCGCCAGCTTTTCATCCCGGATATCACACCGGGTAAAG 223
;
; QY 835 TTCACGGAGACTTTTATCTGACAGAGAGCTGCACTGGCCAGGGGGATCACCATCCGTCG 894
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 222 TTCACGGAGACTTTTATCTGACAGAGAGCTGCACTGGCCAGGGGGATCACCATCCGTCG 163
;
; QY 895 CCCGGCGGTGCAATAATATCACTCTGTACATCCAGAACACAGACGATACGGCTCTCTCT 954
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 162 CCCGGCGGTGCAATAATATCACTCTGTACATCCAGAACACAGACGATACGGCTCTCTCT 103
;
; QY 955 TTTATAGGTGTAACCTTAAACTGCATT 982
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 102 TTTATAGGTGTAACCTTAAACTGCATT 75
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Job time : 213.004 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 1296.69 Seconds

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Perfect score: 4863

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Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5893172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

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14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	4863	100.0	17862	15	US-10-055-001A-23
2	4112.4	84.6	17476	15	US-10-055-001A-24
3	4112.4	84.6	17476	15	US-10-385-546-7
4	4077.2	83.8	17691	15	US-10-055-001A-26
5	4042	83.1	17458	15	US-10-055-001A-25
6	3985.4	82.0	18621	15	US-10-055-001A-13
7	1645	33.8	17862	15	US-10-055-001A-23
8	1207.4	24.8	4470	15	US-10-151-690-21
9	1207.4	24.8	4892	16	US-10-357-268-1
10	1207.4	24.7	5584	15	US-10-151-690-61
11	1201	24.7	4428	15	US-10-151-690-62
12	1194.6	24.6	4627	15	US-10-151-690-63
13	1194.6	24.6	4627	15	US-10-151-690-64
14	1174.2	24.1	17691	15	US-10-055-001A-26

c 15	1089.4	22.4	17476	15	US-10-055-001A-24	Sequence 24, Appl
c 16	1089.4	22.4	17476	15	US-10-385-546-7	Sequence 7, Appl
c 17	1079.4	22.2	17458	15	US-10-055-001A-25	Sequence 25, Appl
c 18	842	17.3	18691	15	US-10-055-001A-13	Sequence 13, Appl
c 19	780	16.0	786	15	US-10-385-521-9	Sequence 9, Appl
c 20	737.8	15.2	2116	12	US-10-644-335-3	Sequence 3, Appl
c 21	737.8	15.2	2873	15	US-10-356-088-55	Sequence 55, Appl
c 22	737.8	15.2	2873	15	US-10-353-454-38	Sequence 38, Appl
c 23	736.2	15.1	3002	13	US-10-353-454-57	Sequence 57, Appl
c 24	735.8	15.1	3034	15	US-10-356-088-48	Sequence 48, Appl
c 25	735.8	15.1	3034	15	US-10-353-454-31	Sequence 31, Appl
c 26	713	14.7	4947	9	US-09-118-276-21	Sequence 21, Appl
c 27	710.2	14.6	7599	15	US-10-027-880-5	Sequence 5, Appl
c 28	703.4	14.5	2867	15	US-10-176-884-9	Sequence 9, Appl
c 29	703.4	14.5	2867	15	US-10-177-478-20	Sequence 20, Appl
c 30	597	12.3	1846	15	US-10-023-208-63	Sequence 63, Appl
c 31	597	12.3	5558	15	US-10-241-596-137	Sequence 137, App
c 32	597	12.3	6464	15	US-10-151-690-20	Sequence 20, Appl
c 33	597	12.3	7278	17	US-10-097-034A-37	Sequence 37, Appl
c 34	597	12.3	9249	16	US-10-389-120-2	Sequence 2, Appl
c 35	597	12.3	10463	16	US-10-389-120-1	Sequence 1, Appl
c 36	597	12.3	12789	13	US-10-686-778-9	Sequence 9, Appl
c 37	593.8	12.2	11180	9	US-09-887-576-581	Sequence 581, App
c 38	505.8	10.4	4470	15	US-10-151-690-21	Sequence 21, Appl
c 39	505.8	10.4	4892	16	US-10-357-268-1	Sequence 1, Appl
c 40	505.8	10.4	5584	15	US-10-151-690-61	Sequence 61, Appl
c 41	499.4	10.3	4428	15	US-10-151-690-62	Sequence 62, Appl
c 42	492.6	10.1	4627	15	US-10-151-690-63	Sequence 63, Appl
c 43	492.6	10.1	4627	15	US-10-151-690-64	Sequence 64, Appl
c 44	478.8	9.8	528	15	US-10-162-214-4	Sequence 4, Appl
c 45	323.4	6.7	2877	13	US-09-861-925-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match	100.0%;	Score 4863;	DB 15;	Length 17862;
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			Indels	0;
			Gaps	0;
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Db	13000	TTTCAATTTGGAGAGACACGCTCGAGGCTAGCATCGATCTCGGGCCCAATAATGATT	13059	
QY	61	TATTTTGACTAGTACCTGCTTCTGTTGCAACAAATGATGAGCAATGCTTTTATATA	120	
Db	13060	TATTTTGACTAGTACCTGCTTCTGTTGCAACAAATGATGAGCAATGCTTTTATATA	13119	
QY	121	TGCCAACTTGTACAAAAAGCTGACGAGAAACGTAATGATATATATATATATATAT	180	

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Db	13180	TAAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAAACAACAATATCCAGT	13239
Qy	241	CACATAGAAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCCTTCGAA	300
Db	13240	CACATAGAAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCCTTCGAA	13299
Qy	301	ATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGCAGCAGCCTTCCAAATGTTCTTCTCA	360
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Qy	361	AACGGAAATCGTGTATTCGAGCCTTACTGCGTATTGTCTCAATGCCGTATTAAATCATAAA	420
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Qy	421	AAGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAACATCTACC	480
Db	13420	AAGAAATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAATATAAACATCTACC	13479
Qy	481	TATTCATATACGCTAGTGTGCATAGTCTCGAAATCATCTGCATCAAGAACAAATTTCAAA	540
Db	13480	TATTCATATACGCTAGTGTGCATAGTCTCGAAATCATCTGCATCAAGAACAAATTTCAAA	13539
Qy	541	CTCTTATACCTTTCTTTACAGTCCGCTTCGCTTCATCTGGATTTTCAGCCTCATAGCT	600
Db	13540	CTCTTATACCTTTCTTTACAGTCCGCTTCGCTTCATCTGGATTTTCAGCCTCATAGCT	13599
Qy	601	ACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGAT	660
Db	13600	ACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGAT	13659
Qy	661	AAGGAGCCTGCATATTATATTCGCCAGAACATCAGTTAATGGCGTTTTTGATGTCATT	720
Db	13660	AAGGAGCCTGCATATTATATTCGCCAGAACATCAGTTAATGGCGTTTTTGATGTCATT	13719
Qy	721	TTCCGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGGAGACCGGCACATCGGCCAT	780
Db	13720	TTCCGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGGAGACCGGCACATCGGCCAT	13779
Qy	781	ATCGGTGGTCAATATGCGCAGCTTTTCATCCCGATATGCAACAACGGGTAAAGTTCAG	840
Db	13780	ATCGGTGGTCAATATGCGCAGCTTTTCATCCCGATATGCAACAACGGGTAAAGTTCAG	13839
Qy	841	GGAGACTTTATCTGACAGCAGATGCTGCTGGCCAGGGGATCACCATCCGTCGCCGG	900
Db	13840	GGAGACTTTATCTGACAGCAGATGCTGCTGGCCAGGGGATCACCATCCGTCGCCGG	13899
Qy	901	CGTGTCAATTAATACCTCTGTATCATCCCAACACAGACGATTAACCGCTCTCTTTTATA	960
Db	13900	CGTGTCAATTAATACCTCTGTATCATCCCAACACAGACGATTAACCGCTCTCTTTTATA	13959
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Db	13960	GGTGTAAACCTTAACTGCAATTCACAGTCCGTTCTCGTCAGCAAAAGACCGTTCAC	14019
Qy	1021	TTTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCGGCTTTCCAGCGTCCG	1080
Db	14020	TTTCAATAAACCCGGGCGACCTCAGCCATCCCTTCTCTGATTTTCGGCTTTCCAGCGTCCG	14079
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Db	14080	CACGAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACAGACCGGAGATATTGACAT	14139
Qy	1141	CATATATGCCCTTGAGCAACTGATAGCTGTGCCTGTCAACTGTCACTGTAAATACGCTGCT	1200
Db	14140	CATATATGCCCTTGAGCAACTGATAGCTGTGCCTGTCAACTGTCACTGTAAATACGCTGCT	14199
Qy	1201	CATAGCACACCTCTTTTTTGACATACTTTCCGGTGTGTCGGATCAAGCTCTCATTTTCGCCA	1260
Db	14200	CATAGCACACCTCTTTTTTGACATACTTTCCGGTGTGTCGGATCAAGCTCTCATTTTCGCCA	14259

QY	1261	AAAGTTGGCCACGGGCTTCCCGGTATCAACAGGGACACAGAGTTATTATTATCTGCGAA	1320
DB	14260	AAAGTTGGCCACGGGCTTCCCGGTATCAACAGGGACACAGAGTTATTATTATCTGCGAA	14319
QY	1321	GTGATCTTCGGTCACAGGTATTTATTCGGCGCAAAAGTCGTCGGGTGATGCTGCCAATT	1380
DB	14320	GTGATCTTCGGTCACAGGTATTTATTCGGCGCAAAAGTCGTCGGGTGATGCTGCCAATT	14379
QY	1381	AGTCGACTACAGGTCACTAATACCATCTAAGPAGTTGATTCATAGTCACTCGATATGTTG	1440
DB	14380	AGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTCACTCGATATGTTG	14439
QY	1441	TGTTTTACAGTATTATGTTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATT	1500
DB	14440	TGTTTTACAGTATTATGTTAGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATATT	14499
QY	1501	TATATCATTTTACGTTTTCGTTTCAGCTTTCCTGTACAAAGTTGCAATTAAAGAAAGCA	1560
DB	14500	TATATCATTTTACGTTTTCGTTTCAGCTTTCCTGTACAAAGTTGCAATTAAAGAAAGCA	14559
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DB	14560	TTGCTTATCAATTTGTTGCAACGACAGGTCACTATCAGTCAAAATAAATCATTATTG	14619
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DB	14620	CCATCCAGCTGCACTCCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATAAATTATT	14679
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DB	14680	TTCTTTTTCCTTTTAGTATAAAATAGTTAAAGTAGTAAATTAGTAGTATTAATAAAT	14739
QY	1741	ATAGTTGTTATTAATTCGTAAGAAAAATAAATTTAATAATATATCTGTTACATAAACAATAG	1800
DB	14740	ATAGTTGTTATTAATTCGTAAGAAAAATAAATTTAATAATATATCTGTTACATAAACAATAG	14799
QY	1801	TAATGTAAAAAAATATGACAAAGTGATGTCTAAGACGAAGAGATAAAAAGTTGAGAGTAAG	1860
DB	14800	TAATGTAAAAAAATATGACAAAGTGATGTCTAAGACGAAGAGATAAAAAGTTGAGAGTAAG	14859
QY	1861	TATATTAATTTTAAATGAATTTGATCGAAATGCTAGTAGATGATATCTAGCATTAATATTG	1920
DB	14860	TATATTAATTTTAAATGAATTTGATCGAAATGCTAGTAGATGATATCTAGCATTAATATTG	14919
QY	1921	TTTTTAATCATAAATAGTAAATTTAGCTGGTTGATGAAATTAATATCAATGATAAAATACT	1980
DB	14920	TTTTTAATCATAAATAGTAAATTTAGCTGGTTGATGAAATTTAAATAATCAATGATAAAATACT	14979
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DB	14980	ATAGTAAAAATAGATATAAATAATTAATTAATTTTATGATTAATAGTTTATTA	15039
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DB	15100	TTAGAAATTCCAATCTGCTGTAATTTATTAATAAATAATTAATAACACAGCTAAA	15159
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QY	2221	GCTAATAATAACAAAGCGCAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATTC	2280
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Db 15460 TGGATCCCTCTAGAGAGCTGCGAGCTGGATGGCAATAATGATTTTATTTTGGATGATAGTG 15519
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Db 15520 ACCTGTTCTGTCACAAATTTGATAAGCAATGCTTTCTTATAATGCCAACTTTTGACAAAG 15579
QY 2581 AAAGCTGAACGAGAAACGCTAAATGATATAAATATCAATATATAAATTTAGATTTTGGAT 2640
Db 15580 AAAGCTGAACGAGAAACGCTAAATGATATAAATATCAATATATAAATTTAGATTTTGGAT 15639
QY 2641 AAAAAACGACTACATATACTGTAAACACAAACATATCCAGTCACTATGATGAATCAACTAC 2700
Db 15640 AAAAAACGACTACATATACTGTAAACACAAACATATCCAGTCACTATGATGAATCAACTAC 15699
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Db 15700 TTAGATGGTATTAGTACACCTGTAGTCGACTAAGTTGGCAGCATCAACCGACGCACTTTGC 15759
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Db 15760 GCCGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAATCCTGGTGCCT 15819
QY 2821 GTTGATACCGGAAGCCCTGGCCAACTTTTCGCAAAATGAGAGTGTGATCGGCACCTAC 2880
Db 15820 GTTGATACCGGAAGCCCTGGCCAACTTTTCGCAAAATGAGAGTGTGATCGGCACCTAC 15879
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Db 16000 TGGCTGTGATAAGGAGCTGACATTTATATTTCCCGAACAATCAGGTTAATGGGTTTT 16059
QY 3061 TTGATGTCATTTTCGGGTTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGC 3120
Db 16060 TTGATGTCATTTTCGGGTTGGCTGAGATCAGCCACTTCTTCCCGGATAACGGAGACCGGC 16119
QY 3121 AACTGGCCATATCGGTGTGATCATGCGCCAGCTTTTCATCCCGGATATGCACACCGGG 3180
Db 16120 AACTGGCCATATCGGTGTGATCATGCGCCAGCTTTTCATCCCGGATATGCACACCGGG 16179
QY 3181 TAAAGTTTACGGAGACTTTTATCTGACAGCAGACGTGCATCGCCAGGGGGATCACCATC 3240
Db 16180 TAAAGTTTACGGAGACTTTTATCTGACAGCAGACGTGCATCGCCAGGGGGATCACCATC 16239
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Db 16240 CGTGGCCCGGGTGTCATTAATATCACTCTGTACATPCCAAACAGACGATAACGGCTC 16299
QY 3301 TCTCTTTTATAGTGTAACCTTAACTGATTTTCACTGATTTCCAGTCCCTGTTCTCGTCACAAA 3360
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QY 3361 AGAGCCGTTTCAATTAACACGGGGGACCTCAGCCATCCCTTCCCTGATTTTCCGCTTT 3420
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QY 3421 CCAGCGTTCCGCGACGACGAGCGGGCTTCATTTCTGATGGTTGTGTTTACCAGACGGGA 3480

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Db 16480 GATATTGACATCATATATGCTTGGCAACTGATAGTGTGCTGTCAACTGTCACTGTA 16539
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Db 16600 TCAGGACTATGACACTAGCTGATATGATAGGTAGATGTTTATTTTGTTCACACAAAA 16659
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QY 3781 ACTAAGTTGGCAGCATCACCCGAAAGAACATTTGGAGGCTGTGGTTCGACTACAGGTCCAC 3840
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Db 16840 TAAATACCATCTAAGTAGTTGATTCATAGTACTGATATGTTGTTTACAGTATTATG 16899
QY 3901 TAGTCTGTTTTTATGCAAAATCTAAATTAATATATATGATATTTATATCATTTTACGTTT 3960
Db 16900 TAGTCTGTTTTTATGCAAAATCTAAATTAATATATATGATATTTATATCATTTTACGTTT 16959
QY 3961 CTGTTTCAAGCTTTTGTGACAAAGTTGCAATTTAAAGAGCATGCTCATCAATTTGTT 4020
Db 16960 CTGTTTCAAGCTTTTGTGACAAAGTTGCAATTTAAAGAGCATGCTCATCAATTTGTT 17019
QY 4021 GCAACGACAGCTCACTATCAGTCAAAATAAATCAATTTTGGGGCCCGAGATCCATGC 4080
Db 17020 GCAACGACAGCTCACTATCAGTCAAAATAAATCAATTTTGGGGCCCGAGATCCATGC 17079
QY 4081 TAGCTCTAGAGTCTGCTTTTAAATGAGATATGAGACGCTATGATCGCATGATTTTGC 4140
Db 17080 TAGCTCTAGAGTCTGCTTTTAAATGAGATATGAGACGCTATGATCGCATGATTTTGC 17139
QY 4141 TTTCAATTTCTGTTGCGAGTTGTAAGAACCTGAGCATGTGTAGCTCAGATCCTTACCG 4200
Db 17140 TTTCAATTTCTGTTGCGAGTTGTAAGAACCTGAGCATGTGTAGCTCAGATCCTTACCG 17199
QY 4201 CCGGTTTCGGTTTCATTTCAATGAATATATCAACCGTTACTATCGTATTTTATGATTAAT 4260
Db 17200 CCGGTTTCGGTTTCATTTCAATGAATATATCAACCGTTACTATCGTATTTTATGATTAAT 17259
QY 4261 ATTCCTCGTTTCAATTTCTGATGTGACCTACTACTATATGATGATTAATTAATGAA 4320
Db 17260 ATTCCTCGTTTCAATTTCTGATGTGACCTACTACTATATGATGATTAATTAATGAA 17319
QY 4321 ACAATATATGCTGTAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAAATAACAA 4380
Db 17320 ACAATATATGCTGTAATAGGTTTATAGCGACATCTATGATAGAGCGCCACAAATAACAA 17379
QY 4381 ACAATTGGCTTTTATTTATTAACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAAACC 4440
Db 17380 ACAATTGGCTTTTATTTATTAACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAAACC 17439
QY 4441 TAAAAAGCTGATTAACATAAATCTTATTTCAAAATTTCAAAAGGCCCGGAGGTAGTATCTA 4500
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QY 4501 CGACACACGAGCGGCGAATTAACGTTTCACTGAGGGAATCCCGTTCCCGCGCGC 4560

Db 17500 CGACACCGGCGGCGGAACTAATTAACGTTCACTGAAAGGAACTCCGGTTCCCGCGCGG 17559
Qy 4561 GCGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGG 4620
Db 17560 GCGCATGGGTGAGATTCCTTGAAGTTGAGTATGCGCGTCCGCTCTACCGAAAGTTACGG 17619
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Db 17800 GACCTGCGGCGATGCAAGCTAGCTTACTAGTGCATATCTATAGTGTCAACCTAAATC 17859
Qy 4861 TGC 4863
Db 17860 TGC 17862

RESULT 2

US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellmwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATES
US-10-055-001A-24

Query Match 84.6%; Score 4112.4; DB 15; Length 17476;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 4446; Conservative 0; Mismatches 6; Indels 290; Gaps 4;

Qy 122 GCCAACTTTGTACAAAAAGCTGAACGAGAAAGTAAATGATATAAATCAATATATT 181
Db 13025 GACAAGTTTGTACAAAAAGCTGAACGAGAAAGTAAATGATATAAATCAATATATT 13084
Qy 182 AATATGATTTTGCATATAAAAAAGAGTACATATATCTGTAAACACATATCCAGTC 241
Db 13085 AATATGATTTTGCATATAAAAAAGAGTACATATATCTGTAAACACATATCCAGTC 13144
Qy 242 ACTATGAATCAACTACTTACTAGTATGTTAGTACCTGTAGTCCAGCAGACGCTCCCAA 301
Db 13145 ACTATGAATCAACTACTTACTAGTATGTTAGTACCTGTAGTCCAGCAGACGCTCCCAA 13204
Qy 302 TGTTCTTCGGGTGATGCTGCCAACTTAGTGCAGCAGCGCTTCCCAATGTTCTTCTCAA 361
Db 13205 TGTTCTTCGGGTGATGCTGCCAACTTAGTGCAGCAGCGCTTCCCAATGTTCTTCTCAA 13264
Qy 362 ACGGAATCGTGTATCGAGCCTACTCGCTATGTCCTCAATGCGGTATTAATCATATAAA 421
Db 13265 ACGGAATCGTGTATCGAGCCTACTCGCTATGTCCTCAATGCGGTATTAATCATATAAA 13324

Qy 422 AGAATTAAGAAAAAGAGCTCGAGCCTCTTTTGTGTGACAAATAAATAACATCTACCT 481
Db 13325 AGAATTAAGAAAAAGAGCTCGAGCCTCTTTTGTGTGACAAATAAATAACATCTACCT 13384
Qy 482 ATTCATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCATCAAGAACAAATTTCAAC 541
Db 13385 ATTCATATACGCTAGTGTCTATAGTCTGAAAAATCATCTGCATCAAGAACAAATTTCAAC 13444
Qy 542 TCTTATATCTTTTCTCTTACAAAGTCGTTCCGCTTCATCTGGAATTTTACGCTCTATACCTTA 601
Db 13445 TCTTATATCTTTTCTCTTACAAAGTCGTTCCGCTTCATCTGGAATTTTACGCTCTATACCTTA 13504
Qy 602 CTTAAAGTGTATAAAGTTTCTGTATTTCTACTGTATCGACTGCAGACTGCTGTGTATA 661
Db 13505 CTTAAAGTGTATAAAGTTTCTGTATTTCTACTGTATCGACTGCAGACTGCTGTGTATA 13564
Qy 662 AGGAGAGCTCGACATTTATATTTCCCCAGAACATCAAGTTTAATGGCGTTTTTGAATCAATTT 721
Db 13565 AGGAGAGCTCGACATTTATATTTCCCCAGAACATCAAGTTTAATGGCGTTTTTGAATCAATTT 13624
Qy 722 TCGCGGTGGCTGAGATCGACCATCTTCTTCCCGATTAACGAGACCGGACACATCGCCATA 781
Db 13625 TCGCGGTGGCTGAGATCGACCATCTTCTTCCCGATTAACGAGACCGGACACATCGCCATA 13684
Qy 782 TCGGTGGTCAATCATCGCGCAGCTTTTCATCCCGATATGCACACCGGTTAAAGTTCAAG 841
Db 13685 TCGGTGGTCAATCATCGCGCAGCTTTTCATCCCGATATGCACACCGGTTAAAGTTCAAG 13744
Qy 842 GAGACTTTTATCTGACAGACGCTGCACTGGCCAGGGGATCAACATCCGTCGCGCGCGG 901
Db 13745 GAGACTTTTATCTGACAGACGCTGCACTGGCCAGGGGATCAACATCCGTCGCGCGCGG 13804
Qy 902 GTGTCAATTAATCACTCTGTACATCCACAAACAGAGATTAACGGCTCTCTCTTTATAG 961
Db 13805 GTGTCAATTAATCACTCTGTACATCCACAAACAGAGATTAACGGCTCTCTCTTTATAG 13864
Qy 962 GTGTAAACCTTTAACTGCAATTTCAACAGTCCCTCTCTGTGACAAAGACCGCTTCAT 1021
Db 13865 GTGTAAACCTTTAACTGCAATTTCAACAGTCCCTCTCTGTGACAAAGACCGCTTCAT 13924
Qy 1022 TTCATAAACCGGCGAGCTCAGCCATCCCTTCTGTATTTTCCGCTTTCCAGCGTTCCGC 1081
Db 13925 TTCATAAACCGGCGAGCTCAGCCATCCCTTCTGTATTTTCCGCTTTCCAGCGTTCCGC 13984
Qy 1082 ACGGACAGACGGGCTTCAATTCGATGTTGTGTTACAGACCGGAGATTAAGACATC 1141
Db 13985 ACGGACAGACGGGCTTCAATTCGATGTTGTGTTACAGACCGGAGATTAAGACATC 14044
Qy 1142 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCACTGTCACTGTATTAACGCTGCTTC 1201
Db 14045 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCACTGTCACTGTATTAACGCTGCTTC 14104
Qy 1202 ATAGCACACCTCTTTTGTACATATCTCGGTAGTGCCTCAACGCTCTCATTTTCGCCAA 1261
Db 14105 ATAGCACACCTCTTTTGTACATATCTCGGTAGTGCCTCAACGCTCTCATTTTCGCCAA 14164
Qy 1262 AAGTTGGCCCGGGCTTCCCGGTATCAACAGGACACACAGGATTTATTTATTCGCGAAG 1321
Db 14165 AAGTTGGCCCGGGCTTCCCGGTATCAACAGGACACACAGGATTTATTTATTCGCGAAG 14224
Qy 1322 TGATCTTCGCTCAGAGGATTTTATTCGCGCAAGTGGTCCGGTGTATGCTGCCAACTTA 1381
Db 14225 TGATCTTCGCTCAGAGGATTTTATTCGCGCAAGTGGTCCGGTGTATGCTGCCAACTTA 14284
Qy 1382 GTCGACTACAGTCACTAATACCATCTAAGTGTGATTCATAGTACCTGGATGTGTGT 1441
Db 14285 GTCGACTACAGTCACTAATACCATCTAAGTGTGATTCATAGTACCTGGATGTGTGT 14344
Qy 1442 GTTTTACAGTATATGATGCTGTGTTTTTATGCCAAATCTAATTTAATATATATGATATTT 1501
Db 14345 GTTTTACAGTATATGATGCTGTGTTTTTATGCCAAATCTAATTTAATATATATGATATTT 14404

QY 1502 ATATCATTTTACGTTTCTCGTTACGTTTCTTGTAACAAAGTTGGCAATTAAGAAGCAT 1561
Db 14405 ATATCATTTTACGTTTCTCGTTACGTTTCTTGTAACAAAGTTGG 14447
QY 1562 TGCTTATCAATTTGTTGCAAGACAGGTGACATCATAGTCAAAATAAAATCAATTTTGC 1621
Db 14448 ----- 14447
QY 1622 CATCCAGCTGAGCTCCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAATAATATTTT 1681
Db 14448 -----TCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAATAATATTTT 14492
QY 1682 TCTTTTTCCTTTTAGTATTAATAATAGTTAGTGATGTTAATAGTATGATTAATAATA 1741
Db 14493 TCTTTTTCCTTTTAGTATTAATAATAGTTAGTGATGTTAATAGTATGATTAATAATA 14552
QY 1742 TAGTTGTTATTAATTTGTAAGAAATAATTTTATAATATATTTGTTACATAAAACAAATAGT 1801
Db 14553 TAGTTGTTATTAATTTGTAAGAAATAATTTTATAATATATTTGTTACATAAAACAAATAGT 14612
QY 1802 AATGTAAAAAATAATGACAAGTGATGCTAAAGCAAGAAAGATAAAAGTTGAGAGTAAGT 1861
Db 14613 AATGTAAAAAATAATGACAAGTGATGCTAAAGCAAGAAAGATAAAAGTTGAGAGTAAGT 14672
QY 1862 AATTTATTTTAAATGCAATTTGATCGAAATGATGTAAGATGATATAGTATTAATTTTGT 1921
Db 14673 AATTTATTTTAAATGCAATTTGATCGAAATGATGTAAGATGATATAGTATTAATTTTGT 14732
QY 1922 TTTAATCATATAGTAATTTAGCTGGTTTGTATGAATTAATAATATCAATGATAAAATACTA 1981
Db 14733 TTTAATCATATAGTAATTTAGCTGGTTTGTATGAATTAATAATATCAATGATAAAATACTA 14792
QY 1982 TAGTAAAAATAAGAAATAATAATTAATAATATTTTATGATTAATAGTTATTTAT 2041
Db 14793 TAGTAAAAATAAGAAATAATAATTAATAATATTTTATGATTAATAGTTATTTAT 14852
QY 2042 ATAAATTAATATCTATACCATTAATAATATTTTAAAGTTAAATAATAATTTTGT 2101
Db 14853 ATAAATTAATATCTATACCATTAATAATATTTTAAAGTTAAATAATAATTTTGT 14912
QY 2102 TAGAAATTCATCTGCTTGTAAATTTATCAATTAATAATAATAATAAGCTAAAG 2161
Db 14913 TAGAAATTCATCTGCTTGTAAATTTATCAATTAATAATAATAATAAGCTAAAG 14972
QY 2162 TAACAAATAATATCAAACTAATAGAAACAGTAACTAATGTAACAAACATTAATCTAATG 2221
Db 14973 TAACAAATAATATCAAACTAATAGAAACAGTAACTAATGTAACAAACATTAATCTAATG 15032
QY 2222 CTAATATAACAAAGCGCAAGATCTATCAATTTATATAGTATTAATTTCAATCAATCT 2281
Db 15033 CTAATATAACAAAGCGCAAGATCTATCAATTTATATAGTATTAATTTCAATCAATCT 15092
QY 2282 TATTAATTTCTAAATAATACCTGTAGTTTATTAATCTTAAATGGAATGACTAATTAAT 2341
Db 15093 TATTAATTTCTAAATAATACCTGTAGTTTATTAATCTTAAATGGAATGACTAATTAAT 15152
QY 2342 AAATGAATTAGTGAACATGAATAAACAAGTAACATGATAGTATCATGCTGTTAT 2401
Db 15153 AAATGAATTAGTGAACATGAATAAACAAGTAACATGATAGTATCATGCTGTTAT 15212
QY 2402 CATTTGATCTTACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCCAAATCCGATAGCTT 2461
Db 15213 CATTTGATCTTACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCCAAATCCGATAGCTT 15272
QY 2462 GGATCCTCTAGAGAGCTGACGCTGGATGGCAAAATAATGATTTTATTTTGCATGATAGTA 2521
Db 15273 GGATCCTCTAGA ----- 15284
QY 2522 CCTGTTGTTGCAACAAATGATAAGCAATGCTTTCTTATATGCCAACTTTGTACAAGA 2581
Db 15285 -----CCACTTTGTAACA 15299
QY 2582 AAGCTGAACGAGAAACGTAATAATGATATAATAATATCAATATTAATAATTTAGATTTGCATA 2641

Db 15300 AAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATTAATAATTTAGATTTGCATA 15359
QY 2642 AAAAAACAGACTACATAATACTGTAAAAACAAACATATCCAGTCACTATGATGAATCAACTACT 2701
Db 15360 AAAAAACAGACTACATAATACTGTAAAAACAAACATATCCAGTCACTATGATGAATCAACTACT 15419
QY 2702 TAGATGGTATTAAGTGAACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGACGCACTTTGCG 2761
Db 15420 TAGATGGTATTAAGTGAACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGACGCACTTTGCG 15479
QY 2762 CCGAATAAATAACCTGTGACGGAAGATCACCTTCGAGAAATAAATAAATCCCTGGTGTCCCTG 2821
Db 15480 CCGAATAAATAACCTGTGACGGAAGATCACCTTCGAGAAATAAATAAATCCCTGGTGTCCCTG 15539
QY 2822 TTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAATGAGAGCTTTGATCGGCACCTACC 2881
Db 15540 TTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAATGAGAGCTTTGATCGGC 15592
QY 2882 CATTTCAAACTCTTATACCTTTTCTCTTCAAGTCTGTTCCGCTTCATCTCGATTTTTCAGC 2941
Db 15593 -ATTTCAAACTCTTATACCTTTTCTCTTCAAGTCTGTTCCGCTTCATCTCGATTTTTCAGC 15651
QY 2942 CTCCTATACTTACTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGAGCT 3001
Db 15652 CTCCTATACTTACTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTCGAGCT 15711
QY 3002 GGCTGTGTAAGGAGGCTGACATTTATTTCCCGAGACATCAGGTTTAATGCGGTTTT 3061
Db 15712 GGCTGTGTAAGGAGGCTGACATTTATTTCCCGAGACATCAGGTTTAATGCGGTTTT 15771
QY 3062 TGATGTCAATTTTCCGGTGGCTGAGATCAGCACTTTCTTCCCGATTAACGGAGACCGGCA 3121
Db 15772 TGATGTCAATTTTCCGGTGGCTGAGATCAGCACTTTCTTCCCGATTAACGGAGACCGGCA 15831
QY 3122 CACTGGGCATATTCGGTGGCTGATCATGCGGCACTTTTCTATCCCGATTAACGGAGACCGGCT 3181
Db 15832 CACTGGGCATATTCGGTGGCTGATCATGCGGCACTTTTCTATCCCGATTAACGGAGACCGGCT 15891
QY 3182 AAGGTTCAACGGAGACTTTATCTGACGACGAGCTGCACTGGCCAGGGGATCACCATCC 3241
Db 15892 AAGGTTCAACGGAGACTTTATCTGACGACGAGCTGCACTGGCCAGGGGATCACCATCC 15951
QY 3242 GTCCGCCGGGCTGTCAATAATATCACTCTGTATCATCCAAACAGACGATTAACGGCTCT 3301
Db 15952 GTCCGCCGGGCTGTCAATAATATCACTCTGTATCATCCAAACAGACGATTAACGGCTCT 16011
QY 3302 CTCCTTTATAGGTGTAAACCTTAAACCTGATTTACAGTCCCTGTTCTCGTCAGCAAAA 3361
Db 16012 CTCCTTTATAGGTGTAAACCTTAAACCTGATTTACAGTCCCTGTTCTCGTCAGCAAAA 16071
QY 3362 GAGCGGTTCAATTTCAATAAACCAGGCGACCTCAGCATCCCTTCTGTATTTTCCGCTTTC 3421
Db 16072 GAGCGGTTCAATTTCAATAAACCAGGCGACCTCAGCATCCCTTCTGTATTTTCCGCTTTC 16131
QY 3422 CAGCGGTTCCGCAACAGACGAGCGGCTTCACTCTGATGTTGCTTACAGACCGGAG 3481
Db 16132 CAGCGGTTCCGCAACAGACGAGCGGCTTCACTCTGATGTTGCTTACAGACCGGAG 16191
QY 3482 ATATTGACATCATATATGCTTTGAGCAACTGATAGTCTGCTGCTCACTGCTGATA 3541
Db 16192 ATATTGACATCATATATGCTTTGAGCAACTGATAGTCTGCTGCTCACTGCTGATA 16251
QY 3542 TACGCTGCTTCTATAGCAACCTTTTGTGACATCTTCTGTTCTTGTAGTGCAGATGATTTT 3601
Db 16252 TACGCTGCTTCTATAGCAACCTTTTGTGACATCTTCTGTTCTTGTAGTGCAGATGATTTT 16311
QY 3602 CAGGACTATGACACTAGCGTATATGAATAGGTPAGATGTTTTTATTTTGTCACAAAAAA 3661
Db 16312 CAGGACTATGACACTAGCGTATATGAATAGGTPAGATGTTTTTATTTTGTCACAAAAAA 16371
QY 3662 GAGGCTCGCACTCTTTTCTTATTTTATGATTTAATACGGCATTTGAGGACAATA 3721

Db 16372 GAGGCTCGACCTCTTTTCTTTTCTTTTATGATTAATACGGCANTGAGGACAA 16431
QY 3722 GCGAGTAGGCTGGATACGACGATTCGGTTTGAGAGAAACATTTGGAAGGCTGTGGTTCGA 3781
Db 16432 GCGAGTAGGCTGGATACGACGATTCGGTTTGAGAGAAACATTTGGAAGGCTGTGGTTCGA 16491
QY 3782 CTAAGTTGGCAGCATCACCCGGAAGAACATTTGGAAGGCTGTGGTTCGAGCTACAGGTCACT 3841
Db 16492 CTAAGTTGGCAGCATCACCCGGAAGAACATTTGGAAGGCTGTGGTTCGAGCTACAGGTCACT 16551
QY 3842 AATACATCTAAGTAGTGAATTCATAGTCACTGATATGTTGTTTACAGTATATGTT 3901
Db 16552 AATACATCTAAGTAGTGAATTCATAGTCACTGATATGTTGTTTACAGTATATGTT 16611
QY 3902 AGTCTGTTTTTATGCAAAATCTAATTTAATATATTTGATATTTATATCATTTTACGTTTC 3961
Db 16612 AGTCTGTTTTTATGCAAAATCTAATTTAATATATTTGATATTTATATCATTTTACGTTTC 16671
QY 3962 TCGTTCAGCTTTTTGTACAAAGTTGGCATTTAATAAAGCATTTGCTCATCAATTTGTTG 4021
Db 16672 TCGTTCAGCTTTTTGTACAAACTTG----- 16697
QY 4022 CAAAGAACAGGTCACTATCAGTCAAAATAAATCATTTATTTGGGGCCCGAGATCCATGCT 4081
Db 16698 ----- 16697
QY 4082 AGCTCTAGAGTCTGTTTAAATGAGATATCGGAGCGCTATGATCGCATGATATTTGCT 4141
Db 16698 ---TCTAGAGTCTGTTTAAATGAGATATCGGAGCGCTATGATCGCATGATATTTGCT 16754
QY 4142 TTCAATCTGTTGTCAGCTGTGAAAAACCTGAGCATGTGTAGTCACTCTTACCGC 4201
Db 16755 TTCAATCTGTTGTCAGCTGTGAAAAACCTGAGCATGTGTAGTCACTCTTACCGC 16814
QY 4202 CGGTTTCGGTTCACTTCTAATGATATATCACCGTTTACTATCGTATTTTATGAATAATA 4261
Db 16815 CGGTTTCGGTTCACTTCTAATGATATATCACCGTTTACTATCGTATTTTATGAATAATA 16874
QY 4262 TTCCTCGTTCAATTTACTGATGTCACCTACTACTTATATGTAATATTAATGAATAA 4321
Db 16875 TTCCTCGTTCAATTTACTGATGTCACCTACTACTTATATGTAATATTAATGAATAA 16934
QY 4322 CATATATTTGCTGATAGTTTATAGGACATCTATGATAGCGCCGACAAATCAAA 4381
Db 16935 CAATATTTGCTGATAGTTTATAGGACATCTATGATAGCGCCGACAAATCAAA 16994
QY 4382 CAATTCGGTTTTATTTAATAATCCAAATTTTAAAAAAGCGCGAGAACCGTCAAACT 4441
Db 16995 CAATTCGGTTTTATTTAATAATCCAAATTTTAAAAAAGCGCGAGAACCGTCAAACT 17054
QY 4442 AAAAGTCTGATTAATTAATTTTAAATTTTAAAGGCCCGGCTAGTATCTAC 4501
Db 17055 AAAAGTCTGATTAATTAATTTTAAATTTTAAAGGCCCGGCTAGTATCTAC 17114
QY 4502 GACACACGAGCGGCACTAATAACCTTCACTGAAGGGAACCTCCGGTTCGCCCGCGCG 4561
Db 17115 GACACACGAGCGGCACTAATAACCTTCACTGAAGGGAACCTCCGGTTCGCCCGCGCG 17174
QY 4562 CGCATGGGTGAGATTCCTTGAAGTTGATATGCGCGTCCGCTACCGAAAGTTACGGG 4621
Db 17175 CGCATGGGTGAGATTCCTTGAAGTTGATATGCGCGTCCGCTACCGAAAGTTACGGG 17234
QY 4622 CACCATTCACCGGTCAGCACGCGCGCGGTTAACGGACTTCTGCGCCCGGAGATTAT 4681
Db 17235 CACCATTCACCGGTCAGCACGCGCGCGGTTAACGGACTTCTGCGCCCGGAGATTAT 17294
QY 4682 GCACATTTTTTGTGTATGCGGCCCCAAATGAAAGTGAAGTCAAACTTGCACGTGA 4741
Db 17295 GCACATTTTTTGTGTATGCGGCCCCAAATGAAAGTGAAGTCAAACTTGCACGTGA 17354
QY 4742 CGACAAATCGTTGGCGGCTCCAGGCGGAATTTTGCACAAACATGTGCGAGCTCAGCAG 4801
Db 17355 CGACAAATCGTTGGCGGCTCCAGGCGGAATTTTGCACAAACATGTGCGAGCTCAGCAG 17414

QY 4802 ACTGCGAGGCATGCAAGCTAGCTTACTAGTGATGCATATTTCTATAGTGTCACTAAATCT 4861
Db 17415 ACTGCGAGGCATGCAAGCTAGCTTACTAGTGATGCATATTTCTATAGTGTCACTAAATCT 17474
QY 4862 GC 4863
Db 17475 GC 17476
RESULT 3
US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid PHELLSGATE 8
US-10-385-546-7
Query Match 84.6%; Score 4112.4; DB 15; Length 17476;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 4446; Conservative 0; Mismatches 6; Indels 290; Gaps 4;
QY 122 GCCAATTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATT 181
Db 13025 GACAAAGTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATT 13084
QY 182 AAATTAGATTTTGCATAAAAAAGCACTACATAATCTGTATAAAACACAACTATCCAGTC 241
Db 13085 AAATTAGATTTTGCATAAAAAAGCACTACATAATCTGTATAAAACACAACTATCCAGTC 13144
QY 242 ACTATGAATCAACTACTTAGATGTTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 301
Db 13145 ACTATGAATCAACTACTTAGATGTTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 13204
QY 302 TGTTCCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 361
Db 13205 TGTTCCTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 13264
QY 362 ACGGAATCGTGTATCCAGCCTTACTCGCTATTTGCTCAATGCGGTATTTAAATCATATAA 421
Db 13265 ACGGAATCGTGTATCCAGCCTTACTCGCTATTTGCTCAATGCGGTATTTAAATCATATAA 13324
QY 422 AGAATTAAGAAAAAGAGGTCGAGCCTCTTTTTTGTGTGACAAATAAATAATCACTACCT 481
Db 13325 AGAATTAAGAAAAAGAGGTCGAGCCTCTTTTTTGTGTGACAAATAAATAATCACTACCT 13384
QY 482 ATTATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAACAAATTTCAACAC 541
Db 13385 ATTATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAACAAATTTCAACAC 13444
QY 542 TCTTATACATTTTCTTCTTACAGTCGTTGCGCTTCTATGGAATTTTTCAGCCTCTATCTT 601
Db 13445 TCTTATACATTTTCTTCTTACAGTCGTTGCGCTTCTATGGAATTTTTCAGCCTCTATCTT 13504
QY 602 CTAAACGTCATTAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACCTGGCTGTGTATA 661
Db 13505 CTAAACGTCATTAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACCTGGCTGTGTATA 13564

Db	15540	TTGATACGGGAAGCCCTGGGCCAACTTTTGGGAAAATGAGACGTTGATCGG-----	15592
QY	2882	CATTTCACAACTCTTATACTTTTCTCTTACAAAGTCGTTCCGGCTTCATCTGATTTTCAGC	2941
Db	15593	-ATTTCACAACTCTTATACTTTTCTCTTACAAAGTCGTTCCGGCTTCATCTGATTTTCAGC	15651
QY	2942	CTCTATACTTACTAAACGCGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCAGACT	3001
Db	15652	CTCTATACTTACTAAACGCGATAAAGTTTCTGTAAATTTCTACTGTATCGACTGCAGACT	15711
QY	3002	GGCTGTGTATAGGAGGCTGCACATTTATATCCCGAGAAACATCAGGTTAATGGCGTTTT	3061
Db	15712	GGCTGTGTATAGGAGGCTGCACATTTATATCCCGAGAAACATCAGGTTAATGGCGTTTT	15771
QY	3062	TGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCA	3121
Db	15772	TGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCA	15831
QY	3122	CACTCGGCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGATATGCACCACCGGCT	3181
Db	15832	CACTCGGCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGATATGCACCACCGGCT	15891
QY	3182	AAAGTTTCAGGAGACTTTTATCTGCAGCAGACGTGCACCTGGCCAGGGGGATCACCATCC	3241
Db	15892	AAAGTTTCAGGAGACTTTTATCTGCAGCAGACGTGCACCTGGCCAGGGGGATCACCATCC	15951
QY	3242	GTCCGCCGGCGGTGCAATAATATCACTCTGTACATCCCAAAACAGACGATACGGCTCT	3301
Db	15952	GTCCGCCGGCGGTGCAATAATATCACTCTGTACATCCCAAAACAGACGATACGGCTCT	16011
QY	3302	CTCTTTTATAGTGTAAACCTTAAACCTGCATTTACACAGTCCCTGTTCTCGTCAGCAAAA	3361
Db	16012	CTCTTTTATAGTGTAAACCTTAAACCTGCATTTACACAGTCCCTGTTCTCGTCAGCAAAA	16071
QY	3362	GAGCGGTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTCCCGTTTC	3421
Db	16072	GAGCGGTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTCCCGTTTC	16131
QY	3422	CAGCGTTCCGACGCGAGACGAGCGGGCTTCATCTCGATGGTGTGCTTACAGACCGGAG	3481
Db	16132	CAGCGTTCCGACGCGAGACGAGCGGGCTTCATCTCGATGGTGTGCTTACAGACCGGAG	16191
QY	3482	ATATTACACATCATATATGCTTCAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTA	3541
Db	16192	ATATTACACATCATATATGCTTCAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTA	16251
QY	3542	TACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCTGTTCTGTGATGAGATGATTTT	3601
Db	16252	TACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCTGTTCTGTGATGAGATGATTTT	16311
QY	3602	CAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTACACAAAAA	3661
Db	16312	CAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTACACAAAAA	16371
QY	3662	GAGGCTCGACCTCTCTTTTCTTATTTTATGATTTTAATACGGCATTTGAGGACAATA	3721
Db	16372	GAGGCTCGACCTCTCTTTTCTTATTTTATGATTTTAATACGGCATTTGAGGACAATA	16431
QY	3722	GCAGTAGGCTGGATACGACGATTCGTTTGTAGGAAGAACATTTGGAAGGCTGTCGGTCGA	3781
Db	16432	GCAGTAGGCTGGATACGACGATTCGTTTGTAGGAAGAACATTTGGAAGGCTGTCGGTCGA	16491
QY	3782	CTAAGTTGGCAGCATCACCCGAGAACATTTGGAAGGCTGTCGGTCGACTACAGTCACT	3841
Db	16492	CTAAGTTGGCAGCATCACCCGAGAACATTTGGAAGGCTGTCGGTCGACTACAGTCACT	16551
QY	3842	AATACCATCTAAGTAGTTGATTCATGATGACTGGATATGTTGTGTTTTACAGTATATGT	3901
Db	16552	AATACCATCTAAGTAGTTGATTCATGATGACTGGATATGTTGTGTTTTACAGTATATGT	16611
QY	3902	AGTCGTGTTTTTATGCAAAATCTAATTTAATATATGATATTTATATCATTTTACGTTTC	3961

; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 83.8%; Score 4077.2; DB 15; Length 17681;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 68; Indels 309; Gaps 5;

QY 122 GCGAATCTTGTACAAAAAGCTGACGAGAAAGCTGAAATGATATAAATATCAATATTT 181
Db 13025 GACAACTTGTACAAAAAGCTGACGAGAAAGCTGAAATGATATAAATATCAATATTT 13084

QY 182 AATTAGATTTGCATAAAAAGCTGACGAGAAAGCTGAAATGATATAAATATCAATATTT 241
Db 13085 AATTAGATTTGCATAAAAAGCTGACGAGAAAGCTGAAATGATATAAATATCAATATTT 13144

QY 242 ACTATGAATCAACTACTAGATGGTATTTAGTACCTGTAGTCAGCCGACGAGCCCTCCAAA 301
Db 13145 ACTATGAATCAACTACTAGATGGTATTTAGTACCTGTAGTCAGCCGACGAGCCCTCCAAA 13204

QY 302 TGTCTTCGGGTGATGCTGCAACTAGTCGACGAGCCCTTCCAAAATGCTTCTCTCAA 361
Db 13205 TGTCTTCGGGTGATGCTGCAACTAGTCGACGAGCCCTTCCAAAATGCTTCTCTCAA 13264

QY 362 ACCGAATCGTGTATCCAGCTACTCGCTATTTGCTCAATGCGGTATTAATATCAATAA 421
Db 13265 ACCGAATCGTGTATCCAGCTACTCGCTATTTGCTCAATGCGGTATTAATATCAATAA 13324

QY 422 AGAAATAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 481
Db 13325 AGAAATAAGAAAAAGAGTGGAGCCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 13384

QY 482 ATTCAATAGCTAGTGTATGCTGCAATCAATCTGATCAAGAACAAATTTCAAC 541
Db 13385 ATTCAATAGCTAGTGTATGCTGCAATCAATCTGATCAAGAACAAATTTCAAC 13444

QY 542 TCTTATATCTTTCTCTTACAAAGTGGTTCGGCTTCTATCTGATTTTTCAGCCCTCTATCTTA 601
Db 13445 TCTTATATCTTTCTCTTACAAAGTGGTTCGGCTTCTATCTGATTTTTCAGCCCTCTATCTTA 13504

QY 602 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGATATGCACTGAGAGCTGGCTGTGATA 661
Db 13505 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGATATGCACTGAGAGCTGGCTGTGATA 13564

QY 662 AGGAGCCCTGACATTTATATTTCCCGAGACATCAAGTTTAAATGCGGTTTGTGATCTATTT 721
Db 13565 AGGAGCCCTGACATTTATATTTCCCGAGACATCAAGTTTAAATGCGGTTTGTGATCTATTT 13624

QY 722 TCGGGTGGCTGAGATCAGCCACTTTCTTCCCGAGATACGGAGACCGGACACTGGCCATA 781
Db 13625 TCGGGTGGCTGAGATCAGCCACTTTCTTCCCGAGATACGGAGACCGGACACTGGCCATA 13684

QY 782 TCGGTGGTCAATCATGCGCCAGCTTTCTATCCCGATATGACACACGGGGTAAAGTTTCAGG 841
Db 13685 TCGGTGGTCAATCATGCGCCAGCTTTCTATCCCGATATGACACACCGGGTAAAGTTTCAGG 13744

QY 842 GAGACTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCACATCCGTCGCGCCGGC 901
Db 13745 GAGACTTTATCTGACAGCAGCTGCTGCTGCGGAGGATCACATCCGTCGCGCCGGC 13804

QY 902 GTGTCAATAATATCACTGTGTACATCCACAAACAGACGATACCGCTCTCTCTTTATAG 961
Db 13805 GTGTCAATAATATCACTGTGTACATCCACAAACAGACGATACCGCTCTCTCTTTATAG 13864

QY 962 GTGTAAACCTTAAACCTGCAATTTACAGTCCCTGTTCTGTCAGCAAAAGACCGTTTCAT 1021
Db 13865 GTGTAAACCTTAAACCTGCAATTTACAGTCCCTGTTCTGTCAGCAAAAGACCGTTTCAT 13924

QY 1022 TTCAATAAACCGGGCGACTCAGCCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCGGC 1081
Db 13925 TTCAATAAACCGGGCGACTCAGCCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCGGC 13984

QY 1082 ACGCAGACGACGGGCTTCATTTCTGATGGTTGTCTTACACAGACCGAGATATTCACATC 1141
Db 13985 ACGCAGACGACGGGCTTCATTTCTGATGGTTGTCTTACACAGACCGAGATATTCACATC 14044

QY 1142 ATATATGCTTGTAGCAACTGATAGTGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1201
Db 14045 ATATATGCTTGTAGCAACTGATAGTGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 14104

QY 1202 ATAGCACACCTCTTTTTCACATACCTTCGGGTAGTGCCTGATCAACCTCTCATTTTCGCCAA 1261
Db 14105 ATAGCACACCTCTTTTTCACATACCTTCGGGTAGTGCCTGATCAACCTCTCATTTTCGCCAA 14164

QY 1262 AAGTTGGCCCGAGGCTTCCCGGTATCAACAGGACACAGAGATTTATTTCTCGGAAG 1321
Db 14165 AAGTTGGCCCGAGGCTTCCCGGTATCAACAGGACACAGAGATTTATTTATTTCTCGGAAG 14224

QY 1322 TGATCTTTCGTCACAGGATTTTATTTGGCGCAAGTGGTCGGGTGATGCTGCCAACTTA 1381
Db 14225 TGATCTTTCGTCACAGGATTTTATTTGGCGCAAGTGGTCGGGTGATGCTGCCAACTTA 14284

QY 1382 GTCGACTACAGTCTCAATATACCATCTAAGTAGTTGATTCATAGTACCTGGATATGTTGT 1441
Db 14285 GTCGACTACAGTCTCAATATACCATCTAAGTAGTTGATTCATAGTACCTGGATATGTTGT 14344

QY 1442 GTTTTACAGTATTAATGATGCTGTTTATGCAAAATCAATTTAAATATGATATTT 1501
Db 14345 GTTTTACAGTATTAATGATGCTGTTTATGCAAAATCAATTTAAATATGATATTT 14404

QY 1502 ATATCATTTTACGTTTCTGTTACGTTTCTGTACAAAGTTGGCATTATTAAGAAAGCAT 1561
Db 14405 ATATCATTTTACGTTTCTGTTACGTTTCTGTACAAAGTTGGCATTATTAAGAAAGCAT 14447

QY 1562 TGCTTATCAATTTGTTGCAACGAAACAGTCACTATCAGTCAAAATCAATATTTTGC 1621
Db 14448 TGCTTATCAATTTGTTGCAACGAAACAGTCACTATCAGTCAAAATCAATATTTTGC 14447

QY 1622 CATCCAGTGCAGCTCCTCAGGAATTCGGTACCCAGCTTGGTAAGGAATAATATTTT 1681
Db 14448 CATCCAGTGCAGCTCCTCAGGAATTCGGTACCCAGCTTGGTAAGGAATAATATTTT 14492

QY 1682 TCTTTTTCCTTTTGTATATAAATAGTAAAGTATGATGTTAATAGTATGATATAAATA 1741
Db 14493 TCTTTTTCCTTTTGTATATAAATAGTAAAGTATGATGTTAATAGTATGATATAAATA 14552

QY 1742 TAGTGTGTTAAATGTTGCAAAAAATAATTTATAAATATTTGTTTACATAAACATAGT 1801
Db 14553 TAGTGTGTTAAATGTTGCAAAAAATAATTTATAAATATTTGTTTACATAAACATAGT 14612

QY 1802 AATGTAAAAAATAATGACAAAGTATGTAAGAGAGAGATATAAAGTTGACAGTAAGT 1861
Db 14613 AATGTAAAAAATAATGACAAAGTATGTAAGAGAGAGATATAAAGTTGACAGTAAGT 14672

QY 1862 ATATTTATTTTATGATTTGATCGAACATGTAAGTATGATATACTAGCATTAATTTGT 1921
Db 14673 ATATTTATTTTATGATTTGATCGAACATGTAAGTATGATATACTAGCATTAATTTGT 14732

QY 1922 TTTAATCATATATGATTAATCTAGCTGGTTTGTGATGAAATTAATATCAATGATAAATACTA 1981
Db 14733 TTTAATCATATATGATTAATCTAGCTGGTTTGTGATGAAATTAATATCAATGATAAATACTA 14792

QY 1982 TAGTAAAAATAAGAAATAAATAAATAAATAATTTTTTATGATTAATAGTTTATTAT 2041


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;
; OTHER INFORMATION: acceptor vector PHELLSGATE11
US-10-055-001A-25

Query Match      83.1%; Score 4042; DB 15; Length 17458;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 4419; Conservative 0; Mismatches 15; Indels 308; Gaps 6;

QY 4090 AGTCCTGCTTTAATGAGATATGCGAGACGCCCTATGATCGCATGATATTTGCTTCAATTC 4149
Db 16908 AGTCCTGCTTTAATGAGATATGCGAGACGCCCTATGATCGCATGATATTTGCTTCAATTC 16967
QY 4150 TGTGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCTCTTACCGCGGTTTCG 4209
Db 16968 TGTGTGACGCTGTGAAAAACCTGAGCATGTGTAGCTCAGATCTCTTACCGCGGTTTCG 17027
QY 4210 GTTCATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATATCTCCGT 4269
Db 17028 GTTCATCTTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATATCTCCGT 17087
QY 4270 TCAATTTACTGATGTGACCTACTATATATGTACAAATATTTAAATGAAACAATATAT 4329
Db 17088 TCAATTTACTGATGTGACCTACTATATATGTACAAATATTTAAATGAAACAATATAT 17147
QY 4330 TGTGCTGATAGTGTATAGGACATCTATGAGCGCCACAATAACAAACAATTTGCG 4389
Db 17148 TGTGCTGATAGTGTATAGGACATCTATGAGCGCCACAATAACAAACAATTTGCG 17207
QY 4390 TTTTATTTATCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACT 4449
Db 17208 TTTTATTTATCAAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACT 17267
QY 4450 GATTACATAATCTTATTTCAAAATTTTCAAAAGGCCCGGAGGCTAGTATCTACGACACAC 4509
Db 17268 GATTACATAATCTTATTTCAAAATTTTCAAAAGGCCCGGAGGCTAGTATCTACGACACAC 17327
QY 4510 GAGCGCGCAACTAATAACGTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCATGGG 4569
Db 17328 GAGCGCGCAACTAATAACGTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCATGGG 17387
QY 4570 TGAGATTCCTTGAAGTTGAGTATTTGGCGTCCGCTCTACCGAAAGTTACGGGCACCATTC 4629
Db 17388 TGAGATTCCTTGAAGTTGAGTATTTGGCGTCCGCTCTACCGAAAGTTACGGGCACCATTC 17447
QY 4630 AACCCGCTCCAGCACGCGCGCGGTAACCGACTTGTGTCGCCGAGAAATTTATGCGAAT 4689
Db 17448 AACCCGCTCCAGCACGCGCGCGGTAACCGACTTGTGTCGCCGAGAAATTTATGCGAAT 17507
QY 4690 TTTTGTGTATGTGGSCCCCAAAATGAAGTGCAGGTCAAACTTGACAGTGACGACAAAT 4749
Db 17508 TTTTGTGTATGTGGSCCCCAAAATGAAGTGCAGGTCAAACTTGACAGTGACGACAAAT 17567
QY 4750 GTTGGCGGGTCCAGCGCGAATTTTCGACACATGTGCGGCTCAGAGGACCTGCAG 4809
Db 17568 GTTGGCGGGTCCAGCGCGAATTTTCGACACATGTGCGGCTCAGAGGACCTGCAG 17627
QY 4810 GCATGCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTTAAATCTGC 4863
Db 17628 GCATGCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTACCTTAAATCTGC 17681

RESULT 5
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835N1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELUGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
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; OTHER INFORMATION: acceptor vector PHELLSGATE11
US-10-055-001A-25

Query Match      83.1%; Score 4042; DB 15; Length 17458;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 4419; Conservative 0; Mismatches 15; Indels 308; Gaps 6;

QY 122 GCCAACCTTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAAATATCAATATATT 181
Db 13025 GACAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAAATATCAATATATT 13084
QY 182 AAATTTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACAATATCCAGTC 241
Db 13085 AAATTTAGATTTTGCATAAAAACAGACTACATAATCTGTAAAAACACAATATCCAGTC 13144
QY 242 ACTATGAATCAACTACTTCTAGATGGTATTAGTGAACCTGTAGTCGACGACGCTTCCAAA 301
Db 13145 ACTATGAATCAACTACTTCTAGATGGTATTAGTGAACCTGTAGTCGACGACGCTTCCAAA 13204
QY 302 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 361
Db 13205 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 13264
QY 362 ACGGAATCGTGTATCCAGCCTTACTCGCTATTGTCTCAATGCCGCTATTAAATCATATAA 421
Db 13265 ACGGAATCGTGTATCCAGCCTTACTCGCTATTGTCTCAATGCCGCTATTAAATCATATAA 13324
QY 422 AGAATATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 481
Db 13325 AGAATATAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACCT 13384
QY 482 ATTCTATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAACAATTCACAAC 541
Db 13385 ATTCTATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAACAATTCACAAC 13444
QY 542 TCTTATACCTTTCTCTTACAAAGTGGTTCGGCTTCATCTGGATTTTCAGCCTCTATACCTA 601
Db 13445 TCTTATACCTTTCTCTTACAAAGTGGTTCGGCTTCATCTGGATTTTCAGCCTCTATACCTA 13504
QY 602 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACACTGGCTGTGTATA 661
Db 13505 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGACACTGGCTGTGTATA 13564
QY 662 AGGAGCCTTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGTTTTTGTATGTCATTT 721
Db 13565 AGGAGCCTTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGTTTTTGTATGTCATTT 13624
QY 722 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGAGACCGGACACTGGGCATA 781
Db 13625 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATACCGAGACCGGACACTGGGCATA 13684
QY 782 TCGGTGTGTCATATCGCCGACGCTTTTCATCCCGCATATGCACCAACCGGGTAAAGTTCA 841
Db 13685 TCGGTGTGTCATATCGCCGACGCTTTTCATCCCGCATATGCACCAACCGGGTAAAGTTCA 13744
QY 842 GAGACTTTATCTGACAGCAGACGTCGACCTGGCCAGGGGATACCATTCCTGCCCGGGC 901
Db 13745 GAGACTTTATCTGACAGCAGACGTCGACCTGGCCAGGGGATACCATTCCTGCCCGGGC 13804
QY 902 GTGTCAATATATATCTCTGTATATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG 961
Db 13805 GTGTCAATATATATCTCTGTATATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG 13864
QY 962 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTCGTACGAAAAAGAGCGGTTTAT 1021
Db 13865 GTGTAAACCTTAAACTGCAATTTTCCAGTCCCTGTTCTCGTACGAAAAAGAGCGGTTTAT 13924
QY 1022 TTCAATTAACCGGCGGACCTCAGCCATCTCTGATTTTTCGCTTTCCAGGTTTCGGC 1081
Db 13925 TTCAATTAACCGGCGGACCTCAGCCATCTCTGATTTTTCGCTTTTCAGGTTTCGGC 13984
QY 1082 ACGCAGACGAGCGGCTTCAATTCGTGATGTTGTGCTTACACAGCCGGAGATATTGACATC 1141
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Db	13985	ACGCAGCAGCGGGCTTCATTTCTGCAATGGTTGTCTTCCACGACCGGAGATATTGACATC	14044
Qy	1142	ATATATGCTTGGACCACTGATAGCTGTCGCTGTCAACTGTCTACCTGTAATAGCTGCTTC	1201
Db	14045	ATATATGCTTGGACCACTGATAGCTGTCGCTGTCAACTGTCTACCTGTAATAGCTGCTTC	14104
Qy	1202	ATAGCACACCTCTTTTTGACATACTTCGGGTAGTGCAGATCAAGCTCTCATTTTCGCCAA	1261
Db	14105	ATAGCACACCTCTTTTTGACATACTTCGGGTAGTGCAGATCAAGCTCTCATTTTCGCCAA	14164
Qy	1262	AAGTTGGCCAGGGCTTCCCGGTATCAACAGGACACACAGGATTTATTTATTTCTGCGAAG	1321
Db	14165	AAGTTGGCCAGGGCTTCCCGGTATCAACAGGACACACAGGATTTATTTATTTCTGCGAAG	14224
Qy	1322	TGATCTTCGGTCACAGGTATTTATTTCCGGCGAAAGTGGCTCGGTGATGCTGCGCAACTTA	1381
Db	14225	TGATCTTCGGTCACAGGTATTTATTTCCGGCGAAAGTGGCTCGGTGATGCTGCGCAACTTA	14284
Qy	1382	GTCGACTACAGTCTACTAATACATCTAGTAGTTCATTCATAGTCACATGGATATCTTGT	1441
Db	14285	GTCGACTACAGTCTACTAATACATCTAGTAGTTCATTCATAGTCACATGGATATCTTGT	14344
Qy	1442	GTTTTACAGTATATGTAAGTCTGTTTTTATGCAAAATCTAAATTTAATATATTTGATTT	1501
Db	14345	GTTTTACAGTATATGTAAGTCTGTTTTTATGCAAAATCTAAATTTAATATATTTGATTT	14404
Qy	1502	ATATCAATTTACGTTTCTCGTTCAGCTTCTTGTGACAAAGTTGGCATTTAAGAAAGCAT	1561
Db	14405	ATATCAATTTACGTTTCTCGTTCAGCTTCTTGTGACAAAGTTGGCATTTAAGAAAGCAT	14448
Qy	1562	TGCTTATCAATTTGTTGCAACGAAAGGTCACATCAGTCAAAATAAAATCATTATTTGC	1621
Db	14449	-----	14448
Qy	1622	CATCCAGCTGCAGCTCCTCGAGAAATTCGGTACCCGAGCTTGGTAAGGAATTAATTTT	1681
Db	14449	-----CTCGAGAAATTCGGTACC-----AACTGTGAAGGAATTAATTTT	14488
Qy	1682	TCCTTTTTCCTTTTAGTATATAATAGTTAAAGTGATGTTAATTTAGTATGATTAATAATA	1741
Db	14489	TCCTTTTTCCTTTTAGTATATAATAGTTAAAGTGATGTTAATTTAGTATGATTAATAATA	14548
Qy	1742	TAGTTGTTATAATTTGTGAAAAATAATTTATAATAATTTGTTTACATAAACACATAGT	1801
Db	14549	TAGTTGTTATAATTTGTGAAAAATAATTTATAATAATTTGTTTACATAAACACATAGT	14608
Qy	1802	AATGTAAAAAATAATGACAACTGATGTGAAGCGAAGAGATATAAAGTTTCAGAGTAAGT	1861
Db	14609	AATGTAAAAAATAATGACAACTGATGTGAAGCGAAGAGATATAAAGTTTCAGAGTAAGT	14668
Qy	1862	ATATTTATTTTAAATGAATTTGATCGAATCTGTAAGATGATATCTAGCATTTAATTTGT	1921
Db	14669	ATATTTATTTTAAATGAATTTGATCGAATCTGTAAGATGATATCTAGCATTTAATTTGT	14728
Qy	1922	TTTAATCATAAATAGTAATCTAGCTGTTTCATGAAATTAATATCAATGATAAATACTA	1981
Db	14729	TTTAATCATAAATAGTAATCTAGCTGTTTCATGAAATTAATATCAATGATAAATACTA	14788
Qy	1982	TAGTAAAAATAAGATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	2041
Db	14789	TAGTAAAAATAAGATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	14848
Qy	2042	ATAATTAATAATCTATACCATTTACTAAATATTTTATAGTTTAAAGTTAATAATTTTGT	2101
Db	14849	ATAATTAATAATCTATACCATTTACTAAATATTTTATAGTTTAAAGTTAATAATTTTGT	14908
Qy	2102	TAGAAATTTCCATCTGCTGTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAG	2161
Db	14909	TAGAAATTTCCATCTGCTGTGTAATTTATCAATAAACAATAATTAATAACAAGCTAAAG	14966
Qy	2162	TAACAAAATAATCAAACTAATAGAAACAGTAAATCTAATGTAAACAAAAACATAATCTAATG	2221

14969	Db	TACAAATAATATCAAACTAATAAGAAACAGTAATCTAATGTAAACAAACATAATCTTAAG	15028
2222	Qy	CTAATAATAACAAAGCGAAGTCTCATATTTTATATAGTATTATTTTCAATCAACATCTCT	2281
15029	Db	CTAATAATAACAAAGCGAAGTCTCATATTTTATATAGTATTATTTTCAATCAACATCTCT	15088
2282	Qy	TATTAATTTCTAAATAATACCTGTAGTGTTTATTAACCTCTAAATGGATGACTATTATTT	2341
15089	Db	TATTAATTTCTAAATAATACCTGTAGTGTTTATTAACCTCTAAATGGATGACTATTATTT	15148
2342	Qy	AAATGAATTAGTCGAACATGAAATAAACAAGCTAAACATGATAGATCATGCTCATTTGGTTAT	2401
15149	Db	AAATGAATTAGTCGAACATGAAATAAACAAGCTAAACATGATAGATCATGCTCATTTGGTTAT	15208
2402	Qy	CATTGATCTTACATTTGGATTGATTAACAGTTGGGAAGCTGGTTCGAAATCGATAAGCTTT	2461
15209	Db	CATTGATCTTACATTTGGATTGATTAACAGTTTACCTCTTACCTCTTACCTCTTACCTCT	15254
2462	Qy	GGATCCTCTAGAGAGCTGCAGCTGGATGGCAATAAATGATTTTATTTGACTGATAGTA	2521
15255	Db	GGATCCTCTAGA-----	15266
2522	Qy	CCTGTTCTGTGCAACAAATTGATAAGCAATGCTTTCTTATATGCGCAACTTTGTATCAAGA	2581
15267	Db	-----CCACTTTGTACAAGA	15281
2582	Qy	AAGCTGAACGAGAAACGTAAAAATGATATAAATATCAATATATAAATPAGATTTTGCATA	2641
15282	Db	AAGCTGAACGAGAAACGTAAAAATGATATAAATATCAATATATAAATPAGATTTTGCATA	15341
2642	Qy	AAAAACAGACTACATAATCTGTAAAAACAAACATATCCAGTCACTATGAATCAACTACT	2701
15342	Db	AAAAACAGACTACATAATCTGTAAAAACAAACATATCCAGTCACTATGAATCAACTACT	15401
2702	Qy	TAGATGGTATTAGTGACCTGTAGTCGACTPAAGTTGGCAGCATCACCGCAGCACTTTGGG	2761
15402	Db	TAGATGGTATTAGTGACCTGTAGTCGACTPAAGTTGGCAGCATCACCGCAGCACTTTGGG	15461
2762	Qy	CGGAATAAATACCTGTGACGGAGATCACTTCGCAGAAATAAATAAATCCTGGTGTCCCTG	2821
15462	Db	CGGAATAAATACCTGTGACGGAGATCACTTCGCAGAAATAAATAAATCCTGGTGTCCCTG	15521
2822	Qy	TTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAAATGAGACGTTGATCGGCATCAC	2881
15522	Db	TTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAAATGAGACGTTGATCGG-----	15574
2882	Qy	CATTTCAGAACTCTTATCTTTTCTTCTTACAGTCGTTGGCTTCATCTGGATTTTCAGC	2941
15575	Db	-ATTTCACRACCTCTTATCTTTTCTTCTTACAGTCGTTGGCTTCATCTGGATTTTCAGC	15633
2942	Qy	CTCTATATCTTACTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACT	3001
15634	Db	CTCTATATCTTACTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACT	15693
3002	Qy	GGCTGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGTTAATGCGGTTTT	3061
15694	Db	GGCTGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGTTAATGCGGTTTT	15753
3062	Qy	TGATGTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGGATTAACGAGACCGGCA	3121
15754	Db	TGATGTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGGATTAACGAGACCGGCA	15813
3122	Qy	CACCTGGCCATATCGGTGGTCAATCATATGCGCAGCTTTTATCCCGATATGACCAACCGGT	3181
15814	Db	CACCTGGCCATATCGGTGGTCAATCATATGCGCAGCTTTTATCCCGATATGACCAACCGGT	15873
3182	Qy	AAAGTTACCGGAGACTTTATCTCACAGCAGACGTGCACTGGCCAGGGGATCACCATCC	3241
15874	Db	AAAGTTACCGGAGACTTTATCTCACAGCAGACGTGCACTGGCCAGGGGATCACCATCC	15933
3242	Qy	GTGCGCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCT	3301
15934	Db	GTGCGCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGATAACGGCTCT	15993

QY	3302	CTCTTTTATAGGTGTAACCTTTAAACTGCAATTTCAACCACTCCCTGTTCTCGTCAGCAAAA	3361
Db	15994	CTCTTTTATAGGTGTAACCTTTAAACTGCAATTTCAACCACTCCCTGTTCTCGTCAGCAAAA	16053
QY	3362	GAGCGGTTCAATTTCAATAAACCGGGGAGCACTCAGCCATCCCTTCCGTGATTTCCCGTTTC	3421
Db	16054	GAGCGGTTCAATTTCAATAAACCGGGGAGCACTCAGCCATCCCTTCCGTGATTTCCCGTTTC	16113
QY	3422	CAGCGTTCCGGACGACAGACGCGGCTTCATTTCTGTCATGGTTGTGCTTACCCAGACCGGAG	3481
Db	16114	CAGCGTTCCGGACGACAGACGCGGCTTCATTTCTGTCATGGTTGTGCTTACCCAGACCGGAG	16173
QY	3482	ATATTGACATCATATATGCTTGTAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTATA	3541
Db	16174	ATATTGACATCATATATGCTTGTAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTATA	16233
QY	3542	TACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTTCTGTCATGTCAGATGATTTT	3601
Db	16234	TACGCTGCTTCATAGCACACCTCTTTTTCACATACCTTTCTGTCATGTCAGATGATTTT	16293
QY	3602	CAGGACTATGACACTAGCGTATATAGTAAGTAGATGTTTTTATTTGTGCACAAAAA	3661
Db	16294	CAGGACTATGACACTAGCGTATATAGTAAGTAGATGTTTTTATTTGTGCACAAAAA	16353
QY	3662	GAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTAATAAGCGCATTCAGGACAATA	3721
Db	16354	GAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTAATAAGCGCATTCAGGACAATA	16413
QY	3722	GGAGTAGGCTGGATACGACGATTCGGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGA	3781
Db	16414	GGAGTAGGCTGGATACGACGATTCGGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGA	16473
QY	3782	CTAAGTTGCGACATCACCGAAGACATTTGGAAGGCTGTCGGTCGACTACAGGTCAC	3841
Db	16474	CTAAGTTGCGACATCACCGAAGACATTTGGAAGGCTGTCGGTCGACTACAGGTCAC	16533
QY	3842	AATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGT	3901
Db	16534	AATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGT	16593
QY	3902	AGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATTAATATATCATTTTACGTTTC	3961
Db	16594	AGTCTGTTTTTATGCAAAATCTAAATTAATATATTGATTAATATATCATTTTACGTTTC	16653
QY	3962	TCGTTTCAGCTTTTTTCGACAAAGTCGCAATTAATAAAAAACAATTCATCAATTTCTTG	4021
Db	16654	TCGTTTCAGCTTTTTTCGACAAAGTCGCAATTAATAAAAAACAATTCATCAATTTCTTG	16679
QY	4022	CAACGAACAGGTCACATCAGTCAAAATAAAATCATTTTGGGGCCCGAGATCCATGCT	4081
Db	16680	-----	16679
QY	4082	AGCTCTAGAGTCCTGCTTTTAATGAGATATGCGAGAGCCCTATGATCGCATGATTTTGCT	4141
Db	16680	-----TCTAGAGTCCTGCTTTTAATGAGATATGCGAGAGCCCTATGATCGCATGATTTTGCT	16736
QY	4142	TTCAATTCCTGTTGTGCACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATTCCTTACCGC	4201
Db	16737	TTCAATTCCTGTTGTGCACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATTCCTTACCGC	16796
QY	4202	CGGTTTCGGTTCAATCTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATA	4261
Db	16797	CGGTTTCGGTTCAATCTAATGAATATATCAACCGTTACTATCGTATTTTATGAATAATA	16856
QY	4262	TTCTCCGTTCAATTTACTGATTTGTAACCTACTCTTATATGTACAATATTTAAATGAATA	4321
Db	16857	TTCTCCGTTCAATTTACTGATTTGTAACCTACTCTTATATGTACAATATTTAAATGAATA	16916
QY	4322	CAATATATTTGCTGAATAGGTTTATAGGACATCTATGATAGAGCGCCCAATATAAATA	4381
Db	16917	CAATATATTTGCTGAATAGGTTTATAGGACATCTATGATAGAGCGCCCAATATAAATA	16976

QY	4382	CAATTGCGTTTATTATTACAAATCAATTTAAAAAGCGCGACGACCGTCAAACT	4441
Db	16977	CAATTGCGTTTATTATTACAAATCAATTTAAAAAGCGCGACGACCGTCAAACT	17036
QY	4442	AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTAC	4501
Db	17037	AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTAC	17096
QY	4502	GAACACCGAGCGCGGAACCTAATAACGTTCACTGAAGGGAACTCCCGTTCCCGCCCGCGG	4561
Db	17097	GAACACCGAGCGCGGAACCTAATAACGTTCACTGAAGGGAACTCCCGTTCCCGCCCGCGG	17156
QY	4562	CGCATGGGTGAGATTCCTTTGAAAGTTCAGTATGGCCGTCGCTCTACCGAAAGTTACGGG	4621
Db	17157	CGCATGGGTGAGATTCCTTTGAAAGTTCAGTATGGCCGTCGCTCTACCGAAAGTTACGGG	17216
QY	4622	CACCAATTCAAACCCGGTCCAGCAGCGCGCGGGTAAACCGACTTGTCTGCCCGAGAAATTAT	4681
Db	17217	CACCAATTCAAACCCGGTCCAGCAGCGCGCGGGTAAACCGACTTGTCTGCCCGAGAAATTAT	17276
QY	4682	GGAGCAATTTTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACCTTGACAGTGA	4741
Db	17277	GGAGCAATTTTGGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACCTTGACAGTGA	17336
QY	4742	CGACAAATCGTTGGGCGGTCCAGAGCGGAATTTTGGCAACAATGTCAGGCTCAGCAGG	4801
Db	17337	CGACAAATCGTTGGGCGGTCCAGAGCGGAATTTTGGCAACAATGTCAGGCTCAGCAGG	17396
QY	4802	ACCTGAGCGATGCAAGCTAGCTTACTAGTATGCATATTTCTATAGTGTCACTTAAATCT	4861
Db	17397	ACCTGAGCGATGCAAGCTAGCTTACTAGTATGCATATTTCTATAGTGTCACTTAAATCT	17456
QY	4862	GC 4863	
Db	17457	GC 17458	

RESULT 6

US-10-055-001A-13

Sequence 13, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Waterhouse, Peter

APPLICANT: Helliwell, Christopher A.

TITLE OF INVENTION: Method and means for producing efficient silencing constr

TITLE OF INVENTION: using recombinational cloning

FILE REFERENCE: HELIGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 18691

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: acceptor vector pHELLSGATE

FEATURE:

NAME/KEY: misc feature

LOCATION: (7922)..(9985)

OTHER INFORMATION: spectinomycin resistance

FEATURE:

NAME/KEY: misc feature

LOCATION: (10706)..(11324)

OTHER INFORMATION: right T-DNA border fragment

FEATURE:

NAME/KEY: misc feature

LOCATION: (11674)..(13019)

OTHER INFORMATION: CamV35S promoter fragment

FEATURE:

NAME/KEY: misc feature

LOCATION: (17890)..(17659)

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; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17610)..(16855)
; OTHER INFORMATION: codb selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14650)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15002)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: codb selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13
;
; Query Match 82.0%; Score 3985.4; DB 15; Length 18691;
; Best Local Similarity 85.1%; Pred.No. 0; Mismatches 16; Indels 831; Gaps 2;
; Matches 4846; Conservative 0;
;
QY 1 TTTTCAATTTGGAGAGGACGCTCGAGCTAGCATGGATCTCGGGCCCCAAAATAATGATTT 60
DB 13000 TTTCAATTTGGAGAGGACGCTCGAGCTAGCATGGATCTCGGGCCCCAAAATAATGATTT 13059
QY 61 TATTTTGACTGATGATGACCTGTTCTGTCACAAATTCGATGAGCAATGCTTTTATATAA 120
DB 13060 TATTTTGACTGATGATGACCTGTTCTGTCACAAATTCGATGAGCAATGCTTTTATATAA 13119
QY 121 TGCACATTTTGTACAAAAGCTGGAACGAGAAAGCTAAATGATATAAATATCAATATAT 180
DB 13120 TGCACATTTTGTACAAAAGCTGGAACGAGAAAGCTAAATGATATAAATATCAATATAT 13179
QY 181 TAAATAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACATATCCAGT 240
DB 13180 TAAATAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACATATCCAGT 13239
QY 241 CACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGAGCGGACGCTTCCAA 300
DB 13240 CACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGAGCGGACGCTTCCAA 13299
QY 301 ATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGGACGCTTCCAAATGTTCTTCTCA 360
DB 13300 ATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGGACGCTTCCAAATGTTCTTCTCA 13359
QY 361 AACGGAATCGTGGTATCCAGCCTACTCGCTATTGTCTCAATCGGTATTAAATCATATAA 420
DB 13360 AACGGAATCGTGGTATCCAGCCTACTCGCTATTGTCTCAATCGGTATTAAATCATATAA 13419
QY 421 AAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACC 480
DB 13420 AAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAACATCTACC 13479
QY 481 TATTATATACGCTAGTGTGATAGTCTGAAATCATCTGATCAAGAAATCTCAAA 540
DB 13480 TATTATATACGCTAGTGTGATAGTCTGAAATCATCTGATCAAGAAATCTCAAA 13539
QY 541 CTCCTTATACCTTTCTCTTACAAAGTCGTTTCGGCTTCTCTGATTTTCAGGCTCTATATCTT 600
DB 13540 CTCCTTATACCTTTCTCTTACAAAGTCGTTTCGGCTTCTCTGATTTTCAGGCTCTATATCTT 13599
QY 601 ACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTCGAGCTGGCTGTGAT 660
DB 13600 ACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTCGAGCTGGCTGTGAT 13659
QY 661 AAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTGTGATGTCATT 720
DB 13660 AAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTGTGATGTCATT 13719
QY 721 TTCGGGTGGCTGAGATCAGCCACTTTCTTCCCGGATAACGAGACCCGGCACACTGGCCAT 780
DB 13720 TTCGGGTGGCTGAGATCAGCCACTTTCTTCCCGGATAACGAGACCCGGCACACTGGCCAT 13779
QY 781 ATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATGACACCCGGGTAAAGTTACG 840
DB 13780 ATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATGACACCCGGGTAAAGTTACG 13839
QY 841 GGAGACTTTTATCTGACAGCAGCTGACCTGCGCAGGGGGATCACCATCCGTCGCCCGG 900
DB 13840 GGAGACTTTTATCTGACAGCAGCTGACCTGCGCAGGGGGATCACCATCCGTCGCCCGG 13899
QY 901 CGTGTCAATAATATCACTCTGTATACACAAACAGACGATACCGGCTCTCTCTTTTATA 960
DB 13900 CGTGTCAATAATATCACTCTGTATACACAAACAGACGATACCGGCTCTCTCTTTTATA 13959
QY 961 GGTGTAAACCTTAACTGCATTTACAGTCCTGTTCTCTGTCAGCAAAAGACGGTCA 1020
DB 13960 GGTGTAAACCTTAACTGCATTTACAGTCCTGTTCTCTGTCAGCAAAAGACGGTCA 14019
QY 1021 TTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTCCAGCGCTTCGG 1080
DB 14020 TTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTCCAGCGCTTCGG 14079
QY 1081 CACGACAGACGCGGCTTCATTTGTCATGTTGTGTTTACAGACCGGAGATATTGACAT 1140
DB 14080 CACGACAGACGCGGCTTCATTTGTCATGTTGTGTTTACAGACCGGAGATATTGACAT 14139
QY 1141 CATATATGCTTTGACAACTGATAGCTGCTGCTCACTGCTCACTGTAATACGCTGCTT 1200
DB 14140 CATATATGCTTTGACAACTGATAGCTGCTGCTCACTGCTCACTGTAATACGCTGCTT 14199
QY 1201 CATAGCACACCTCTTTTGTGACATCTTCGGGTAGTGGCGGATCAACGCTCTCACTTTTCGCCA 1260
DB 14200 CATAGCACACCTCTTTTGTGACATCTTCGGGTAGTGGCGGATCAACGCTCTCACTTTTCGCCA 14259
QY 1261 AAAGTTGCGCCAGGCTTCCCGGTATCAACAGGGACACACAGATTTATTTATTTCTGCGAA 1320
DB 14260 AAAGTTGCGCCAGGCTTCCCGGTATCAACAGGGACACACAGATTTATTTATTTCTGCGAA 14319
QY 1321 GTGATCTTCGCTCAGGATTTATTTCCGCGCAAGTCGCTGGGTGATGCTGCCAATCT 1380
DB 14320 GTGATCTTCGCTCAGGATTTATTTCCGCGCAAGTCGCTGGGTGATGCTGCCAATCT 14379
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QY	1381	AGTCGACTACAGGTCACATAACCACTAAGPAGTTGATGATGACTGATGATGTTG	1440
Db	14380	AGTCGACTACAGGTCACATAACCACTAAGPAGTTGATGATGACTGATGATGTTG	14439
QY	1441	TGTTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATATT	1500
Db	14440	TGTTTTACAGTATTATGATGCTGTTTTTTATGCAAAATCTAATTTAATATATGATATT	14499
QY	1501	TATATCAITTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTTGGCATTATAAGAAAGCA	1560
Db	14500	TATATCAITTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTTGGCATTATAAGAAAGCA	14559
QY	1561	TTGCTTATCAATTTGTTGCAACGAACAGGTCTACTATCAGTCAAAATCAATTTATTG	1620
Db	14560	TTGCTTATCAATTTGTTGCAACGAACAGGTCTACTATCAGTCAAAATCAATTTATTG	14619
QY	1621	CCATCCAGCTGAGCTCCCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATAATTATT	1680
Db	14620	CCATCCAGCTGAGCTCCCTCGAGGAATTCGGTACCCCA-ATTGGTAAAGAAATAATTATT	14678
QY	1681	TTCTTTTTTCTTTTGTATATAAAATAGTTTAAAGTGAATTTAGTATGATTTAATAAT	1740
Db	14679	TTCTTTTTTCTTTTGTATATAAAATAGTTTAAAGTGAATTTAGTATGATTTAATAAT	14738
QY	1741	ATAGTTGTTTATTAATTTGTGAAAAATAATTTTATAATATATTTTACATAAACACATAG	1800
Db	14739	ATAGTTGTTTATTAATTTGTGAAAAATAATTTTATAATATATTTTACATAAACACATAG	14798
QY	1801	TAATGTAAAAAATATGACAGTGTGTGTAAGACGAAGATAAAAAGTTGAGAGTAAG	1860
Db	14799	TAATGTAAAAAATATGACAGTGTGTGTAAGACGAAGATAAAAAGTTGAGAGTAAG	14858
QY	1861	TATATATTTTAAATGAATTTGATCGAACATGTAGATGATATCTAGCAITTA	1914
Db	14859	TATATATTTTAAATGAATTTGATCGAACATGTAGATGATATCTAGCGCGTAAAGAGTT	14918
QY	1915	-----	1914
Db	14919	CCAACTTTCACCATTAATGAAATAAGATCACTACCGGGCGGTATTTTGTAGTTATCGAGAT	14978
QY	1915	-----	1914
Db	14979	TTTTCAGGACTAAGGAAGCTAAATAATGAGAAATAAATCACTGATATACCACCGTTGATA	15038
QY	1915	-----	1914
Db	15039	TATCCCAATGGCATCGTAAAGAACATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTACCT	15098
QY	1915	-----	1914
Db	15099	ATAACGAGACCGTTCAGCTGGATATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGC	15158
QY	1915	-----	1914
Db	15159	ACHAAGTTTATCCGGCCTTTATTCACATTTCTTGCCCGCGCTGATGAATGCTCATCCGGAAT	15218
QY	1915	-----	1914
Db	15219	TCCGTATGCAATGAAGAAGCGGTGAGCTGGTGATATGGGATAGTTTCACCCCTTGTACA	15278
QY	1915	-----	1914
Db	15279	CCGTTTTCCATGAGCAAACTGAACCGTTTTCATCGCTCTGGAGTGAATACCAGCAGATT	15338
QY	1915	-----	1914
Db	15339	TCCGGCAGTTTTCACACATATATTCGCAGATGTGGCGTGTACGGGTGAACCTGGCCT	15398
QY	1915	-----	1914
Db	15399	ATTTCCCTAAAGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTT	15458
QY	1915	-----	1914
Db	15459	TCACCAGTTTGTATTTAAACGTGCCCAATATGGACAACTTCTTCCGCCCCCGTTTTCACCA	15518
QY	1915	-----	1914
Db	15519	TGGGCAAAATATTATACGCAAGCGACCAAGGTGCTGATGCCCGTGGCGATTCCAGTTTCATC	15578
QY	1915	-----	1914
Db	15579	ATGCCGTCTGTGATGGCTTCCATGTCCGCAAGATGCTTTAATGAATTTACAACAGTACTGCG	15638
QY	1915	-----	1914
Db	15639	ATGAGTGGCAGGGCGGGCGGTAAATCGCGGTGATCGGGCTTACTAAAAGCCAGATAACAGT	15698
QY	1915	-----TATTTGTTTTTAATCAT	1930
Db	15699	ATGCCGTATTTTCGGCGTGAATTTTTCGGGTAATAAGAAATATATCTGATATGTCGGGCCCAT	15758
QY	1931	AATAGTAAATTTCTAGCTGGTTTGTGATGAATTAATATCAATGATAAAATCTATAGTAAAAA	1990
Db	15759	AATAGTAAATTTCTAGCTGGTTTGTGATGAATTAATATCAATGATAAAATCTATAGTAAAAA	15818
QY	1991	TAAGAAATAAAATAAAATAATATTTTATGATTAAATAGTTTATATATAATTTAAA	2050
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QY	2051	TATCTATACCATTAATAAATATTTAGTTTAAAAAGTTAAATAAATTTTGTAGAAATTC	2110
Db	15879	TATCTATACCATTAATAAATATTTAGTTTAAAAAGTTAAATAAATTTTGTAGAAATTC	15938
QY	2111	CAATCTGCTTGTATTTATCAATAAACAATAATTTAATAACACAGCTAAAGCTACAAATA	2170
Db	15939	CAATCTGCTTGTATTTATCAATAAACAATAATTTAATAACACAGCTAAAGCTACAAATA	15998
QY	2171	ATATCAAACTAATAAGAACAGTAAATCTAATGTAAACAAACATAATCTAATGCTAATAATA	2230
Db	15999	ATATCAAACTAATAAGAACAGTAAATCTAATGTAAACAAACATAATCTAATGCTAATAATA	16058
QY	2231	CAAGCGCAAGATCTATCATTTTATATAGTATTTATTTCAATCAACATCTTATTATTAATTT	2290
Db	16059	CAAGCGCAAGATCTATCATTTTATATAGTATTTATTTCAATCAACATCTTATTATTAATTT	16118
QY	2291	CTAATATATCTGTAGTTTATTAACCTTCTAATAATGGAATTCACATTTAATTTAAATGAATTT	2350
Db	16119	CTAATATATCTGTAGTTTATTAACCTTCTAATAATGGAATTCACATTTAATTTAAATGAATTT	16178
QY	2351	AGTCGAACATGAATAAACAAGCTAACATGATAGATCATGTCTATTTGTATTCAATGTATCT	2410
Db	16179	AGTCGAACATGAATAAACAAGCTAACATGATAGATCATGTCTATTTGTATTCAATGTATCT	16238
QY	2411	TACATTTGGATTGATTACAGTTGGGAAGCTGGTTTGGAAATCGATAAGCTTTGGATCTCT	2470
Db	16239	TACATTTGGATTGATTACAGTTGGGAAGCTGGTTTGGAAATCGATAAGCTTTGGATCTCT	16298
QY	2471	AGAGAGCTGCAGCTGGATGGCAATAATAATTTTATTTTGTAGTGTAGTGCCTGTCTGT	2530
Db	16299	AGAGAGCTGCAGCTGGATGGCAATAATAATTTTATTTTGTAGTGTAGTGCCTGTCTGT	16358
QY	2531	TGCAACAAATTTGATGAAGCAATGCTTTTCTTATAATGCCAACTTTTGPACAAAGCTGAAC	2590
Db	16359	TGCAACAAATTTGATGAAGCAATGCTTTTCTTATAATGCCAACTTTTGPACAAAGCTGAAC	16418
QY	2591	GAGAAACGTAAATGATATAAATATCAATATATTAATTAGATTTTGTATATAAACAACA	2650
Db	16419	GAGAAACGTAAATGATATAAATATCAATATATTAATTAGATTTTGTATATAAACAACA	16478
QY	2651	CTACATAATCTGTAAAAACACACATATCCAGTCTACTATGAATCAACTTCTAGATGGTA	2710
Db	16479	CTACATAATCTGTAAAAACACACATATCCAGTCTACTATGAATCAACTTCTAGATGGTA	16538
QY	2711	TTAGTGACCTGTAGTCGATGAATTTGGCAGCATCACCGACGCACTTTTGGCCCGCAATAA	2770

Db 16539 TTAGTGACCTGTAGTGCATAGTGTGGCAGCATCACCCGAGCAGCATTTTCGCCGCGAATAAA 16598
QY 2771 TACCTGTGACGGAAGATCACTTCCGAGATAAATAAATCCTGGTGTCCCTGTGTATACCG 2830
Db 16599 TACCTGTGACGGAAGATCACTTCCGAGATAAATAAATCCTGGTGTCCCTGTGTATACCG 16658
QY 2831 GGAGCCCTGGCCCAACTTTTGGCGAAATGAGAGCTTCATCGGCACCTACCCATTTCACA 2890
Db 16659 GGAAGCCCTGGCCCAACTTTTGGCGAAATGAGAGCTTCATCGGCACCTACCCATTTCACA 16718
QY 2891 ACTCTTATATCTTTCTCTTACAGTCCGTTCGGCTTCATCTGGATTTTCAGGCTCTATATCT 2950
Db 16719 ACTCTTATATCTTTCTCTTACAGTCCGTTCGGCTTCATCTGGATTTTCAGGCTCTATATCT 16778
QY 2951 TACTAAACGTGATAAAGTTCCTGTAAATTTCTACTGTATCGACTGAGACTGGCTGTGTGA 3010
Db 16779 TACTAAACGTGATAAAGTTCCTGTAAATTTCTACTGTATCGACTGAGACTGGCTGTGTGA 16838
QY 3011 TAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTTTGTATGTCAT 3070
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QY 3071 TTTTCGGGTGGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACCGGCCACACTGGCCA 3130
Db 16899 TTTTCGGGTGGCTGAGATCAGCCACTTTCTTCCCGATAACGGAGACCGGCCACACTGGCCA 16958
QY 3131 TATCGGTGTATCATGCGCAGCTTTGATCCCGATATGACACCGGGTAAAGTTTAC 3190
Db 16959 TATCGGTGTATCATGCGCAGCTTTGATCCCGATATGACACCGGGTAAAGTTTAC 17018
QY 3191 GGGAGACTTTATCTGACAGCAGCTGTCAGTCCGAGGGGATCACCATCCGTCGCCCGG 3250
Db 17019 GGGAGACTTTATCTGACAGCAGCTGTCAGTCCGAGGGGATCACCATCCGTCGCCCGG 17078
QY 3251 GGGTGTCAATAATPACTCTGTATATCCAAACAGAGATTAACGGCTCTCTCTTTTAT 3310
Db 17079 GGGTGTCAATAATPACTCTGTATATCCAAACAGAGATTAACGGCTCTCTCTTTTAT 17138
QY 3311 AGGTGTAAACCTTAACCTGATTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGGTC 3370
Db 17139 AGGTGTAAACCTTAACCTGATTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGGTC 17198
QY 3371 ATTTCAATAAACCGGCGACCTCAGCCATCCCTTCCTGATTTTCGCTTTCCAGCGGTCG 3430
Db 17199 ATTTCAATAAACCGGCGACCTCAGCCATCCCTTCCTGATTTTCGCTTTCCAGCGGTCG 17258
QY 3431 GCACGACGACGCGGCTTCAITCTGATGTTGTGCTTACAGACCGGAGATATTGACA 3490
Db 17259 GCACGACGACGACGCGGCTTCAITCTGATGTTGTGCTTACAGACCGGAGATATTGACA 17318
QY 3491 TCATATATGCTTGTAGCACTGATAGTGTGCTGCTGCTCAACTGTCACTGTAAATACGCTGCT 3550
Db 17319 TCATATATGCTTGTAGCACTGATAGTGTGCTGCTGCTCAACTGTCACTGTAAATACGCTGCT 17378
QY 3551 TCATAGCACACCTCTTTTGTACATCTCTGTTCTTGTGATGAGATGATTTTCAGGACTAT 3610
Db 17379 TCATAGCACACCTCTTTTGTACATCTCTGTTCTTGTGATGAGATGATTTTCAGGACTAT 17438
QY 3611 GACACTAGGATATGAATAGGTAGATGTTTATTTTGTATGATGATGATGATGATGATGATGAT 3670
Db 17439 GACACTAGGATATGAATAGGTAGATGTTTATTTTGTATGATGATGATGATGATGATGATGAT 17498
QY 3671 ACCTCTTTTCTTTTCTTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 3730
Db 17499 ACCTCTTTTCTTTTCTTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 17558
QY 3731 CTGGATACGAGATTCGGTTTGTAGAGAACATTTTGAAGGCTGTCCGTGCACTAAAGTTGG 3790
Db 17559 CTGGATACGAGATTCGGTTTGTAGAGAACATTTTGAAGGCTGTCCGTGCACTAAAGTTGG 17618
QY 3791 CAGCANTCACCGAAGAACATTTTGGAGGCTGTCCGTGCACTACAGTCACTAATACCATC 3850

Db 17619 CAGCATCACCGGAGAACATTTTGGAGGCTGTCCGTGCACTACAGGTCACTAAATACCATC 17678
QY 3851 TAAGTAGTGTGATTCATAGTGACTGGATATGTTGTGTTTTCAGTATTAATGATGCTGTTT 3910
Db 17679 TAAGTAGTGTGATTCATAGTGACTGGATATGTTGTGTTTTCAGTATTAATGATGCTGTTT 17738
QY 3911 TTTATGCAAAATCTAAATTAAT 3970
Db 17739 TTTATGCAAAATCTAAATTAAT 17798
QY 3971 TTTTGTGACAAAGTGTGCATTTATAAAAGCAATTTGTCTCATCAATTTTGTGCAAGAAC 4030
Db 17799 TTTTGTGACAAAGTGTGCATTTATAAAAGCAATTTGTCTCATCAATTTTGTGCAAGAAC 17858
QY 4031 GGTCACTATCAGTCAAAATAAATCAATTTATTTGGGCCCCGAGATCCATGCTAGCTCTAGA 4090
Db 17859 GGTCACTATCAGTCAAAATAAATCAATTTATTTGGGCCCCGAGATCCATGCTAGCTCTAGA 17918
QY 4091 GTCCCTGCTTTAATGAGATATCGAGACGCTTATGATCGCATGATTTTGTCTTTCAATTTCT 4150
Db 17919 GTCCCTGCTTTAATGAGATATCGGAGACGCTTATGATCGCATGATTTTGTCTTTCAATTTCT 17978
QY 4151 GTTGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGG 4210
Db 17979 GTTGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGG 18038
QY 4211 TTTCACTTAATGAAT 4270
Db 18039 TTTCACTTAATGAAT 18098
QY 4271 CAATTTACTGATTTACCCCTACTTATATATGTATCAATATTTAAAAATGAAAAAATATAT 4330
Db 18099 CAATTTACTGATTTACCCCTACTTATATATGTATCAATATTTAAAAATGAAAAAATATAT 18158
QY 4331 GTGCTGAATAGTGTATAGCAGCATCTATGATAGAGCGCCAAATAAACAATTTGGT 4390
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QY 4391 TTTTATATATACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAAAGACTG 4450
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QY 4451 ATTAATCAATATCTTATTTCAAAATTTTCAAAAGGCCCCAGGGGCTTAGTATCTACGACACCG 4510
Db 18279 ATTAATCAATATCTTATTTCAAAATTTTCAAAAGGCCCCAGGGGCTTAGTATCTACGACACCG 18338
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Db 18339 ACCGCGCAATTAATTAACGTTCACTGAAGGAACTCCGGTTCCTCCGCGCGCGGCGATGGT 18398
QY 4571 GAGATTCCTTGAAGTTGAGTATTTGGCCGCTTACCGGAAAGTTTACGGGCACTTCA 4630
Db 18399 GAGATTCCTTGAAGTTGAGTATTTGGCCGCTTACCGGAAAGTTTACGGGCACTTCA 18458
QY 4631 ACCCGGTCCAGCACGCGCGCGGTTAAACCGCTTGTCTCCCGGAGAAATTTATGAGCAATTT 4690
Db 18459 ACCCGGTCCAGCACGCGCGCGGTTAAACCGCTTGTCTCCCGGAGAAATTTATGAGCAATTT 18518
QY 4691 TTTTGGTGTATGTGGGCCCCAAATGAGTGCAGGTCAAACTTGTACAGTGCAGCAAAATC 4750
Db 18519 TTTTGGTGTATGTGGGCCCCAAATGAGTGCAGGTCAAACTTGTACAGTGCAGCAAAATC 18578
QY 4751 GTTGGCGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGGACCTGCAGG 4810
Db 18579 GTTGGCGGGTCCAGGGCGAAATTTTTCGACAAACATGTGAGGCTCAGCAGGACCTGCAGG 18638
QY 4811 CATGCAAGCTAGCTTACTAGTGTATGATGATATTTCTATAGTGTCACTTAAATCTGC 4863
Db 18639 CATGCAAGCTAGCTTACTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 18691

RESULT 7

US-10-055-001A-23/c

Db	15295	ATTAGAAATTAATAAGAAATGTTGATGAAATAATATCTATATAAATGATAGATCTTGC	15236	Db	14226	AAGTATGTCAAAAGAGGCTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGC	14170
Qy	1864	ATTATTTTAAATGAATTTGATCGAATGTAAGATGATATACTAGCAATTAATTTGTTT	1923	Qy	2944	CTATACCTTAATAACGTTGATAAAGTTTCTGTATTTCTACTGTATCGACCTGACAGCTGG	3003
Db	15235	GCTTGTATATTAGCAATTAGATTATGTTTGTACATAGATTACTGTTTCTATTAGTT	15176	Db	14169	GACAGCTATCAGTTTGTCTCAAGGCATATATGATGTCAATATCTCCGCTCTGTAAGCAAA	14110
Qy	1924	TAATCATATAGTAATCTAGCTGTTTGTAGTAATTAATTAATCAATGATTAATACTATA	1983	Qy	3004	CTGTGTATTAAGGGAGCTGACATTTATATCCCCAGAACATACAGTTTAATCGCGCTTTTGG	3063
Db	15175	TGATATTATTTTACTTGTAGCTTGTATTTAATATTTTGTATTTATGATTAATTAAGC	15116	Db	14109	CCATGCAATGAAGACCGCTGCTCTCGGTGCC---GAACGCTGAAAGCGGAATCAGG	14053
Qy	1984	GTAATAAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	2043	Qy	3064	ATGTCAATTTTCGGTGTGCTGAGATCAGCCATCTTCTTCCCGATAACGAGACCGGACAA	3123
Db	15115	AGATTGGAATTTCTTCAACAAAATATTATTAACTTTTAAACTAAATATTATTAGTAAGTA	15056	Db	14052	AAGGATGGCTGAGGTGCGCCGCTTTATTGAATGAACCGCTCTTTTGTCTGACGAGAACA	13993
Qy	2044	AAATTAATATCTATACCATCTACTAATAATTTTAGTTTAAAGTTAATAAATTTTGTGA	2103	Qy	3124	CTGGCCATATCGGTGGTTCATCATGGCCAGCTTTTATCCCGATATGCACCACCGGTAA	3183
Db	15055	TAGATATTTAATTAATAATAAATACTATTAAATCAATAAATAAATAATTATTATTATTTA	14996	Db	13992	GGGA-----CTGTGAAATGCACTTTAAGGTTTACACCTTAATAAGAGAGAGCGTTAT	13939
Qy	2104	GAAATCCAAATCTGTTGTAAATTTATCAATAAACAATAATTAATAAACAAGCTAAAGTA	2163	Qy	3184	AGTTTCAAGGAGACCTTTATCTGACAGCAGACGTCACCTGGCCAGGGGATCACCATCCGT	3243
Db	14995	TTCTTATTTTACTATAGTATTATTATCATTTGATTTTAAATCATCAACACGCTAGAATT	14936	Db	13938	CGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCCCGCGCGAGATGGTGATC	13879
Qy	2164	ACAAATTAATCAAACTAATAGAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGCT	2223	Qy	3244	CGCCGGCGGTGTCTAATAATATCTCTGTACATCCACAAACACAGATTAAGGCTCTCT	3303
Db	14935	ACTATTATGATTAACAATAATATTANTGCTAGTATATCATCTTACATGTTTCGATCAAAAT	14876	Db	13878	CCCTGGCCAGTGCACGCTCTGCTGTACAGATAAAGTCTCCCGTGAACCTTTTACCCGGTGGT	13819
Qy	2224	AAATTAACAAAGCGCAAGATCTATCATTTTATATAGTATATTTTCAATCAACATCTTTA	2283	Qy	3304	CTTTTATAGGTGTAACCTTAAACTGCACTTTTACCAGT-----CCCTGTTCTCGTCAGC	3357
Db	14875	CATTAAAAATAATATCTTACTCTCACTTTTATCTTCTGCTTACACATCCTTTGTC	14816	Db	13818	CATATCGGGATGAAGCTGGCGCATGATGACACCGATATGGCCAGTGTCCGCTCTCC	13759
Qy	2284	TTAATTTCTAAATAAATCTGTGTAGTTTATTAATCTTAAAGGATGCTATTAAATTA	2343	Qy	3358	AAAAAGAGCGTTTCAPTTCAATAAACCAGGCGCACTCAGCCATCCCTTCTGATTTTCGC	3417
Db	14815	ATATTTTTTTACATTAATCTATGTTGTTTATGTAACAATAATATTATAAATTTTTC	14756	Db	13758	GTTATCGGGAGAGAGTGGCTGATCTCAGCCACCGCAAAATGACATCAAAAACCCCAT	13699
Qy	2344	ATGAAATTAGTCGAACATGATAAACAAGGTAAACATGATAGATCATGCTCATTTGTTTATCA	2403	Qy	3418	TTTCCAGCGTTC---GGCAGCAGCAGCAGCGGCTTCATCTGCACTGG---TTGCTTAC	3471
Db	14755	CAATTATACAACTATATTATTTATATATCATCATCTTAAATCACTTAACTATTATTATAC	14696	Db	13698	AACTCTGATGTTCTGGGGAATATAAATGTGAGCTCCCTTATACACAGCCAGTCTGCAAGT	13639
Qy	2404	TTGATCTTACATTTGGATGATTACAGTTGGGAGCTGGGTTGGAATCGATNAAGCTGG	2463	Qy	3472	CAGACCGGAGATTTGACATCATATATGCTTTGACCACTGATAGCTCTGCTGCTGCAACT	3531
Db	14695	TAAAAAGAAAAGAAAATAATTA-----TTTCTTACCAAGCTGGGATCCGA	14647	Db	13638	CGATACAGTAGAATAATACAGAACTTTATCAGTTTAGTATAGAGGCTGAAATCC	13579
Qy	2464	ATCCTCTAGAGAGCTGAGCTGCAATTAATGATTTTATTTTGTGACTGATAGTACC	2523	Qy	3532	GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTGACATATCTTCTTCTTGTATGC	3591
Db	14646	ATTCTCGAGAGGCTGAGCTGGAATGCAATTAATGATTTTATTTTGTGATGATGACC	14587	Db	13578	AGATGAAGCCGAACGACTTGTAAAGAAAAGATTAAGAGTTGTGAAATTTTCTTGTATGC	13519
Qy	2524	TGTTCTGTGCAACAAATTTGATAAGCAATGCTTCTTATAATGCCAATTTTGTACAAGAA	2583	Qy	3592	AGATGATTTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGT	3651
Db	14586	TGTTCTGTGCAACAAATTTGATAAGCAATGCTTCTTATAATGCCAATTTTGTACAAGAA	14527	Db	13518	AGATGATTTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGT	13459
Qy	2584	GCTGAAGCAGAAAGCTAAATGATATAAATATCATATATAATTAATTAATTAATTAATTA	2643	Qy	3652	ACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAATACGGCAAT	3711
Db	14526	GCTGAACGAGAAAGCTAAATGATATAAATATCATATATAATTAATTAATTAATTAATTA	14467	Db	13458	ACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAATACGGCAAT	13399
Qy	2644	AAACAGACTACATAATCTGTAATAACCAACATATCCAGTCACTATCAATCAACTACTTA	2703	Qy	3712	GAGGCAATATAGCGAGTGGCTGGATCGACGATTCGTTTTGAGAAAGCAATTTGGAGGC	3771
Db	14466	AAACAGACTACATAATCTGTAATAACCAACATATCCAGTCACTATCAATCAACTACTTA	14407	Db	13398	GAGGCAATATAGCGAGTGGCTGGATCGACGATTCGTTTTGAGAAAGCAATTTGGAGGC	13339
Qy	2704	GATGGTATTAGTACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGCC	2763	Qy	3772	TGTCGGTCCACTAAGTTGGCAGCATCACCCGAGCAATTTGGAAGGCTGTCGGTGCAT	3831
Db	14406	GATGGTATTAGTACCTGTAGTCCGACTAAGTTGGCAGCATCACCCGACGCACTTTGGCC	14347	Db	13338	TGTCGGTCCACTAAGTTGGCAGCATCACCCGAGCAATTTGGAAGGCTGTCGGTGCAT	13279
Qy	2764	GAATTAATACCTGTGACGGAAGATCACTTCCAGATTAATAATTAATTAATTAATTAATTA	2823	Qy	3832	ACAGGTCACTAATACCATCTAAAGTAGTTGATTCATAGTACCTGGATATGTTGTTTTAC	3891
Db	14346	GAATTAATACCTGTGACGGAAGATCACTTCCAGATTAATAATTAATTAATTAATTAATTA	14287	Db	13278	ACAGGTCACTAATACCATCTAAAGTAGTTGATTCATAGTACCTGGATATGTTGTTTTAC	13219
Qy	2824	GATACCGGAGAGCCTGGGCCAACTTTTGGGAAAAATGAGACGTTGATCGGCACTACCCA	2883	Qy	3892	AGTATTATGATGATCTGTTTTTANGCAAAATCTAATTAATTAATTAATTAATTAATTAAT	3951
Db	14286	GATACCGGAGAGCCTGGGCCAACTTTTGGGAAAAATGAGACGTTGATCGGCACTACCCG	14227	Db	13218	AGTATTATGATGATCTGTTTTTANGCAAAATCTAATTAATTAATTAATTAATTAATTAAT	13159
Qy	2884	TTTCAACACTCTTATACCTTTTCTCTTACAGTCTGCTGCTTCTATCTGGATTTTCACT	2943	Qy	3952	TTTACGTTTCTGTTTCTGCTTTTGTACAAAGTTGGCATTTATAAAGGCAATTTGCTCAT	4011
				Db	13158	TTTACGTTTCTGTTTCTGCTTTTGTACAAAGTTGGCATTTATAAAGGCAATTTGCTCAT	13099

QY	4012	CAATTTGTTGCACACGACAGGTCAC	TATCAGTCACAAATAAATCAT	TATTTGGGGCCGA	4071
DB	13098	CAATTTGTTGCACACGACAGGTCAC <td>TATCAGTCACAAATAAATCAT <td>TATTTGGGGCCGA</td> <td>13039</td> </td>	TATCAGTCACAAATAAATCAT <td>TATTTGGGGCCGA</td> <td>13039</td>	TATTTGGGGCCGA	13039
QY	4072	GATCCATGCTAGC	4084		
DB	13038	GATCCATGCTAGC	13026		

RESULT 8

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US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470

```

QY	85	CGTTGCAACAAA	TTGATGAGCAAAATGCTTTT	TATAATGCAACTTTTGTA	CAAAAAAGCTG	144
DB	65	CGTTGCAACAAA	TTGATGAGCAAAATGCTTTT	TATAATGCAAAAGCTG	124	
QY	145	AACGAGAAACGT	AAAAATGATATAAAATATCAA	TATATTAATATAGATTTT	TGCATAAAAAAC	204
DB	125	AACGAGAAACGT	AAAAATGATATAAAATATCAA	TATATTAATATAGATTTT	TGCATAAAAAAC	184
QY	205	AGACTACATAAT	TACTGTAAAAACAACATATCC	AGTCACTATGAAATCAACTACT	TAGATG	264
DB	185	AGACTACATAAT	TACTGTAAAAACAACATATCC	AGTCACTATGAAATCAACTACT	TAGATG	244
QY	265	GTATATGTAG	CTGTAGTGACCGACGCGACG	CTTCCAAATGTTCTTCGGGT	GATGCTGCCAA	324
DB	245	GTATATGTAG	CTGTAGTGACCGACGCGACG	CTTCCAAATGTTCTTCGGGT	GATGCTGCCAA	304
QY	325	CTTAGT	CGACCGACAGCGCTTCCAAAT	TGTTCTTCTCAAAAGGAATCGT	CTGATCCAGCCTA	384
DB	305	CTTAGT	CGACCGACAGCGCTTCCAAAT	TGTTCTTCTCAAAAGGAATCGT	CTGATCCAGCCTA	364
QY	385	CTCGCTATTG	TCTCAATGCCGATTAATAAT	TCATAAAGAAATATAAAGAG	AGGTGCGA	444
DB	365	CTCGCTATTG	TCTCAATGCCGATTAATAAT	TCATAAAGAAATATAAAGAG	AGGTGCGA	424
QY	445	GCCTCTTTT	TGTGTGCAAAAATAAAAA	CATCTCACTATCATATACGT	TAGTGTCTATG	504
DB	425	GCCTCTTTT	TGTGTGCAAAAATAAAAA	CATCTCACTATCATATACGT	TAGTGTCTATG	484
QY	505	TCCTGAAAAT	CATCTGCATCAAGAAACAAT	TTCAAACTTTTATACCTTTCT	CTTACAAGT	564
DB	485	TCCTGAAAAT	CATCTGCATCAAGAAACAAT	TTCAAACTTTTATACCTTTCT	CTTACAAGT	544
QY	565	CGTTGGGTTT	CATCTGGAATTTT	CAGCCTCTATATCTTAAC	CGTGATAAAGTTTCTGTA	624
DB	545	CGTTGGGTTT	CATCTGGAATTTT	CAGCCTCTATATCTTAAC	CGTGATAAAGTTTCTGTA	604
QY	625	ATTTCTACTG	TATCGACTCGACTGGCTGT	GTATAAGGAGCGCTGACAT	TTTATATATTC	684
DB	605	ATTTCTACTG	TATCGACTCGACTGGCTGT	GTATAAGGAGCGCTGACAT	TTTATATATTC	664
QY	685	CCAGAAATCA	GAGTAAATGGCGTTTTT	TGATGTCATTTTCGCGTGG	CTGAGATCAGCCAC	744
DB	665	CCAGAAATCA	GAGTAAATGGCGTTTTT	TGATGTCATTTTCGCGTGG	CTGAGATCAGCCAC	724
QY	745	TTCTTCCCGA	TAAAGGAGACCGGCA	CACATGGCCATATCGTGGT	CTCATCATGCGCCAGCT	804
DB	725	TTCTTCCCGA	TAAAGGAGACCGGCA	CACATGGCCATATCGTGGT	CTCATCATGCGCCAGCT	784
QY	805	TTTCATCCCG	ATATGTCACACCGGGTAAAG	TTTACCGGGAGACTTATCT	TCACAGCAGACG	864
DB	785	TTTCATCCCG	ATATGTCACACCGGGTAAAG	TTTACCGGGAGACTTATCT	TCACAGCAGACG	844
QY	865	TGCACTGCC	ACGAGGGATACCAATCG	TGCGCGGGCGTGTCAATA	TATATCATCTGTATC	924
DB	845	TGCACTGCC	ACGAGGGATACCAATCG	TGCGCGGGCGTGTCAATA	TATATCATCTGTATC	904
QY	925	ATCCCAAA	ACAGATAAACGGCTCTCT	TTTTATAGTGTAAACCTTAA	ACTTGAATTC	984
DB	905	ATCCCAAA	ACAGATAAACGGCTCTCT	TTTTATAGTGTAAACCTTAA	ACTTGAATTC	964
QY	985	ACCAGTCC	CTGTCTCGTCAGCAAAA	AGACCGTTCATTTCAATAA	ACCGGGCGACCTCAG	1044
DB	965	ACCAGTCC	CTGTCTCGTCAGCAAAA	AGACCGTTCATTTCAATAA	ACCGGGCGACCTCAG	1024
QY	1045	CCATCCCT	TCTGTATTTTCCGTTT	CCAGCGTTTCGGACGACG	ACGGGCTTCATCT	1104
DB	1025	CCATCCCT	TCTGTATTTTCCGTTT	CCAGCGTTTCGGACGACG	ACGGGCTTCATCT	1084
QY	1105	GCATGGT	GTGCTTACACAGACCG	GAGATATTGACATATAT	TGCTTTGAGCAACTGATA	1164
DB	1085	GCATGGT	GTGCTTACACAGACCG	GAGATATTGACATATAT	TGCTTTGAGCAACTGATA	1144

QY 1165 GCTGCGCTGCAACTGTCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA 1224
DB 1145 GCTGCGCTGCAACTGTCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA 1204
QY 1225 CTTCCGGGTA 1233
DB 1205 CTTCCGGGTA 1213

RESULT 10
US-10-151-690-61/c
; Sequence 61, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 24.8%; Score 1207.4; DB 15; Length 5584;
Best Local Similarity 99.9%; Pred. No. 4.3e-175; Indels 0; Gaps 0;
Matches 1208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 AGCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACTGATGACCTGTT 84
DB 5580 ACCTAGCATGATCTCGGCGCCCAATAATGATTTTATTTGACTGATGACCTGTT 5521
QY 85 CGTTGCAACAATGATGACATGCTTTTATATATGCAATGCTTTGACAAAAGCTG 144
DB 5520 CGTTGCAACAATGATGACATGCTTTTATATATGCAATGCTTTGACAAAAGCTG 5461
QY 145 AACGAGAAAGTAAATGATATATATATCAATATATTAATTAATGATTTTGCATAAAAAC 204
DB 5460 AACGAGAAAGTAAATGATATATATATCAATATATTAATTAATGATTTTGCATAAAAAC 5401
QY 205 AGACTACATAATCTGTAAACACACATATCCAGTCATCATGAATCAACTACTTAGATG 264
DB 5400 AGACTACATAATCTGTAAACACACATATCCAGTCATCATGAATCAACTACTTAGATG 5341
QY 265 GTATTAGTACCTGATGTCGACGACGCTTCCAAATGCTTCTCGGTGATGCTGCAA 324
DB 5340 GTATTAGTACCTGATGTCGACGACGCTTCCAAATGCTTCTCGGTGATGCTGCAA 5281
QY 325 CTTAGTCGACGACGCTTCCAAATGCTTCTTCAACGGAATCGTCGATCCAGCTA 384
DB 5280 CTTAGTCGACGACGCTTCCAAATGCTTCTTCAACGGAATCGTCGATCCAGCTA 5221
QY 385 CTGCTATTCTCCTCAATCGGCTTAAATCATATAAAGAAATAAGAAAGAGGTGCGA 444
DB 5220 CTGCTATTCTCCTCAATCGGCTTAAATCATATAAAGAAATAAGAAAGAGGTGCGA 5161
QY 445 GCCTCTTTTGTGCAAAATAAACAATCTACCTATTATATAGCTAGTGTATAG 504
DB 5160 GCCTCTTTTGTGCAAAATAAACAATCTACCTATTATATAGCTAGTGTATAG 5101

QY 505 TCCTGAAATCATCTGCATCAAGACAAATTTTCAAACTCTTATCTTCTCTTACAGT 564
DB 5100 TCCTGAAATCATCTGCATCAAGACAAATTTTCAAACTCTTATCTTCTCTTACAGT 5041
QY 565 CGTTGCGCTTCATCTGGATTTTTCAGCCCTCTATCTTAAACGTTGATAAAGTTTCTGTA 624
DB 5040 CGTTGCGCTTCATCTGGATTTTTCAGCCCTCTATCTTAAACGTTGATAAAGTTTCTGTA 4981
QY 625 ATTCTACTGTATCGACCTGACAGACTGGCTGTATATAGGAGGCTGACATTTATTTCC 684
DB 4980 ATTCTACTGTATCGACCTGACAGACTGGCTGTATATAGGAGGCTGACATTTATTTCC 4921
QY 685 CCAGAACATCAGTTTAAATGCGGCTTTTTCATGTCATTTTCGCGTGGCTGAGATCAGCCAC 744
DB 4920 CCAGAACATCAGTTTAAATGCGGCTTTTTCATGTCATTTTCGCGTGGCTGAGATCAGCCAC 4861
QY 745 TTCTTCCCCTGATAACGAGACCGGCACATCGGCCATATCGGTGGTTCATCATGGCCAGCT 804
DB 4860 TTCTTCCCCTGATAACGAGACCGGCACATCGGCCATATCGGTGGTTCATCATGGCCAGCT 4801
QY 805 TTCTTCCCCTGATAACGAGACCGGCATCGGTAAAGTTTCAGGAGACTTTATCTGACGACGACG 864
DB 4800 TTCTTCCCCTGATAACGAGACCGGCATCGGTAAAGTTTCAGGAGACTTTATCTGACGACGACG 4741
QY 865 TGCACTGCGCAGGGGGATCACCATCGCTCGCCGCGGCGTGTCAATAATATCACTCTGTAC 924
DB 4740 TGCACTGCGCAGGGGGATCACCATCGCTCGCCGCGGCGTGTCAATAATATCACTCTGTAC 4681
QY 925 ATCCACAAACAGACGATAAACGCTCTCTTTTATGAGTAAACCTTAAACCTGCAATTC 984
DB 4680 ATCCACAAACAGACGATAAACGCTCTCTCTTTTATGAGTAAACCTTAAACCTGCAATTC 4621
QY 985 ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAACGGGCGACCTCAG 1044
DB 4620 ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAACGGGCGACCTCAG 4561
QY 1045 CCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGGCAGCGACGAGCGGCTTCATTCT 1104
DB 4560 CCATCCCTTCTCTGATTTTCCGCTTTCCAGCGTTCGGCAGCGACGAGCGGCTTCATTCT 4501
QY 1105 GCATGCTGTGTTTACCAAGACCGGAGATATTGACATATATATGCTTGTAGCAACTGATA 1164
DB 4500 GCATGCTGTGTTTACCAAGACCGGAGATATTGACATATATATGCTTGTAGCAACTGATA 4441
QY 1165 GCTGTCGCTGTCACACTGTCAATAGCTGCTTCATAGCACACCTCTTTTGCACATA 1224
DB 4440 GCTGTCGCTGTCACACTGTCAATAGCTGCTTCATAGCACACCTCTTTTGCACATA 4381
QY 1225 CTTCCGGGTA 1233
DB 4380 CTTCCGGGTA 4372

RESULT 11
US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64

QY	925	ATCCACAAACAGACGATAACGGCTCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTTC	984
Db	1742	ATCCACAAACAGACGATAACGGCTCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTTC	1801
QY	985	ACCAGTCCCTGTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAAAACGGGCGACCTCAG	1044
Db	1802	ACCAGTCCCTGTCTCGTCAGCAAAAGAGCGGTTCAATTTCAATAAAACGGGCGACCTCAG	1861
QY	1045	CCATCCCTTCTCGTGAATTTCCGGCTTTCCAGCGTTTCGGCAGCGACGACGCGGCTTCATTTCT	1104
Db	1862	CCATCCCTTCTCGTGAATTTCCGGCTTTCCAGCGTTTCGGCAGCGACGACGCGGCTTCATTTCT	1921
QY	1105	GCATGTTGTGCTTACACGACCGGAGATATGACATCAATATGCTTTGAGCAACTGATA	1164
Db	1922	GCATGTTGTGCTTACACGACCGGAGATATGACATCAATATGCTTTGAGCAACTGATA	1981
QY	1165	GCTGTGCGCTCAACCTGTCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTGTGACATA	1224
Db	1982	GCTGTGCGCTCAACCTGTCACCTGTAATACGCTGCTTCATAGCACACCTCTTTTGTGACATA	2041
QY	1225	CTTCGGGTA 1233	
Db	2042	CTTCGGGTA 2050	
RESULT 12			
US-10-151-690-63			
; Sequence 63, Application US/10151690			
; Publication No. US20030124555A1			
; GENERAL INFORMATION:			
; APPLICANT: BRASCH, MICHAEL A.			
; APPLICANT: CHEO, DAVID			
; APPLICANT: LI, XIAO			
; APPLICANT: ESPOSITO, DOMINIC			
; APPLICANT: BYRD, DEVON R.N.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC			
; FILE REFERENCE: 0942.5120001			
; CURRENT APPLICATION NUMBER: US/10/151,690			
; CURRENT FILING DATE: 2002-05-21			
; PRIOR APPLICATION NUMBER: US 10/151,690			
; PRIOR FILING DATE: 2002-05-21			
; PRIOR APPLICATION NUMBER: US 60/291,973			
; PRIOR FILING DATE: 2001-05-21			
; NUMBER OF SEQ ID NOS: 64			
; SOFTWARE: Patentin version 3.1			
; SEQ ID NO 63			
; LENGTH: 4627			
; TYPE: DNA			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: plasmid pDONR212			
US-10-151-690-63			
Query Match 24.6%; Score 1194.6; DB 15; Length 4627;			
Best Local Similarity 99.7%; Pred. No. 3.6e-173;			
Matches 1197; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	33	ATCGATCTCGGGCCCCCAAAATAATGATTTTATTTTGTAGTAGTAGTACCTGTTTCGTTGCAA	92
Db	1	ATGGAATCGGGCCCCCAAAATAATGATTTTATTTTGTAGTAGTAGTACCTGTTTCGTTGCAA	60
QY	93	CAAAATTGATGAGCAATGCTTTTTTATAATGCGCACTTTGTACAAAAAGCTGAACAGAA	152
Db	61	CAAAATTGATGAGCAATGCTTTTTTATAATGCGCACTTTGTACAAAAAGCTGAATCGAA	120
QY	153	ACGTAAAAATGATATAAATATCAATATATTAATTAATGATTTTGTACATAAAAAACAGACTACA	212
Db	121	ACGTAAAAATGATATAAATATCAATATATTAATTAATGATTTTGTACATAAAAAACAGACTACA	180
QY	213	TAATACTGTAAAAACAAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGT	272
Db	181	TAATACTGTAAAAACAAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGT	240

QY 273 GACCTGTAGTCACGACGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCG 332
DB |||||
QY 241 GACCTGTAGTCACGACGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCG 300
DB |||||
QY 333 ACCGACAGCTTCCAAATGTTCTTCAAACGGAATCGTCGATCGAGCTTACTCGCTAT 392
DB |||||
QY 301 ACCGACAGCTTCCAAATGTTCTTCAAACGGAATCGTCGATCGAGCTTACTCGCTAT 360
DB |||||
QY 393 TGTCTCAATCGCGTATTAATAATCAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 452
DB |||||
QY 361 TGTCTCAATCGCGTATTAATAATCAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 420
DB |||||
QY 453 TTTGTGTGACAAATAAATAAATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAA 512
DB |||||
QY 421 TTTGTGTGACAAATAAATAAATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAA 480
DB |||||
QY 513 ATCATCTGCATCAAGAACAAATTTCAAACTCTTATATCTTCTTACAAAGTCGTTCCGC 572
DB |||||
QY 481 ATCATCTGCATCAAGAACAAATTTCAAACTCTTATATCTTCTTACAAAGTCGTTCCGC 540
DB |||||
QY 573 TTTCACTGGAATTTTCAGCTCTATATCTTAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 632
DB |||||
QY 541 TTTCACTGGAATTTTCAGCTCTATATCTTAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 600
DB |||||
QY 633 TGTATCGACCTCGACAGCTGGCTGTGTATAAGGAGGCTGACATTTATATTCGCCAGAAC 692
DB |||||
QY 601 TGTATCGACCTCGACAGCTGGCTGTGTATAAGGAGGCTGACATTTATATTCGCCAGAAC 660
DB |||||
QY 693 TCAGGTTAATGCGGTTTGTATGATCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCC 752
DB |||||
QY 661 TCAGGTTAATGCGGTTTGTATGATCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCC 720
DB |||||
QY 753 CGATACGAGACCGGACACCTGGCCATATCGTGTATCATGCGCAGCTTTCATCCC 812
DB |||||
QY 721 CGATACGAGACCGGACACCTGGCCATATCGTGTATCATGCGCAGCTTTCATCCC 780
DB |||||
QY 813 CGATATGACACCGGTTAAGTTTCACGGGAGACTTTATCTGACAGCAGCTGCACTGG 872
DB |||||
QY 781 CGATATGACACCGGTTAAGTTTCACGGGAGACTTTATCTGACAGCAGCTGCACTGG 840
DB |||||
QY 873 CGAGGGGATACCATTCGTCGCGCGGCTGTCAATAATATCACTCTGTATCATCCACAA 932
DB |||||
QY 841 CGAGGGGATACCATTCGTCGCGCGGCTGTCAATAATATCACTCTGTATCATCCACAA 900
DB |||||
QY 933 ACAGCGATAACGCTCTCTCTTTATAGTGTAAACCTTAACTTAACTTCAACAGTCC 992
DB |||||
QY 901 ACAGCGATAACGCTCTCTCTTTATAGTGTAAACCTTAACTTAACTTCAACAGTCC 960
DB |||||
QY 993 CTGTTCTCGTCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGCGGACCTCAGCCATCCCT 1052
DB |||||
QY 961 CTGTTCTCGTCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGCGGACCTCAGCCATCCCT 1020
DB |||||
QY 1053 TCGTGAATTTTCAGGTTTCGACGAGCTGCGACGAGAGCGGCTTCTATCTGCAATGTT 1112
DB |||||
QY 1021 TCGTGAATTTTCAGGTTTCGACGAGCTGCGACGAGAGCGGCTTCTATCTGCAATGTT 1080
DB |||||
QY 1113 GTGCTTACAGACCGGAGATTTGACATCATATATGCTTGTAGCAACTGATAGTCTGCG 1172
DB |||||
QY 1081 GTGCTTACAGACCGGAGATTTGACATCATATATGCTTGTAGCAACTGATAGTCTGCG 1140
DB |||||
QY 1173 TGTCAACTGTCACTGTAATACGCTGCTTATAGCAGACACCTCTTTTGAATCTTCGGT 1232
DB |||||
QY 1141 TGTCAACTGTCACTGTAATACGCTGCTTATAGCAGACACCTCTTTTGAATCTTCGGT 1200
DB |||||
QY 1233 A 1233
DB 1201 A 1201

RESULT 13

US-10-151-690-64

; Sequence 64, Application US/10151690

; Publication No. US2003012455A1

; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151.690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151.690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 24.6%; Score 1194.6; DB 15; Length 4627;

Best Local Similarity 99.7%; Pred. No. 3.6e-173;

Matches 1197; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB |||||
QY 61 CAAATGTGATGAGCAATGCTTTTATATATGCAACTTTGTACAAAAGAGCTGAATCGAA 120
DB |||||
QY 153 ACCTAAATGATATAAATATCAATATATATAATAGATTTTGCATAAAAAAGAGCTGAA 212
DB |||||
QY 121 ACCTAAATGATATAAATATCAATATATATAATAGATTTTGCATAAAAAAGAGCTGAA 180
DB |||||
QY 213 TAATAGCTGTAACAACAACATATCCAGTCATATGAATCAACTCTTATAGATGTTAGT 272
DB |||||
QY 181 TAATAGCTGTAACAACAACATATCCAGTCATATGAATCAACTCTTATAGATGTTAGT 240
DB |||||
QY 273 GACCTGTAGTCAGCGACGAGCTTCCAAATGTTCTTCGSGTGATGCTGCCAACTTAGTCG 332
DB |||||
QY 241 GACCTGTAGTCAGCGACGAGCTTCCAAATGTTCTTCGSGTGATGCTGCCAACTTAGTCG 300
DB |||||
QY 333 ACCGACAGCTTCCAAATGTTCTTCTCAAAACGGAATCGTCGTATCCAGCTTACTCGCTAT 392
DB |||||
QY 301 ACCGACAGCTTCCAAATGTTCTTCTCAAAACGGAATCGTCGTATCCAGCTTACTCGCTAT 360
DB |||||
QY 393 TGTCTCAATCGCGTATTAATAATCAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 452
DB |||||
QY 361 TGTCTCAATCGCGTATTAATAATCAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 420
DB |||||
QY 453 TTTGTGTGACAAATAAATAAATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAA 512
DB |||||
QY 421 TTTGTGTGACAAATAAATAAATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAA 480
DB |||||
QY 513 ATCATCTGCATCAAGAACAAATTTCAAACTCTTATATCTTCTTCAAGTCGTTCCGC 572
DB |||||
QY 481 ATCATCTGCATCAAGAACAAATTTCAAACTCTTATATCTTCTTCAAGTCGTTCCGC 540
DB |||||
QY 573 TTTCACTGGAATTTTCAGCTCTATATCTTAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 632
DB |||||
QY 541 TTTCACTGGAATTTTCAGCTCTATATCTTAATAAAGAAATAAGAAAAAGAGGTCGAGCTCTTT 600
DB |||||
QY 633 TGTATCGACCTCGACAGCTGGCTGTGTATAAGGAGGCTGACATTTATATTCGCCAGAAC 692
DB |||||
QY 601 TGTATCGACCTCGACAGCTGGCTGTGTATAAGGAGGCTGACATTTATATTCGCCAGAAC 660
DB |||||
QY 693 TCAGGTTAATGCGGTTTGTATGATCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCC 752
DB |||||

Db 661 TCAGGTTAATGGGCTTTTTCATGTCATTTTCGGGGTGGCTGAGATCAGCCACTCTCTCC 720
QY 753 CGATAACGGAGACCGCACACTCGGCATATCGGTGTCATCGCCGCGCTTTCATCC 812
Db 721 CGATAACGGAGACCGGCACACTCGGCATATCGGTGTCATCGCCGCGCTTTCATCC 780
QY 813 CGATATGCACCCACCGGTAAGTTTCACGGGAGACTTTATCTGACAGCAGCGTGCCTGG 872
Db 781 CGATATGCACCCACCGGTAAGTTTCACGGGAGACTTTATCTGACAGCAGCGTGCCTGG 840
QY 873 CCAGGGGATCAGCATCCGTCGCGCGGCGTGTCAATAATACATCTGTGACATCCACAA 932
Db 841 CCAGGGGATCAGCATCCGTCGCGCGGCGTGTCAATAATACATCTGTGACATCCACAA 900
QY 933 ACAGACGATACCGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACCACTCC 992
Db 901 ACAGACGATACCGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTCACCACTCC 960
QY 993 CTGTTCTGTCAGCAAAAGCGCTTCATTTCAATAAACCGGCGACCTCAGCCATCCCT 1052
Db 961 CTGTTCTGTCAGCAAAAGCGCTTCATTTCAATAAACCGGCGACCTCAGCCATCCCT 1020
QY 1053 TCCTGATTTCCGCTTCCAGCGTTCGGCAGCAGCGGCTTCATTTCTGCATGGTT 1112
Db 1021 TCCTGATTTCCGCTTCCAGCGTTCGGCAGCAGCGGCTTCATTTCTGCATGGTT 1080
QY 1113 GTGCTTACCAAGCGGAGATTTGACATCATATATGCTTTGAGCAACTGATAGCTGCGC 1172
Db 1081 GTGCTTACCAAGCGGAGATTTGACATCATATATGCTTTGAGCAACTGATAGCTGCGC 1140
QY 1173 TGTCACCTGTCATGTAATGCTGCTTATAGCAGCACTCTTTTGAATATCTGCGGT 1232
Db 1141 TGTCACCTGTCATGTAATGCTGCTTATAGCAGCACTCTTTTGAATATCTGCGGT 1200
QY 1233 A 1233
Db 1201 A 1201

RESULT 14
US-10-055-001A-26/c
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 24.1%; Score 1174.2; DB 15; Length 17681;
Best Local Similarity 59.5%; Pred. No. 8e-170;
Matches 2327; Conservative 0; Mismatches 1508; Indels 78; Gaps 17;
QY 122 GCCAATTTGTACAAAAGCTGACGAGAAAGTAAATGATATATATCAATATTT 181
Db 16904 GACAGTTTGTACAAAAGCTGACGAGAAAGTAAATGATATATATCAATATTT 16845
QY 182 AAATTAGATTTGCAATAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 241

Db 16844 AAATTAGATTTGCAATAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 16785
QY 242 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTACCGCAGCAGCTTCCAAA 301
Db 16784 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTACCGCAGCAGCTTCCAAA 16725
QY 302 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACCGCAGCTTCCAAATGTTCTTCTCAA 361
Db 16724 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACCGCAGCAGCTTCCAAATGTTCTTCTCAA 16665
QY 362 AGGGAATCGTCTATCCAGCCTACTCGGTATTGTCCTCAATGCGGTATTAAATCATAAA 421
Db 16664 AGGGAATCGTCTATCCAGCCTACTCGGTATTGTCCTCAATGCGGTATTAAATCATAAA 16605
QY 422 AGAAATAAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATCTACCT 481
Db 16604 AGAAATAAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATCTACCT 16545
QY 482 ATTATATACGCTAGTGTCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTA 541
Db 16544 ATTATATACGCTAGTGTCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTA 16485
QY 542 TCTTATACCTTTCTCTTACAAGTCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 601
Db 16484 AAAAAGAGGTGCTATGAA---GCAGCGTATTAAGTGAAGTGAAGTGAAGTGAAGTGA 16428
QY 602 CTAAACGCTGATAAAGTCTCTGTAATCTTCTGTAATCTGTAATCTGTAATCTGTAATCT 661
Db 16427 CAGTTGCTCAAGGCATATATGATGTCATATCTCGGTCTGTTAAGCACAACCATGCGA 16368
QY 662 AGGAGCCTGACATTTATATCCCGCAGAACATCAGGTTAATGCGGTTTTTGTATGCAITTT 721
Db 16367 ATGAAGCCGCTGCTGCGGTGCC---GAAAGCTGAAAAGCGGAAAATCAGGAAGGATGG 16311
QY 722 TCGCGTGGCTCAGATCAGCCACTTCTTCCCGATAACCGAGACCGGCACACTGCGCATA 781
Db 16310 CTGAGGTGCGCGGTTTTTGAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 16257
QY 782 TCGGTGCTCATCATCGCCAGCTTTTATCCCGATATGCAACCCCGGTGTAAGTTTCAAGG 841
Db 16256 ACTGGTGAATTCAGTAAAGTTTACACCTATAAAGAGAGAGCGGTTATCGTCTGTTT 16197
QY 842 GAGACTTTTATCTGACAGCAGACGTCGACGCGGAGGATCACCATCGTCCGCGCGGCG 901
Db 16196 GTGGATGTACAGAGTATATTAATGACAGCCCGCGGCGAGCGGATGGTATGCCCTGGCC 16137
QY 902 GTGTCAATAATATCACTCTGTATACATCCACAAACAGACGATACCGGCTCTCTCTTTATAG 961
Db 16136 AGTGCAGCTCTGCTGTGATATAAGTCTCCCGTGAACCTTTACCCGCTGTCATATCGG 16077
QY 962 GTGTAAACCTTAACTGCAATTTTACG-----AGTCCCTGTTCTGTCAGCAAAAGAGCC 1015
Db 16076 GATGAAGCTGGCGCATGATGACCCCGATATGGCCAGTGTGCGGTCTCCGTTATCGG 16017
QY 1016 GTTCTATTTCAATAAACCGGCGACCTCAGCCATCCCTCTGATTTTCCGCTTTCCAGCG 1075
Db 16016 GAAGAAGTGGCTGATCTGAGCCACCGGAAAATGATCAAAACGCCATTAACCTGATG 15957
QY 1076 TTC---GGCAGCAGCAGCGGCTTCAATCTGCTATGTTGTGTTTACAGACCGGAGAT 1132
Db 15956 TTCTGGGGAATATAAATGTACAGGCTCCCTTATACACAG-----CCAGTCTGAGGT 15906
QY 1133 ATTGACATCATATATGCTTGAAGCACTGATAGTGTGCTGTGCTGCTGCTGCTGCTGCTG 1192
Db 15905 CGATACAGTAGAAATTTACAGAACTTTTATCAGGTTTAGTAAGTATAGAGGCTGAAATCC 15846
QY 1193 CGCTGCTTCATAGCACACCTCTTTTGTACATACTTTCGGTAGTG---CCGATCAACGTC 1248
Db 15845 AGATGAGCCGACGACTTGTGAAGAAAGTATGAAGTGTGGAATCCGATCAACGTC 15786
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Db 15785 TCATTTTCCGCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGAGACACCAAGGATTTAT 15726

Db	13557	AGCCAGTCTGCGAGGTCGATACAGTAGAATAATACAGNAACCTTTATCACGTTTAACTAAGTAT	13498
QY	3517	CTGTGCTCTCAACTGCTCACTGTATAAATACGCTGCTTCATAGCACACCTCTTTTIGACATAC	3576
Db	13497	AGAGGGCTGAATAATCCAGATGAAGCCGAACGACTTGTAAAGAGAAAGATATAAGAGTTGTGA	13438
QY	3577	TTCTGTTCTGTATGTCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGA	3636
Db	13437	AATTGTTCTGTATGTCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGA	13378
QY	3637	TGTTTTTATTTTGTACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATG	3696
Db	13377	TGTTTTTATTTTGTACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATG	13318
QY	3697	ATTTAATACGGCAATTGAGGACAAATAGCGAGTAGGCTGGATAGCAGATTCCCGTTTGAGAA	3756
Db	13317	ATTTAATACGGCAATTGAGGACAAATAGCGAGTAGGCTGGATAGCAGATTCCCGTTTGAGAA	13258
QY	3757	GAACATTTGGAAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAAGACATTTGGAA	3816
Db	13257	GAACATTTGGAAGGCTGTCGGTCGACTAAAGTTGGCAGCATCACCCGAAGACATTTGGAA	13198
QY	3817	GGCTGTCGGTCGACTACAGTCACTAATACCATCTAAGTAGTTGATTCTAGTGACTGGA	3876
Db	13197	GGCTGTCGGTCGACTACAGTCACTAATACCATCTAAGTAGTTGATTCTAGTGACTGGA	13138
QY	3877	TATGTTGTGTTTACAGTATATGATAGTCTGTTTTTATGCAAAATCTAATTAATATAT	3936
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QY	3937	TGATATTTATATCATTTTACGTTTCTCGTTTCAGCTTTTTTGTACAAAGTTGGC	3989
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Search completed: May 10, 2004, 00:04:33
Job time : 1354.69 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 7543.25 Seconds
(without alignments)
19251.609 Million cell updates/sec

Title: US-10-055-001B-23_COPY_13000_17862

Perfect score: 4863

Sequence: 1 ttctattggagaggacacg.....atagtgtaacataatgc 4863

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gsl1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C	2	496.6	10.2	713	29 AG000762 Homo sapi
3	437.2	9.0	542	14	CD109790 AGENCOURT
C	4	411.8	8.5	723	29 AG000761 Homo sapi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	5	408.4	8.4	725	29	AG013450	Homo sapi
C	6	404	8.3	522	14	CB997937	AGENCOURT
C	7	398.4	8.2	722	29	AG000763	Homo sapi
C	8	357	7.3	487	14	CB395230	OSTR151B2
C	9	347.4	7.1	487	14	CB395230	OSTR151B2
C	10	340.2	7.0	384	12	BI174407	OSTF043E1
C	11	325.4	6.7	384	12	BI174407	OSTF043E1
C	12	301.4	6.2	337	12	BJ555980	BJ555980
C	13	273.2	5.6	1068	14	CF469981	P7-E11 Pl
C	14	271.8	5.6	1037	14	CF469119	P16A8 Pl
C	15	264.4	5.4	724	29	AG000791	Homo sapi
C	16	262.4	5.4	816	14	CF469496	P22B07 Pl
C	17	257.4	5.3	557	12	BG220129	RST39901
C	18	255.8	5.3	656	14	CK291800	EST754514
C	19	254	5.2	569	14	CF469084	P15E7 Pl
C	20	252.4	5.2	819	14	CF469247	P18G02 Pl
C	21	247.4	5.1	320	29	CG206516	TOS0136 T
C	22	246	5.1	329	28	BH739300	32283V63
C	23	245.4	5.0	1041	14	CF468941	P13A3 Pl
C	24	243.6	5.0	1035	14	CF470036	P8-B8 Pl
C	25	242.8	5.0	1017	14	CF470004	P7-G5 Pl
C	26	232.2	4.9	659	14	CK287298	EST750020
C	27	235.6	4.8	859	14	CF468865	P11-E10 P
C	28	234.8	4.8	506	14	CF468964	P13E12 Pl
C	29	234.8	4.8	657	14	CF468948	P13B3 Pl
C	30	230.2	4.7	712	28	AQ990809	Rfc01638
C	31	230.2	4.7	712	28	AQ990809	Rfc01638
C	32	229	4.7	628	14	CF469215	PL7G11 Pl
C	33	227.2	4.7	968	14	CF469474	P21H01 Pl
C	34	220	4.5	583	14	CB403882	OSTR013H1
C	35	220	4.5	583	14	CB403882	OSTR013H1
C	36	215.2	4.4	393	14	CB403984	OSTR015E7
C	37	215.2	4.4	393	14	CB403984	OSTR015E7
C	38	215.2	4.4	1020	14	CF469337	P2A07 Pl
C	39	214.6	4.4	1017	14	CF468787	P10-C6 Pl
C	40	214.2	4.4	1042	14	CF468958	P13D10 Pl
C	41	213.8	4.4	945	14	CF468807	P10-E8 Pl
C	42	213.2	4.4	509	14	CF468864	P11-D8 Pl
C	43	213.2	4.4	716	29	AG000792	Homo sapi
C	44	204.6	4.2	398	14	CF974207	PSU nepl\
C	45	203.4	4.2	1013	14	CF469353	P20C02 Pl

ALIGNMENTS

RESULT 1
AG012840
LOCUS
DEFINITION Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.
ACCESSION AG012840
VERSION AG012840.1 GI:3435047
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 698)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Published Only in DataBase (1998)

2 (bases 1 to 698)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Submitted (20-AUG-1998) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:0427-78-9561)

Location/Qualifiers

1..698

/organism="Homo sapiens"

/mol_type="genomic DNA"

FEATURES

source

/db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clone="f6SH12X16"

ORIGIN

Query Match 10.7%; Score 518.4; DB 29; Length 698;
 Best Local Similarity 98.9%; Pred. No. 1.1e-81;
 Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

675 TTTATATTTCCCGAGACATCAGTTAAATGGCGTTTGTGATGTCATTTTCGGCGTGGCTGA 734
 Db TTTATATTTCCCGAGACATCAGTTAAATGGCGTTTGTGATGTCATTTTCGGCGTGGCTGA 93
 735 GATCAGCCACTTCTTCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGTCATCA 794
 Db GATCAGCCACTTCTTCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGTCATCA 153
 795 TCGCCAGCTTTTCATCCCCGATATGACACCCGGGTAAAGTTTCAAGGAGACTTTATCTG 854
 Db TCGGCCA-NTTTCATCCCCGATATGACACCCGGGTAAAGTTTCAAGGAGACTTTATCTG 212
 855 ACAGCAGCGTGCATGCGCCAGGGGATCACATCGTCCCGCGGGGTTCAATAATAT 914
 Db ACAGCAGCGTGCATGCGCCAGGGGATCACATCGTCCCGCGGGGTTCAATAATAT 272
 915 CACTCTGTATATCCCAACACAGACGATACGGCTCTCTCTTTTATAGGTGTAACCTTAA 974
 Db CACTCTGTATATCCCAACACAGACGATACGGCTCTCTCTTTTATAGGTGTAACCTTAA 332
 975 ACTGCATTTTCAACGAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCAATTTCAATAACCGG 1034
 Db ACTGCATTTTCAACGAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTCAATTTCAATAACCGG 392
 1035 GCGACTCAGCATCCCTTCTGATTTTCCGCTTCCAGCTTCGCGCAGCAGACGAG 1094
 Db GCGACTCAGCATCCCTTCTGATTTTCCGCTTTCAGCGTTTCGCGCAGCAGACGAG 452
 1095 GCTTCAATCTGATGTTGTTGTTACACGACGGAGATATGACATCATATATGCTTGA 1154
 Db GCTTCAATCTGATGTTGTTGTTACACGACGGAGATATGACATCATATATGCTTGA 510
 1155 GCAACTGATAGTGTGCTGTCAACTGTCACTGTATACGCTGCTTCATAGCACACCTCT 1214
 Db GCAACTGATAGC-GTCGCTGTCAACTGTCACTGTATACGCTGCTTCATAGCACACCTCT 569
 1215 TTTTGACATCTCCGGTA 1233
 Db TTTTGACATCTCCGGTA 588

RESULT 2
 AG000762/c 713 bp DNA linear GSS 06-FEB-1999
 LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
 DEFINITION survey sequence.
 ACCESSION AG000762
 VERSION AG000762.1 GI:2579570
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 713)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Homo sapiens genomic DNA, chromosome 21q
 Published Only in Database (1997)
 2 (bases 1 to 713)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Direct Submission
 Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@sc.ims.u-tokyo.ac.jp)

Tel:0427-78-9732, Fax:0427-78-9561)
 Location/Qualifiers
 1. 713

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clone="64E11X4"

ORIGIN

Query Match 10.2%; Score 496.6; DB 29; Length 713;
 Best Local Similarity 94.2%; Pred. No. 7.9e-78;
 Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

679 TATTCCCGAGAAATCAGTTAAATGGCGTTTGTGATGTCATTTTCGGCGTGGCTGAGATC 738
 Db TATTCCCGCGGANCATCNGTTAAATGGCGTTTGTGAGGNNATTTTCGGCGTGGCTGAGAA 540
 739 AGCCACTTCTTCCCGATAACGGAGACCGGCACACTGSCCATATCGGTGTCATCATCGC 798
 Db CACCAACTTTTCCGATTACGNAGACCGGCACACTGNCATATCGGTGTCATCATCGC 480
 799 CCAGCTTTTCATCCCGATATGCCACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACAG 858
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 859 CAGAGTGCTACGCGCGGGGATCACCATCGTCCCGCGGGGCTGTCATAATATCACT 918
 Db CAGAGTGCTACGCGCGGGGATCACCATCGTCCCGCGGGGCTGTCATAATATCACT 360
 919 CTGTACATCCCAACACAGACGATTAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTG 978
 Db CTGTACATCCCAACACAGACGATTAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTG 300
 979 CATTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCAATTAACCGGGCGA 1038
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 Db CCTCAGCATCCCTTCCGATTTCCGCTTTCAGCGTTTCGCGCAGCAGACGCGGCTT 180
 1099 CATTCGTCATGTTGTGTTTACACGACCGGAGATTTGACATCATATATGCTTTCAGCAA 1158
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 1159 CTGATAGCTGCGCTGTCACACTGTCAGTGAATAGCTGCTTCATAGCACACCTCTTTT 1218
 Db CTGAATANTGTCGCTGTCACACTGTCAGTGAATAGCTGCTTCATAGCACACCTCTTTT 62
 1219 GACATCTTCGGGA 1233
 Db GACATCTTCGGGA 47

RESULT 3
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 LOCUS AGENCOURT_13988518 NIH_MGC_147 Homo sapiens cDNA clone
 DEFINITION IMAGE:30346919 5', mRNA sequence.
 ACCESSION CD109790
 VERSION CD109790.1 GI:30753999
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 542)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: ND4V387 row: c column: 24
 High quality sequence start: 144
 High quality sequence stop: 251.
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 /db_xref="taxon:9606"
 /clone="IMAGE:30346919"
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 /lab_host="PH108 TonA"
 /clone_lib="NIH MGC 147"
 /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamH; Oligo-dT primed using primer
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 insert size 2.3 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

ORIGIN

Query Match 9.0%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 2.7e-67;
 Matches 493; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

QY 642 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA 701
 DB 23 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGTAA 82
 QY 702 TGGCGTTTTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 761
 DB 83 TGGCGTTTTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 142
 QY 762 AGACGGGCACACTGGCCATATCGGTGGTCATATCGCCAGCTTTTCATCCCGATATGCA 821
 DB 143 AGACGGGCACACTGGCCATATCGGTGGTCATATCGGTGGTCATATCGCCAGTATGCA 202
 QY 822 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 881
 DB 203 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 262
 QY 882 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGCAT 941
 DB 263 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGCAT 322
 QY 942 AACGGCTCTCTTTTATAGGTAAACCTTAACTGCACTTTCACAGTCCCTGTCTCG 1001
 DB 323 AACGGCTCTCTTTTATAGGTAAACCTTAACTGCACTTTCACAGTCCCTGTCTCG 382
 QY 1002 TCAGCAAAAGAGCCGTTTCAATTAACCGGGGACCTCAGCCATCCCTTCTGTATT 1061
 DB 383 TCAGCAAAAGAGCCGTTTCAATTAACCGGGGACCTCAGCCATCCCTTCTGTATT 442
 QY 1062 TCGCTTTTCCA-GCGTTCGGCAGCAGCG-ACGGGCTTCATTC--TGATGTTGTGCT 1117
 DB 443 TCGCTTTTCCA-GCGTTCGGCAGCAGCG-ACGGGCTTCATTC--TGATGTTGTGCT 502
 QY 1118 TACCAGACCGG-AGATATTGACATCATATATGCTT 1152
 DB 503 TACCAGACCGGAGATATTGACATCATATATGCTT 538

RESULT 4

AG000761/c
 LOCUS
 DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64B11X4, genomic
 survey sequence.
 ACCESSION AG000761
 VERSION AG000761.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 723)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Homo sapiens genomic DNA, chromosome 21q
 Published Only in Database (1997)
 2 (bases 1 to 723)
 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
 Direct Submission
 Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
 Location/Qualifiers
 1. 723
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"
 /clone="64B11X4"

ORIGIN

Query Match 8.5%; Score 411.8; DB 29; Length 723;
 Best Local Similarity 98.1%; Pred. No. 7.7e-63;
 Matches 416; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 642 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA 701
 DB 450 CTGCAGACTGGCTGTGTATAGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAA 391
 QY 702 TGGCGTTTTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 761
 DB 330 TGGCGTTTTGATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGG 331
 QY 762 AGACGGGCACACTGGCCATATCGGTGGTCATATCGCCAGCTTTTCATCCCGATATGCA 821
 DB 330 AGACGGGCACACTGGCCATATCGGTGGTCATATCGCCAGCTTTTCATCCCGATATGCA 271
 QY 822 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 881
 DB 270 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGA 211
 QY 882 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGCAT 941
 DB 210 TCACCATCGTCCGCGGGCGGTGCATTAATATCATCTGTACATCCCAACACAGCAT 151
 QY 942 AACGGCTCTCTTTTATAGGTAAACCTTAACTGCACTTTCACAGTCCCTGTCTCG 1001
 DB 150 AACGGCTCTCTTTTATAGGTAAACCTTAACTGCACTTTCACAGTCCCTGTCTCG 91
 QY 1002 TCAGCAAAAGAGCCGTTTCAATTAACCGGGGACCTCAGCCATCCCTTCTGTATT 1061
 DB 90 TCAGCAAAAGAGCCGTTTCAATTAACCGGGGACCTCAGCCATCCCTTCTGTATT 31
 QY 1062 TCCG 1065
 DB 30 TCAG 27

RESULT 5
 AG013450/c
 LOCUS
 AG013450 725 bp DNA linear GSS 14-APR-1999

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1998)
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999, this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
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    Best Local Similarity 90.2%; Pred. No. 3.1e-62; Indels 8; Gaps 7;
    Matches 505; Conservative 0; Mismatches 47;
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DB 723 TTATATTCCTCCCGAAGACATCAGTAAAGCGTTTTCGGAAGCCATTTTCGGTGGTGTGAG 664
QY 736 ATCAGGCACTTCTTCCCGAATACGAGACCGGCACACTGGCCATATCGTGGTGTATCAT 795
DB 663 ATCAGCAATTTTCCCGAATACGAGACCGGCACACTGGCCATATCGTGGTGTATCAT 604
QY 796 GGCACAGCTTTCATCCCGATATGCACACCGGTAAGTTCACGGAG-ACCTTATCTG 854
DB 603 GGCACAGCTTTCATCCCGAATACGAGACCGGCACACTGGCCATATCGTGGTGTATCAT 545
QY 855 ACAGCAGAGCTGCACCTGGCC-AGGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAA 913
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DB 485 TCACCTGTACATCCCAACAGACATACCGCTCTCTTTATAGGTGA-ACCTTA 427
QY 974 AACTGCATTTACCAAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAACG 1033
DB 426 AACTGCATTTACCAAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCATTTCAATAAACG 367
QY 1034 GGCAGCTCAGGCATCCCTTCCTGTATTTTCGGTTTCGAGCGTTCGAGCGAGCAGCAGC 1093
DB 366 GGCAGCTCAGGCATCCCTTCCTGTATTTTCGGTTTCGAGCGTTCGAGCGAGCAGCAGC 307
QY 1094 GGCCTTCACTGTGATGTTGTGCTTACCAACCGGAGATTTGACATCATATATGCTTG 1153
DB 306 GGCCTTCACTGTGATGTTGTGCTTACCAACCGGAGATTTGACATC--ATATGCTTG 249
QY 1154 AGCAACTGATAGTGTGCTGTCAACTGTCACTGTAAATAGCTGCTTTCATAGCACACCTTC 1213
DB 248 AGCAACTGATA-NTGTGCTGTCAACTGTCACTGTAAATAGCTGCTTTCATAGCACACCTTC 190
QY 1214 TTTTTCACATCTTCGGGTA 1233

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Db 189 TTTTTCACATCTTCGGGTA 170
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AGENCOURT_13894516 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
CB997937
CB997937.1 GI:30292457
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM391 row: e column: 05
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High quality sequence stop: 256.
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            /note="Organ: placenta; Vector: pBluescriptR; Site 1:
            all-XhoI; Site 2: BamHI; Library is oligo-dT primed and
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            5'-TTTCTTTTCTTTTCTTCTT-3', size-selected for average insert
            size 2.3 kb and normalized to ROT 5. This is a primary
            library enriched for full-length clones and constructed
            using the Cap-trapper method (Carninci, in preparation).
            Library constructed by M. Brownstein (NIH/NHGRI,
            National Institutes of Health). Note: this is a NIH_MGC
            Library."
ORIGIN
    Query Match 8.3%; Score 404; DB 14; Length 522;
    Best Local Similarity 96.2%; Pred. No. 2.1e-61;
    Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
QY 642 CTGCAGACTGGCTGTGTATAGGAGCGCTGACATTTATTTCCCGAGACATGATTAA 701
DB 23 CTGCAGACTGGCTGTGTATAGGAGCGCTGACATTTATTTCCCGACACATCATGTTAA 82
QY 702 TGGCGCTTTTTCATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGAGTAACGG 761
DB 83 TGGCGCTTTTTCATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGAGTAACGG 142
QY 762 AGACCGGCACACTGCCCATATCGGTGGTCAATCATCGCCAGCTTTCATCCCGATATGCA 821
DB 143 AGACCGGCACACTGCCCATATCGGTGGTCAATCATCGCCAGCTTTCATCCCGATATGCA 202
QY 822 CCACCGGTAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGCATCGCCAGGGGGA 881
DB 203 CCACCGGTAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGCATCGCCAGGGGGA 262

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QY 882 TCACCATCGTCGCGCGCGTCAATAATATCACTCTGTACATCCACAAACAGCAT 941
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QY 942 AACGGCTCTCTTTATAGGTGTAACACCTTAAACTGCAATTCACAGTCCCTGTTCTCG 1001
Db 323 AACGGCTCTCTTATAGGTGTAACACCTTAAACTGCAATTCACAGTCCCTGTTCTCG 381
QY 1002 TCAGCAAAAGACCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCC-TTCTGATT 1060
Db 382 TCAGCAAAAGACCGGTTCATTTCAATAAACCAGGCGACCTCAGCCATCCC-TTCTGATT 441
QY 1061 TTCCGCTTTCAGCGTTCGCGACGAGCGAC 1092
Db 442 TTTCGCTTTCAGCGTTCGCGACGCGAC 473

RESULT 7
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LOCUS AG000763 722 bp DNA linear GSS 06-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic survey sequence.
ACCESSION AG000763
VERSION AG000763.1 GI:2579571
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE 2 (bases 1 to 722)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagami-hara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

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        /clone="64E11X4"

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Query Match 8.2%; Score 398.4; DB 29; Length 722;
Best Local Similarity 92.2%; Pred. No. 1.8e-60;
Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7;

QY 697 GTTAATGCGTTTATGATCTATTTTCGCGGTGGTGGATCAGGCACATCTTCCCGCAT 756
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QY 757 AACGAGACCGGCACACTCGGCATATTCGGTGGTGCATCATGCGCGCAGCTTTCATCCCGCAT 816
Db 666 TAAGGAGACCGGCACA-TGGCCATAACGGTGGTGCATCA-CGCGCAGCTTCA-CCCGCAT 610
QY 817 ATGCACACCGGTAAAGTTTCAGGAGACTTTATCTGTACAGCAGCGTCACTGCCAG 876
Db 609 ATGCACACCGGNTAAAGTTTCAGGAGACTTTAACGAGCAGCAGTGCATGCCAG 550
QY 877 GGGGATCACCATCCGTCGCGCGGCGGTGTAATAATATCACTGTACATCCACAAACAG 936
Db 549 GGAATCACCATCCGTCGCGCGGCGGTGTAATAATATCACTGTACATCCACAAACAG 490
QY 937 ACATTAACGGCTCTCTTTTATAGGTGTAACCTTAACTGATTTACACAGTCCCTGT 996

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Db 489 ACGATAACGGCTCTCTCTTTATAGGTGTAAACCTTAACTGCAATTCACAGTCCCTGT 430
QY 997 TCTCGTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCT 1056
Db 429 TCTCGTCAGC-AAAGAGCGGTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCT 371
QY 1057 GATTTTCCGCTTCCAGGTTCCGCGACGACGACGACGCGCTTCATTCGCAATGGTGGC 1116
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Db 310 TTACAGACCGGAGATATTGACATC-ATATGCTTTCAGCAACTGATAG-TGTGCTGCTC 254
QY 1177 AACTGTCACTGTAAATACGCTGCTTCATAGCAACCTCTTTTTCAGCAATCTTCGGGTA 1233
Db 253 AACTGTCACTGTAAATACGCTGCTTCATAGCAACCTCTTTTTCAGCAATCTTCGGGTA 197

RESULT 8
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LOCUS CB395230 487 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR151B2_1 AD-wrmCDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB395230
VERSION CB395230.1 GI:30736941
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
    Marc Vidal Laboratory
    Dana Farber Cancer Institute
    1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
    Tel: 617 632 5180
    Fax: 617 632 5739
    Email: Marc.Vidal@dfci.harvard.edu
    Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
    POLYA=No.
FEATURES
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ORIGIN
Query Match 7.3%; Score 357; DB 14; Length 487;
Best Local Similarity 93.6%; Pred. No. 4.3e-53;
Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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philippe_vaglio@dfci.harvard.edu
POLYA-No_ Location/Qualifiers

1. 384
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/dev_stage="mixed stage"
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

FEATURES
source

ORIGIN

Query Match 7.0%; Score 340.2; DB 12; Length 384;
Best Local Similarity 97.7%; Pred. No. 4.4e-50;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 197 TAAAAACAGACTACATATCTGTAAACACACATATCCAGTCACTATGAATCAACTA 256
|||
Db 32 TAATACACAGACTACATATCTGTAAACACACATATCCAGTCACTATGAATCAACTA 91
|||

QY 257 CTTTAGATGATTAGTACCTGTAGTCGCGGACGCTTCCAAATGTTCTTTCGGGTGAT 316
|||
Db 92 CTTTAGATGTTTAGTGACCTGTAGTCGCGGACGCTTCCAAATGTTCTTTCGGGTGAT 151
|||

QY 317 GCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTTCGAAAGGATCGTGAT 376
|||
Db 152 GCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTTCGAAAGGATCGTGAT 211
|||

QY 377 CGAGCCTACTCGTATGTCCTCAATGCGCTATTAATCAATAAGAAATAGAAAG 436
|||
Db 212 CCAACCTACTCGTATGTCCTCAATGCGCTATTAATCAATAAGAAATAGAAAG 271
|||

QY 437 AGTGGCGAGCTCTTTTGTGACAAATAAATCAATCTACTTATCATACCTAG 496
|||
Db 272 AGTGGCGAGCTCTTTTGTGACAAATAAATCAATCTACTTATCATACCTAG 331
|||

QY 497 TGTCTAGTCTGAAATCATCTGCATCAAGAAATTTTCAACACTTTTATAC 549
|||
Db 332 TGTCTAGTCTGAAATCATCTGCATCAAGAAATTTTCAACACTTTTATAC 384
|||

RESULT 11
BI174407/c
LOCUS
DEFINITION
OSTF043E11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
Fl1F1.5, mRNA sequence.

ACCESSION
BI174407.1 GI:14640210
VERSION
EST.
KEYWORDS
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 384)

REFERENCE
AUTHORS
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome.Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORPome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA-No_ Location/Qualifiers

1. 384
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/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

FEATURES
source

ORIGIN

Query Match 6.7%; Score 325.4; DB 12; Length 384;
Best Local Similarity 98.2%; Pred. No. 1.8e-47;
Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3580 TGTTCCTTGATCGAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATCT 3639
|||
Db 366 TGTTCCTTGATCGAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGTAGATCT 307
|||

QY 3640 TTTTATTTTGTGCACAAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 3699
|||
Db 306 TTTTATTTTGTGCACAAAAAAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGAT 247
|||

QY 3700 TAATACGGATTCAGGACAAATAGCGATAGGCTGGATAGCAGATTCCTTTTGAGAGAA 3759
|||
Db 246 TAATACGGATTCAGGACAAATAGCGATAGGCTGGATAGCAGATTCCTTTTGAGAGAA 187
|||

QY 3760 CATTGGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATACCCGAGAACATTTGGAAGC 3819
|||
Db 186 CATTGGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATACCCGAGAACATTTGGAAGC 127
|||

QY 3820 TGTGGTGCAGTACAGGCTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGGATAT 3879
|||
Db 126 TGTGGTGCAGTACAGGCTCACTAATACCATCTAAGTAGTGTGATTCATAGTACTGGATAT 67
|||

QY 3880 GTTGTGTTTTTACAGTATATATGATGCTGTTTTTA 3914
|||
Db 66 GTTGTGTTTTTACAGTATATATGATGCTGTTTTTA 32
|||

RESULT 12
BJ555980
LOCUS
DEFINITION
BJ555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jmi8n08 5', mRNA sequence.

ACCESSION
BJ555980
VERSION
EST.
KEYWORDS
Ipomoea nil (Japanese morning glory)
ORGANISM
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoea.

REFERENCE
AUTHORS
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T.,
Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.
ESTs of Japanese morning glory
Unpublished (2002)

COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES source
Location/Qualifiers
1..337
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/clone="jmi8n08"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

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Query Match 6.2%; Score 301.4; DB 12; Length 337;
Best Local Similarity 99.4%; Pred. No. 3.3e-43;
Matches 313; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 642 CTGCAGACTGGCTGTATAGGAGCCCTGACATTTATATCCCGAGAACATCAGGTTAA 701
Db 24 CTGCAGACTGGCTGTATAGGAGCCCTGACATTTATATCCCGAGAACATCAGGTTAA 83
QY 702 TGGCGTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGATAAACGG 761
Db 84 TGGC-TTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGATAAACGG 142
QY 762 AGACCGGACACTGGCCATATCGTGGTCATATGCGCCAGCTTTTCATCCCGATATGCA 821
Db 143 AGACCGGACACTGGCCATATCGTGGTCATATGCGCCAGCTTTTCATCCCGATATGCA 202
QY 822 CCACCGGTAAGTTCAAGGAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGA 881
Db 203 CCACCGGTAAGTTCAAGGAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGA 262
QY 882 TCACCATCGTCCCGGGGCTCAATAATATCACTCTGTACATCCACAACAGACGAT 941
Db 263 TCACCATCGTCCCGGGGCTCAATAATATCACTCTGTACATCCACAACAGACGAT 322
QY 942 AACGGCTCTCTCTTT 956
Db 323 AACGGCTCTCTCTTT 337

RESULT 13
CF469981/c
LOCUS
DEFINITION P7-E11 Plasmodium yoelii 17X axenic hepatic stages Plasmodium
yoelii yoelii cDNA, mRNA sequence.
ACCESSION CF469981.1 GI:34487353
VERSION EST.
KEYWORDS
SOURCE Plasmodium yoelii yoelii
ORGANISM Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Wang,Q., Okubo,E., Kaiser,K., Pashrel,E., Kappe,S., Brown,S., Nussenzweig,V. and Bhanot,P.
TITLE Expressed sequence tags from Plasmodium yoelii hepatic stages in axenic culture
JOURNAL Unpublished (2003)
COMMENT Contact: Bhanot P
Department of Pathology
New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop1@med.nyu.edu
similar to NR[GI:23483606 hypothetical protein (Plasmodium yoelii yoelii)] (e-108).

FEATURES source
Location/Qualifiers
1..1068
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/strain="17X"
/sub_species="yoelii"
/db_xref="taxon:73239"
/dev_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii 17X axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million Plasmodium yoelii 17X sporozoites were isolated from salivary glands of infected Anopheles stephensi mosquitoes and purified over a DE52 cellulose column. The sporozoites were cultured for 24h at 37C in the presence of 5% CO2 and 10% FBS as described in 'Transformation of sporozoites into early exoerythrocytic malaria parasites does not require host cells', (J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BD Biosciences SMART cDNA synthesis kit. Double stranded cDNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."

ORIGIN
Query Match 5.6%; Score 273.2; DB 14; Length 1068;
Best Local Similarity 90.0%; Pred. No. 2.2e-38;
Matches 278; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 667 GCCTGACATTTATATCCCGAGAACATCAGGTTAATGCGGTTTGTATGTCATTTCCG 726
Db 562 GCCTGACATTTATATCCCGAGAACATCAGGTTAATGCGGTTTGTATGTCATTTCCG 503
QY 727 GTGGCTGAGATCAGCCACTTCTCCCGATACCGGAGACCGCACATCGGTCATCGT 786
Db 502 GTGGCTGAGATCAGCCACTTCTCCCGATACCGGAGACCGCACATCGGTCATCGT 443
QY 787 GGTATCATGTGGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTCAAGGAGAC 846
Db 442 GGNCATCATGCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTCAAGGAGAC 383
QY 847 TTTATCTGACAGCAGCTGACCTGCGCAGGGGATCACCATCCGTCGCGGGGCTGTC 906
Db 382 TTTATCTGACAGCAGCTGACCTGCGCAGGGGATCACCATCCGTCGCGGGGCTGTC 323
QY 907 AATAATATCACTCTGTATATCCACAACAGACGATACGCTCTCTCTTTATAGGTGTA 966
Db 322 AANAATATCGTTCGNNCATCCACNANCNANGANGCGCTNTNTTTCACAGGTGNA 263
QY 967 AACCTTAA 975
Db 262 AACNTTGA 254

RESULT 14
CF469119/c
LOCUS
DEFINITION CF469119.1 1037 bp mRNA linear EST 05-SEP-2003
yoelii cDNA, mRNA sequence.
ACCESSION CF469119.1 GI:34486491
VERSION EST.
KEYWORDS
SOURCE Plasmodium yoelii yoelii
ORGANISM Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 1037)
AUTHORS Wang,Q., Okubo,E., Kaiser,K., Pashrel,E., Kappe,S., Brown,S., Nussenzweig,V. and Bhanot,P.
TITLE Expressed sequence tags from Plasmodium yoelii hepatic stages in axenic culture
JOURNAL Unpublished (2003)
COMMENT Contact: Bhanot P
Department of Pathology

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:34 ; Search time 11140.1 Seconds
(without alignments)
17418.703 Million cell updates/sec

Title: US-10-055-001b-24_COPY_13000_17476
Perfect score: 4477
Sequence: 1 ttctattggagagacacg.....atagtgccacctaatactgc 4477

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	3234.8	72.3	18691	12	CVE311874	AJ311874 Cloning v	
2	1108.8	24.8	4470	6	BD263377	BD263377 Compositi	
3	1108.8	24.8	4939	6	BD263381	BD263381 Compositi	
C	4	1108.8	24.8	5584	6	BD263402	BD263402 Compositi
	5	989.6	22.1	4165	6	BD263380	BD263380 Compositi
	6	947.8	21.2	4208	6	BD263379	BD263379 Compositi
C	7	827	18.5	4204	6	BD263378	BD263378 Compositi
	8	824.4	18.4	5824	12	CVE311872	AJ311872 Cloning v
C	9	824.4	18.4	6063	12	CVE311873	AJ311873 Cloning v
	10	823.8	18.4	5156	6	BD263382	BD263382 Compositi
11	780	17.4	786	6	BD194641	BD194641 Method an	
12	778.6	17.4	14645	8	F7PDKG	X75095 F.trinervia	
13	747	16.7	7049	6	A23998	A23998 pT4 expres	
C	14	735	16.4	10138	12	AF187951	AF187951 Activatio
	15	728.8	16.3	7566	6	A24783	A24783 plasmid BPS
16	728.8	16.3	7566	6	AR074388	AR074388 Sequence	
17	728.8	16.3	7639	6	A24782	A24782 plasmid pJD	
18	728.8	16.3	7639	6	AR074387	AR074387 Sequence	
19	722.8	16.1	11405	12	AY310901	AY310901 Binary ve	
20	719.4	16.1	22574	12	CVE18556	Y18556 Cloning vec	
21	713	15.9	4947	6	BD217610	BD217610 Method an	
C	22	710.2	15.9	7599	6	AX063413	AX063413 Sequence
	23	709.8	15.9	5399	6	A18050	A18050 DNA for tra
24	709.8	15.9	5399	6	AR095106	AR095106 Sequence	
25	709.8	15.9	5399	6	AR098312	AR098312 Sequence	
26	709.8	15.9	5399	6	I49885	I49885 Sequence 1	
27	709.8	15.9	5399	6	I82373	I82373 Sequence 1	
28	709.8	15.9	5399	6	AX012337	AX012337 Sequence	
C	29	709.8	15.9	6428	12	SYNTIPFPSS	M35007 A.tumefacie
	30	709.8	15.9	6555	6	AR007512	AR007512 Sequence
31	709.8	15.9	6555	6	AR084078	AR084078 Sequence	
32	709.8	15.9	14194	6	AX052541	AX052541 Sequence	
33	708.8	15.8	10907	12	AY310333	AY310333 Cloning v	
34	707	15.8	24595	1	ATACH5	X00493 Agrobacteri	
35	707	15.8	24595	6	E00404	E00404 Ti plasmid	
36	707	15.8	24595	6	E00546	E00546 DNA fragmen	
37	707	15.8	24595	6	AR364803	AR364803 Sequence	
38	707	15.8	24595	6	BD016312	BD016312 Method of	
C	39	707	15.8	194140	1	AF242881	AF242881 Agrobacte
	40	697.2	15.6	6875	12	AF433042	AF433042 Cloning v
41	697.2	15.6	6928	12	AF433043	AF433043 Cloning v	
42	697.2	15.6	27608	12	AF184978	AF184978 Binary ve	
43	697.2	15.6	28708	12	AY218787	AY218787 Cloning v	
44	695.8	15.5	3669	12	ATU414108	AJ414108 Binary ve	
45	695.8	15.5	5341	12	ATU414109	AJ414109 Binary ve	

ALIGNMENTS

RESULT 1	CVE311874	CVE311874	18691 bp	DNA	circular SYN 09-JUL-2002
LOCUS	AJ311874	Cloning vector pHELLSGATE.			
DEFINITION	AJ311874	Cloning vector pHELLSGATE.			
ACCESSION	AJ311874				
VERSION	AJ311874.1	GI:15982218			
KEYWORDS		kanomycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon In7.			
SOURCE		Cloning vector pHELLSGATE			
ORGANISM		Cloning vector pHELLSGATE			
REFERENCE	1	artificial sequences; vectors.			
AUTHORS		Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,			

QY 506 CTAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGCTGTGATA 565
Db 13601 CTAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGCTGCTGTGATA 13660
QY 566 AGGAGGCTGACATTTATTTCCCCAGAACATCAGGTTAAATGGGGTTTTTGATGCAATTT 625
Db 13661 AGGAGGCTGACATTTATTTCCCCAGAACATCAGGTTAAATGGGGTTTTTGATGCAATTT 13720
QY 626 TCGCGGTGGCTGAGATCAGCACATCTTCTCCCGATAACGGAGACCGGCACATCGGCCATA 685
Db 13721 TCGCGGTGGCTGAGATCAGCACATCTTCTCCCGATAACGGAGACCGGCACATCGGCCATA 13780
QY 686 TCGGTGGCTGACATCGGCCAGCTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGG 745
Db 13781 TCGGTGGCTGACATCGGCCAGCTTTCATCCCGATATGCACACCGGGTAAAGTTTCAAGG 13840
QY 746 GAGACTTTATCTGACAGAGAGCTGACATGGCCAGGGGATCACCATCGTTCGCCCGGGC 805
Db 13841 GAGACTTTATCTGACAGAGAGCTGACATGGCCAGGGGATCACCATCGTTCGCCCGGGC 13900
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QY 866 GTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGACCGCTTCA 925
Db 13961 GTGTAAACCTTAAACTGCAATTTCAACAGTCCCTGTTCTCGTCAGCAAAAGACCGCTTCA 14020
QY 926 TTCATTAACCGGGGACCTCAGCCATCCCTTCTGTATTTCCGTTTCCAGCGTTCGGC 985
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QY 986 AGCGAGACGACGGGCTTCAATCTGTATGTTGTGCTTACAGACCGGAGATATGACATC 1045
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QY 1046 ATATATGCTTGAAGCAACTGTATGCTGTGCTGCTCAACTGTCACTGTATAATACGCTGCTTC 1105
Db 14141 ATATATGCTTGAAGCAACTGTATGCTGTGCTGCTCAACTGTCACTGTATAATACGCTGCTTC 14200
QY 1106 ATAGCACACCTCTTTTGTACATCTTCCGGTAGTCCGATCAACGCTCATTTTCGCCAA 1165
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QY 1166 AAGTTGGCCACGAGGCTTCCGGTATCAACAGGAGACCCAGGATTTATTTATTTCTGGAG 1225
Db 14261 AAGTTGGCCACGAGGCTTCCGGTATCAACAGGAGACCCAGGATTTATTTATTTCTGGAG 14320
QY 1226 TGATCTTCGTCACAGGTATTTATTCGGCGCAAGTGGTGGGTGATGCTGCCAATCTTA 1285
Db 14321 TGATCTTCGTCACAGGTATTTATTCGGCGCAAGTGGTGGGTGATGCTGCCAATCTTA 14380
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Db 14381 GTCCAGTACAGGTCACATATACCATCTAAGTAGTGTGATTCATGACCTGGATGTTCT 14440
QY 1346 GTTTTACAGTATTTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATTTGATATTT 1405
Db 14441 GTTTTACAGTATTTATGATCTGTTTTTATGCAAAATCTAAATTTAATATATTTGATATTT 14500
QY 1406 ATATCATTTTACGTTTCTCGTTCAGCTTCTCTGTACAAAGTGG----- 1448
Db 14501 ATATCATTTTACGTTTCTCGTTCAGCTTCTCTGTACAAAGTGGCATTTAAGAAAGCAT 14560
QY 1449 ----- 1448
Db 14561 TGCTTATCAATTTGTTGCAAGAACAGGTCACTATCGTCAAAATAAAATCATTTATTCG 14620
QY 1449 -----TCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTATTT 1493
Db 14621 CATCCAGCTCGAGCTCCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAAATAATTTATTT 14679
QY 1494 TCTTTTTTCTTTTAGTATAAAATAGTTAAGTGATGTTAATTTAGTATGATATAAATA 1553

Db 14680 TCTTTTTTCTTTTAGTATAAAATAGTTAAGTGATGTTAATTTAGTATGATATAAATA 14739
QY 1554 TAGTTGTTAATAATTTGTGAAAAAATAATTTATAAATAATTTGTTTACATAAACAACATAGT 1613
Db 14740 TAGTTGTTAATAATTTGTGAAAAAATAATTTATAAATAATTTGTTTACATAAACAACATAGT 14799
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QY 1674 ATATTTATTTTAAATGAAATTTGATCGAACATCTGAAGATGATATCTAGCATTTAA 1726
Db 14860 ATATTTATTTTAAATGAAATTTGATCGAACATCTGAAGATGATATCGGCCGTAAGAGTTC 14919
QY 1727 ----- 1726
Db 14920 CAACCTTCCACCAATTAATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTTATCGAGATT 14979
QY 1727 ----- 1726
Db 14980 TTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTCGATATACCACCGTTGATAT 15039
QY 1727 ----- 1726
Db 15040 ATCCCAATGGCATCGTAAAGAACATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTPACCTA 15099
QY 1727 ----- 1726
Db 15100 TAAACAGACCGTTCCAGCTGGATATTAACGGCTTTTAAAGACCGTAAAGAAAAATAAGCA 15159
QY 1727 ----- 1726
Db 15160 CAAGTTTATCCGGGCTTTTATTCACATTTCTTGGCCGCTGATGAATGCTCATCCGGAATT 15219
QY 1727 ----- 1726
Db 15220 CGGTATGCAATGAAGAAGCGGTGAGCTGGTGAATATGGGATAGTGTTCACCTTGTTCAC 15279
QY 1727 ----- 1726
Db 15280 CGTTTTCATGAGCAAACTGMAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTT 15339
QY 1727 ----- 1726
Db 15340 CCGGAGTTTCTACACATATATTCGCAAGATGTGGCGTTTACGCGTGAACCTGGCCCTA 15399
QY 1727 ----- 1726
Db 15400 TTTCCCTAAAGGTTTATTTGAGAAATATGTTTTCGTCTCAGCCAATCCCTGGGTGAGTTT 15459
QY 1727 ----- 1726
Db 15460 CACCAGTTTGTATTTAAAGCTGGCCAATATGSAACAATCTTCTCGCCCCCGTTTCCACCAT 15519
QY 1727 ----- 1726
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QY 1727 ----- 1726
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QY 1727 -----TATTTGTTTTTAATCAT 1743
Db 15700 TCGGTATTTTCGCGCTGATTTTTTTCGGGTATAAGAAATATATCTGATATGTCGGGCCATA 15759
QY 1744 ATAGTAATTTCTAGCTGGTTTGTGATGAATTAATAATCAATGATAAAATACTATAGTAAAAAT 1803

Qy	2783	TTCCGGCGTGGCTAGAGATAGCCACATCTCTTCCCGGATAACGAGAGACCGGCACTACCTGGCCAT	2842
Db	16900	TTCCGGCGTGGCTAGAGATACAGCACATCTCTTCCCGGATAACGAGAGACCGGCACTACCTGGCCAT	16959
Qy	2843	ATCGGTGGTGCATCATCGCGCCAGCTTTCACTCCCGGATATGCACCAACCGGGTAAAGTTTCACG	2902
Db	16960	ATCGGTGGTGCATCATGCGCCAGCTTTCACTCCCGGATATGCACCAACCGGGTAAAGTTTCACG	17019
Qy	2903	GGAGACTTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGAATACCATTCGGTCGCCCGGG	2962
Db	17020	GGAGACTTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGAATACCATTCGGTCGCCCGGG	17079
Qy	2963	CGGTGCAATAATATCACTCTGTACATCCAAACAGAGATAAACGGCTCTCTCTTTTATA	3022
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Db	17260	CACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACAT	17319
Qy	3203	CATATATGCCCTTGAGCAACTGATAGCTGTCCGTCTCACTGTCACTGTAAATACGCTGCTT	3262
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Qy	3263	CATAGACACACTCTTTTTCACATACCTCTGTTCTTGATGCACATGATTTTCAGGACTATG	3322
Db	17380	CATAGACACACTCTTTTTCACATACCTCTGTTCTTGATGCACATGATTTTCAGGACTATG	17439
Qy	3323	ACACTAGCGPATATGAATAGGTAGATGTTTTTATTTGTCACAAAAAGAGGCTCGCA	3382
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Qy	3706	TCCTGCTTTAATGAGATATCGGAGACGCCTATGATCGCATGATATTGCTTTCAATTCTG	3765
Db	17920	TCCTGCTTTAATGAGATATCGGAGACGCCTATGATCGCATGATATTGCTTTCAATTCTG	17979

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RESULT 2
BD263377
LOCUS BD263377 4470 bp DNA linear BAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263377
VERSION BD263377.1 GI:33073145
KEYWORDS JP 2002537790-A/155.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 4470)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 155 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/155
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
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ORIGIN
Query Match 24.8%; Score 1108.8; DB 6; Length 4470;
Best Local Similarity 99.8%; Pred. No. 7.1e-151;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATATCAATATATT 85
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QY 86 AATTAGATTTTGCATAAAAACAGACTACATATCTGTAAACACACACATATCCAGTC 145
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Db 282 TGTTCCTCGGTGATGCTGCGCAACTTAGTCACGACGAGCCTTCCAAATGTTCTCTCAA 341
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Db 522 TCTTATCTTTTCTCTTACAAAGTCTGCGGTTCTATCTGGATTTCAGCCTCTATACCTTA 581
QY 506 CTAAACGTTAATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGACTGGCTGTGTATA 565
Db 582 CTAAACGTTAATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCGAGACTGGCTGTGTATA 641
QY 566 AGGAGCCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTTTGTATGTCATT 625
Db 642 AGGAGCCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTTTGTATGTCATT 701
QY 626 TCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGACACTGCGCCATA 685
Db 702 TCGCGGTGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGACACTGCGCCATA 761
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RESULT 3

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BD263381
LOCUS 4939 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
BD263381
VERSION 1 GI:33073149
KEYWORDS JP 2002537790-A/159.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 4939)
REFERENCE Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
AUTHORS Compositions and methods for use in recombinational cloning of
TITLE nucleic acids
JOURNAL Patent: JP 2002537790-A 159 12-NOV-2002;
COMMENT INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PR 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/ PC
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FEATURES

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Query Match 24.8%; Score 1108.8; DB 6; Length 4939;
Best Local Similarity 99.8%; Pred. No. 7e-151;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 85
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QY 86 AAATAGATTTTGCATAAAAAAGAGACTACATATACTGTAAAAACAAACATATCCAGTC 145
Db 3696 AAATAGATTTTGCATAAAAAAGAGACTACATATACTGTAAAAACAAACATATCCAGTC 3755
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Db 4176 AGGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGCGGTTTTTGTATGTCATTT 4235
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RESULT 4
BD263402/c
LOCUS BD263402 5584 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263402
VERSION BD263402.1 GI:33073170
KEYWORDS JP 2002537790-A/180.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 5584)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLES Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/180
PD 12-NOV-2002
PR 02-MAR-2000 JP 2000602252
PR 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
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CC pDONR207
PH Key Location/Qualifiers
FT source 1..5584
FT /organism='Artificial Sequence'.
FEATURES
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ORIGIN
Query Match 24.8%; Score 1108.8; DB 6; Length 5584;
Best Local Similarity 99.8%; Pred. No. 6.9e-151;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAAGCTGAAATGATATTAATCAATATATT 85
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RESULT 5
BD263380 4165 bp DNA linear PAT 17-JUL-2003
LOCUS BD263380
DEFINITION Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263380
VERSION BD263380.1 GI:33073148
KEYWORDS JP 2002537790-A/158.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 4165)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLES Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 158 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/158
PD 12-NOV-2002
PR 02-MAR-2000 JP 2000602252
PR 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744

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LOCUS	BD263379	4208 bp	DNA linear PAT 17-JUL-2003
DEFINITION	Compositions and methods for use in recombinational cloning of nucleic acids.		
ACCESSION	BD263379		
VERSION	BD263379.1	GI:33073147	
KEYWORDS	JP 2002537790-A/157.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	artificial sequences.		
AUTHORS	1 (bases 1 to 4208)		
TITLE	Harley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.		
JOURNAL	Compositions and methods for use in recombinational cloning of nucleic acids		
COMMENT	Patent: JP 2002537790-A 157 12-NOV-2002;		
	INVITROGEN CORP		
	OS Artificial Sequence		
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	PD 12-NOV-2002		
	PF 02-MAR-2000 JP 2000602252		
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	28-MAY-1999 US 60/136744		
	PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC		
	C12N1/05,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/PC		
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	CC ccdB		
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QY	86	AAATTAGATTTCGATAAAAAACAGACTACATAATCTGTAAACACAAACATATCCAGTC	145

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RESULT 7
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DEFINITION BD263378 Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263378
VERSION BD263378.1 GI:33073146
KEYWORDS JP 2002537790-A/156.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 4204)
AUTHORS Hartley, J.L., Bransch, M.A., Temple, G.F. and Chao, D.
TITLE Compositions and methods for use in recombinational cloning of

nucleic acids
Patent: JP 2002537790-A 156 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/156
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/PC
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CC ccdB
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RESULT 9
LOCUS CVE311873 6063 bp DNA circular SYN 09-JUL-2002
DEFINITION Cloning vector pKANIBAL.
ACCESSION AJ311873
VERSION AJ311873.1 GI:15982216
KEYWORDS kan gene; kanamycin resistance protein; pdk gene; promoter.
SOURCE Cloning vector pKANIBAL
ORGANISM Cloning vector pKANIBAL
REFERENCE 1. Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q.,
Gooding, P.S., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P.,
Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
JOURNAL 21461301
MEDLINE 11576441
PUBMED
REFERENCE 2 (bases 1 to 6063)
Waterhouse, P.M.
Direct Submission
TITLE Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
JOURNAL Location/Qualifiers
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Best Local Similarity 92.9%; Pred. No. 8.6e-110;
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DEFINITION			
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Compositions and methods for use in recombinational cloning of nucleic acids.			
ACCESSION			
BD263382			
VERSION			
BD263382.1 GI:33073150			
KEYWORDS			
JP 2002537790-A/160.			
SOURCE			
synthetic construct			
ORGANISM			
artificial sequences.			
REFERENCE			
1 (bases 1 to 5156)			
AUTHORS			
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.			
TITLE			
Compositions and methods for use in recombinational cloning of nucleic acids			
JOURNAL			
Patent: JP 2002537790-A 160 12-NOV-2002;			
COMMENT			
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Artificial Sequence			
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JP 2002537790-A/160			
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12-NOV-2002			
PF			
02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR			
28-MAY-1999 US 60/136744			
PI			
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC			
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N5/00,			
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Matches 825; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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RESULT 13
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 DEFINITION pTE4 expression vector.
 ACCESSION A23998
 VERSION A23998.1 GI:833338
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 7049)
 AUTHORS Nazarov, V., Botterman, J., Stanssens, P. and Sevcik, J.
 TITLE A novel ribonuclease and its inhibitor
 JOURNAL Patent: EP 0537399-A 3 21-APR-1993;
 PLANT GENETIC SYSTEMS, N.V.
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 DB 4542 GTTCCCGCGCGCGCATGGGTGAGATTCTTGAAGTTGAGTATTGGCGCTCCGCTCTA 4601
 QY 4222 CGGAAAGTTTACGGGCACTTCAACCCCGGTCCAGCACCGCGCGCGGTAAACGACTTGGT 4281
 DB 4602 CGGAAAGTTTACGGGCACTTCAACCCCGGTCCAGCACCGCGCGCGGTAAACGACTTGGT 4661
 QY 4282 GCCCGGAGAATTTGCGAGCATTTTGGTGTATGTGGGCGCCCAAAATGAAGTGAGGCA 4341
 DB 4662 GCCCGGAGAATTTGCGAGCATTTTGGTGTATGTGGGCGCCCAAAATGAAGTGAGGCA 4721
 QY 4342 AACCTTGACGTGACGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGCACACACATGT 4401
 DB 4722 AACCTTGACGTGACGACAAATCGTTGGCGGGTCCAGGCGGAATTTTGCACACACATGT 4781
 QY 4402 CGAGGCTCAGCAGGACCTGCGAGGCAATGCAAGCTAG 4436
 DB 4782 CGAGGCTCAGCAGGACCTGCGAGGCAATGCAAGCTAG 4816

RESULT 14
 AF187951/c
 LOCUS AF187951 10138 bp DNA linear SYN 11-MAY-2000
 DEFINITION Activation-tagging vector pSKI015, complete sequence.
 ACCESSION AF187951
 VERSION AF187951.1 GI:6537289
 KEYWORDS
 SOURCE Activation-tagging vector pSKI015
 ORGANISM Activation-tagging vector pSKI015
 REFERENCE 1 (bases 1 to 10138)
 AUTHORS Weigel, D., Ahn, J. H., Blazquez, M. A., Borevitz, J. O.,
 Christensen, S. K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
 Malancharavi, E. J., Neff, M. M., Nguyen, J. T., Saco, S., Wang, Z.,
 Xia, Y., Dixon, R. A., Harrison, M. J., Lamb, C. J., Yanofsky, M. F. and
 Chory, J.
 TITLE Activation tagging in Arabidopsis
 JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000)
 MEDLINE 20223715
 PUBMED 10759496
 REFERENCE 2 (bases 1 to 10138)

AUTHORS Kardailsky, I. and Weigel, D.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES
Location/Qualifiers
source 1..10138
/organism="Activation-tagging vector pSKI015"
/mol_type="genomic DNA"
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12..31
/notes="T7 RNA polymerase promoter"
36..2204
/note="derived from pUC19"
2205..2662
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2663..2829
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2830..2849
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2894..4178
/notes="cauliflower mosaic virus 35S gene promoter enhancer
sequences (tetramer)"
4270..4294
/note="T-DNA right border"
7690..7713
/notes="T-DNA left border"
complement(8054..8784)
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complement(<8785..>9420)
complement(8791..9342)
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complement(9421..10119)
/product="mannopine synthase"
/note="5' end and promoter"

ORIGIN
Query Match 16.4%; Score 735; DB 12; Length 10138;
Best Local Similarity 100.0%; Pred. No. 6.5e-97;
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3700 CTAGAGTCCTGCTTAATGAGATATCGAGACGCTATGATCGCATGATTTGCTTTCA 3759
Db 8772 CTAGATCCCTGCTTAATGAGATATCGAGACGCTATGATCGCATGATTTGCTTTCA 8713
QY 3760 ATTCTGTGTGCGCTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGGT 3819
Db 8712 ATTCTGTGTGCGCTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGGT 8653
QY 3820 TTCGGTTCATCTAAGATATATACCGGTTACTATCGTATTTTATGAATAATTTCT 3879
Db 8652 TTCGGTTCATCTAAGATATATACCGGTTACTATCGTATTTTATGAATAATTTCT 8593
QY 3880 CCGTTCATTTACTGATGTGACCTACTCTATATGTATGTAATTAATAAGAACAT 3939
Db 8592 CCGTTCATTTACTGATGTGACCTACTCTATATGTATGTAATTAATAAGAACAT 8533
QY 3940 ATATTGCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAAT 3999
Db 8532 ATATTGCTGAATAGTTTATAGCGACATCTATGATAGAGCGCCACAATAACAAT 8473
QY 4000 TCGGTTTTATTACAAATCCAAATTTAAAAAGCGGAGAACCGGTCAACCTAAAA 4059

Db 8472 TCGGTTTTATTACAAATCCAAATTTAAAAAGCGGAGAACCGGTCAACCTAAAA 8413
QY 4060 GACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGACA 4119
Db 8412 GACTGATTACATAAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGACA 8353
QY 4120 CACCGAGCGCGCAACTATATACGTTTCACTGAAGGAACTCCGGTTCCTCCCGCGCGCGCA 4179
Db 8352 CACCGAGCGCGCAACTATATACGTTTCACTGAAGGAACTCCGGTTCCTCCCGCGCGCGCA 8293
QY 4180 TGGGTGAGATTCCTTGAAGTTGAGTATTTGGCCGTCTACCGGAAAGTTACGGGACCC 4239
Db 8292 TGGGTGAGATTCCTTGAAGTTGAGTATTTGGCCGTCTACCGGAAAGTTACGGGACCC 8233
QY 4240 ATTCAACCGGTCCAGCACGCGCGGGGTAAACCGACTTGTCTGCCCGGAGAAATTATGAG 4299
Db 8232 ATTCAACCGGTCCAGCACGCGCGGGGTAAACCGACTTGTCTGCCCGGAGAAATTATGAG 8173
QY 4300 CATTTTGTGGTGTATGGGCCCCCAATGAATGAATGAGTCAAGTCAAACTTGACAGTCAAC 4359
Db 8172 CATTTTGTGGTGTATGGGCCCCCAATGAATGAATGAGTCAAGTCAAACTTGACAGTCAAC 8113
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Db 8112 AAATCGTTGGCGCGGTCCAGGGCGCAATTTTGGCAACAATGTGAGGCTCAGCAGACCT 8053
QY 4420 GCAGGATGCAAGCT 4434
Db 8052 GCAGGATGCAAGCT 8038

RESULT 15
A24783
LOCUS A24783 7566 bp DNA linear PAT 24-FEB-1995
DEFINITION plasmid pPS0212 replicable en E.coli.
ACCESSION A24783
VERSION A24783.1 GI:833505
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 7566)
AUTHORS
TITLE MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS
JOURNAL Patent: WO 9309218-A 23-13-MAY-1993;
FEATURES
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ORIGIN
Query Match 16.3%; Score 728.8; DB 6; Length 7566;
Best Local Similarity 99.7%; Pred. No. 5.4e-96;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3698 GTCTAGATCCCTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATTTGCTTT 3757
Db 3692 GTCTAGATCCCTGCTTTAATGAGATATCGAGACGCTATGATCGCATGATTTGCTTT 3751
QY 3758 CAATTCTGTGTGCGCTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGG 3817
Db 3752 CAATTCTGTGTGCGCTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGG 3811
QY 3818 GTTTCGGTTCATCTAATGAATATATCAACCGGTTACTATCGTATTTTATGAATAATTT 3877
Db 3812 GTTTCGGTTCATCTAATGAATATATCAACCGGTTACTATCGTATTTTATGAATAATTT 3871
QY 3878 CTCGGTTCAAATTTACTGATGTGACCTACTTATATGTAATTAATAAGAACAT 3937
Db 3872 CTCGGTTCAAATTTACTGATGTGACCTACTTATATGTAATTAATAAGAACAT 3931
QY 3938 ATATATTGCTGAATAGTTTATAGCGACATCTATGATAGCGCCACAATAACAACA 3997

3932	ATATATTGTGCTGAATAGTGTATTAGCGACATCTATGATAGAGCGCCACCAATATCAACA	3991
3998	ATTGCGTTTTATTATTACAAATCCAAATTTTAAATAAAGCGCGAAGCCGGTCAAACTAA	4057
3992	ATTGCGTTTTATTATTACAAATCCAAATTTTAAATAAAGCGCGAAGCCGGTCAAACTAA	4051
4058	AAGACTGATTACATAAAATCTTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA	4117
4052	AAGACTGATTACATAAAATCTTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA	4111
4118	CACACCGAGCGCGGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGCG	4177
4112	CACACCGAGCGCGGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCGCGCGGCGCG	4171
4178	CATGGGTGAGATTCTCTTGAAGTTTCAGTATTGGCGCTCCGGTCTACCGAAAGTTACGGGCA	4237
4172	CATGGGTGAGATTCTCTTGAAGTTTCAGTATTGGCGCTCCGGTCTACCGAAAGTTACGGGCA	4231
4238	CCATTCAACCCGGTCCAGCACGGCGGCGGGGTAAACCGACTTGTGTGCCCCGAGAAATTATGC	4297
4232	CCATTCAACCCGGTCCAGCACGGCGGCGGGGTAAACCGACTTGTGTGCCCCGAGAAATTATGC	4291
4298	AGCAATTTTTTTGGTGTATGTCGGGCCCCAAATGAAGTGCAGGTCAAACTTTGACAGTCAAG	4357
4292	AGCAATTTTTTTGGTGTATGTCGGGCCCCAAATGAAGTGCAGGTCAAACTTTGACAGTCAAG	4351
4358	ACAAATCGTTCGGGGGTCCAGGCGCAATTTTGGCGAACAATGTCGAGGCTCAGCAGGAC	4417
4352	ACAAATCGTTCGGGGGTCCAGGCGCAATTTTGGCGAACAATGTCGAGGCTCAGCAGGAC	4411
4418	CTGCAGGCATGC	4429
4412	CTGCAGGAATTC	4423

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Job time : 11161.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1031.31 Seconds
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Title: US-10-055-001b-24_COPY_13000_17476

Perfect score: 4477

Sequence: 1 ttctcattgtgagagacacg.....atagtgccacctaatactgc 4477

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
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- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4477	100.0	17476	6 ABQ82141	Abq82141 Acceptor
2	4406.6	98.4	17458	6 ABQ82142	Abq82142 Acceptor
3	4262	95.2	17681	6 ABQ82143	Abq82143 Acceptor
4	3234.8	72.3	18691	6 ABQ82130	Abq82130 Acceptor
5	1277.8	28.5	17458	6 ABQ82142	Abq82142 Acceptor
6	1273	28.4	17476	6 ABQ82141	Abq82141 Acceptor
7	1108.8	24.8	4470	3 AAC55521	Aac55521 Donor pla
8	1108.8	24.8	4470	7 ABZ58767	Abz58767 Destinati
9	1108.8	24.8	4892	8 ADA50329	Ada50329 Plasmid v
10	1108.8	24.8	4939	3 AAC55525	Aac55525 Donor pla
11	1108.8	24.8	5584	3 AAC55632	Aac55632 Donor pla
12	1108.8	24.6	4428	7 ABZ58766	Abz58766 Donor pla
13	1102.4	24.6	4428	7 ABZ58768	Abz58768 Destinati
14	1102.4	24.6	4627	7 ABZ58769	Abz58769 Destinati
15	1102.4	24.6	4627	7 ABZ58770	Abz58770 Destinati
16	1074.8	24.0	17681	6 ABQ82143	Abq82143 Acceptor
17	989.6	22.1	4165	3 AAC55524	Aac55524 Donor pla
18	947.8	21.2	4208	3 AAC55523	Aac55523 Donor pla
19	827	18.5	4204	3 AAC55522	Aac55522 Donor pla
20	823.8	18.4	5156	3 AAC55526	Aac55526 Donor pla
21	780	17.4	786	3 AAZ38603	Aaz38603 Flavaria
22	780	17.4	786	9 ADD44386	Add44386 Flavaria
23	747	16.7	7050	2 AAQ40419	Aaq40419 Sequence

24	728.8	16.3	7566	2	AaQ42160	AaQ42160 Plasmid p	
25	728.8	16.3	7639	2	AaQ42159	AaQ42159 Plasmid p	
26	713	15.9	4947	3	AaZ60627	AaZ60627 Nucleotid	
27	711.4	15.9	3435	8	AcC85049	AcC85049 Nucleotid	
c	28	710.2	15.9	7599	4	AaF25320	AaF25320 Nucleotid
29	709.8	15.9	5399	2	AaQ25706	AaQ25706 pDE108.3	
30	709.8	15.9	6555	2	AaQ53874	AaQ53874 Plasmid p	
31	709.8	15.9	14194	4	AaC66932	AaC66932 Plant sig	
c	32	707	15.8	24596	1	AaU50182	AaU50182 Complete
c	33	703.8	15.7	24593	1	AaU50226	AaU50226 Sequence
34	703	15.7	2867	7	AbZ68391	AbZ68391 Nucleotid	
c	35	617.6	13.8	18691	6	AbQ82130	AbQ82130 Acceptor
36	597	13.3	1846	6	AaQ44626	AaQ44626 Gateway t	
37	597	13.3	5148	6	AaQ27063	AaQ27063 Plasmid p	
c	38	597	13.3	5957	3	AaC55467	AaC55467 Destinati
c	39	597	13.3	5957	3	AaC55464	AaC55464 Destinati
c	40	597	13.3	6025	3	AaC55469	AaC55469 Destinati
c	41	597	13.3	6264	3	AaC55507	AaC55507 Destinati
c	42	597	13.3	6354	3	AaC55491	AaC55491 Destinati
c	43	597	13.3	6422	3	AaC55483	AaC55483 Destinati
c	44	597	13.3	6464	3	AaC55454	AaC55454 Destinati
c	45	597	13.3	6526	3	AaC55471	AaC55471 Destinati

ALIGNMENTS

RESULT 1

ABQ82141
ID ABQ82141 standard; DNA; 17476 BP.

XX
AC ABQ82141;

DT 11-DEC-2002 (first entry)

XX
DE Acceptor vector PHELLSGATE 8 nucleotide sequence SEQ ID NO:24.

XX
KW Chimeric nucleic acid construct; recombinational cloning; silencing;
KW Recombination site; double stranded RNA; plant; ds.

XX
OS Synthetic.

XX
PN WO200259294-A1.

XX
PD 01-AUG-2002.

XX
PF 24-JAN-2002; 2002WO-AU0000073.

XX
PR 26-JAN-2001; 2001US-0264067P.
PR 29-NOV-2001; 2001US-0333743P.

XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Wesley S, Waterhouse P, Helliwell C;

XX
XX WPI; 2002-682659/73.

XX
XX New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

XX
XX Claim 15; Page 74-83; 104pp; English.

XX
XX The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.

XX Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 100.0%; Score 4477; DB 6; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTATTGGAGACACGCTCGAGCAAGTTTCTACAAAAGCTGACGAGAAAGT 60
DB TTTCTATTGGAGACACGCTCGAGCAAGTTTCTACAAAAGCTGACGAGAAAGT 13059

QY 61 AAAATGATATAATATCAATATATTAATAATTAGATTGTCATAAAAAAGACATCAAT 120
DB AAAATGATATAATATCAATATATTAATAATTAGATTGTCATAAAAAAGACATCAAT 13119

QY 121 ACTGTAAACACACATATCCAGTCATGATGAATCACTATAGATGGTATAGTGACC 180
DB ACTGTAAACACACATATCCAGTCATGATGAATCACTATAGATGGTATAGTGACC 13179

QY 181 TGTAGTCGACGACGACGCTTCCAAATGTTCTTCCGGTGATGCTGCCAACTTAGTCGACGG 240
DB TGTAGTCGACGACGACGCTTCCAAATGTTCTTCCGGTGATGCTGCCAACTTAGTCGACGG 13239

QY 241 ACAGCCTTCCAAATGTTCTTCTCAACCGGAATCGTGTATCCAGCCTACTCGCTATTGTC 300
DB ACAGCCTTCCAAATGTTCTTCTCAACCGGAATCGTGTATCCAGCCTACTCGCTATTGTC 13299

QY 301 CTCATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGGAGCCTCTTTTGG 360
DB CTCATGCGGTATTAATCATATAAAGAAATTAAGAAAGAGGTGGAGCCTCTTTTGG 13359

QY 361 TGTGACAAAATAAACAATCTACCTATTTCATATACGCTAGTGTCAAGTCTGAAAAATCA 420
DB TGTGACAAAATAAACAATCTACCTATTTCATATACGCTAGTGTCAAGTCTGAAAAATCA 13419

QY 421 TGTGATCAAGAACAAATTTCAACCTCTTATATCTTTCTTTTACAGTCTGCGCTTCA 480
DB TGTGATCAAGAACAAATTTCAACCTCTTATATCTTTCTTTTACAGTCTGCGCTTCA 13479

QY 481 TCTGGATTTTCAGCCTCTATCTTCAACGCTGATAAGATTCTGTAAATTTCTACTGTA 540
DB TCTGGATTTTCAGCCTCTATCTTCAACGCTGATAAGATTCTGTAAATTTCTACTGTA 13539

QY 541 TCGACCTGACAGCTGGCTGTATAGGAGGCTGACATTTATTTCCCGCAAGACATCAG 600
DB TCGACCTGACAGCTGGCTGTATAGGAGGCTGACATTTATTTCCCGCAAGACATCAG 13599

QY 601 GTTAATGGGGTTTTGATGTCATTTTTCGGGTGGCTGGAGATCAGCCATTTCTCCCGAT 660
DB GTTAATGGGGTTTTGATGTCATTTTTCGGGTGGCTGGAGATCAGCCATTTCTCCCGAT 13659

QY 661 AACGGAGACCGGCACATCGGTCATCGGTCATCGGCGCAGCTTTTCATCCCGAT 720
DB AACGGAGACCGGCACATCGGTCATCGGTCATCGGCGCAGCTTTTCATCCCGAT 13719

QY 721 ATGCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACGACGACGTGCACTGCCAG 780
DB ATGCACACCGGGTAAAGTTTCAAGGAGACTTTTATCTGACGACGACGTGCACTGCCAG 13779

QY 781 GGGGATCACCATCCGTCGCGCGCGCGGTGTCAATAATATCACTCTGTACATCCCAACAG 840

DB 13780 GGGGATCACCATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTATATCCCAACAG 13839
QY 841 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTACAGTCCCTGT 900
DB 13840 ACGATAACGGCTCTCTCTTTTATAGTGTAAACCTTAACTGCAATTTACAGTCCCTGT 13899

QY 901 TCTCGTCAGCAAGAGACGCTTCATTTCAATAAACCGGGGACCTCAGCATCCCTTCCT 960
DB 13900 TCTCGTCAGCAAGAGACGCTTCATTTCAATAAACCGGGGACCTCAGCATCCCTTCCT 13959

QY 961 GATTTTCCGCTTTCCAGCGTTTCGGCAGCGACGACGCGGCTTCATTTCTGCATGTTGTC 1020
DB 13960 GATTTTCCGCTTTCCAGCGTTTCGGCAGCGACGACGCGGCTTCATTTCTGCATGTTGTC 14019

QY 1021 TTACAGACCGGAGATATTGACATCATATATGCTTTCGAGCACTGATAGTGTGCTGTC 1080
DB 14020 TTACAGACCGGAGATATTGACATCATATATGCTTTCGAGCACTGATAGTGTGCTGTC 14079

QY 1081 AACTGTCACTGATAGCTGCTTTATAGACACACTCTTTTTCGACATCTTCGGGTAGTG 1140
DB 14080 AACTGTCACTGATAGCTGCTTTATAGACACACTCTTTTTCGACATCTTCGGGTAGTG 14139

QY 1141 CCGATCAACGCTCTCATTTTCCGCAAAAGTTGGCCGAGGCTTCCGCTATCAACAGGAC 1200
DB 14140 CCGATCAACGCTCTCATTTTCCGCAAAAGTTGGCCGAGGCTTCCGCTATCAACAGGAC 14199

QY 1201 ACCAGGATTTTATTTATCTCGGAAGTGTCTTCCGTCACAGGTATTTATTCGGCGCAAG 1260
DB 14200 ACCAGGATTTTATTTATCTCGGAAGTGTCTTCCGTCACAGGTATTTATTCGGCGCAAG 14259

QY 1261 TGGCTCGGGTGATGCTGCCAACTTAGTCGACTACAGTCTCACTAATACCATCTAAGTAGT 1320
DB 14260 TGGCTCGGGTGATGCTGCCAACTTAGTCGACTACAGTCTCACTAATACCATCTAAGTAGT 14319

QY 1321 GATTCATAGTGACTGGATATGTTGTTTACAGTATTTGTTAGTCTGTTTTTATGCAA 1380
DB 14320 GATTCATAGTGACTGGATATGTTGTTTACAGTATTTGTTAGTCTGTTTTTATGCAA 14379

QY 1381 AATCTAATTTAATATTTATGATTTATATATTTTACGTTTCTCGTTCAGCTTCTTGTA 1440
DB 14380 AATCTAATTTAATATTTATGATTTATATATTTTACGTTTCTCGTTCAGCTTCTTGTA 14439

QY 1441 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTCTTTT 1500
DB 14440 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAAATAATTTCTTTT 14499

QY 1501 TCCTTTTAGTATAAATAGTTAAGTGTAAATAGTATGATTTATATATATATAGTTGT 1560
DB 14500 TCCTTTTAGTATAAATAGTTAAGTGTAAATAGTATGATTTATATATATATAGTTGT 14559

QY 1561 TATAATTTGAAAAATAATTTTATAAATAATATTTTACATAAACAACATAGTAATGTAA 1620
DB 14560 TATAATTTGAAAAATAATTTTATAAATAATATTTTACATAAACAACATAGTAATGTAA 14619

QY 1621 AAAAATATGACAGTGTGTGTAGAGAGAGATAAAAGTTCGAGAGTAAAGTATTTAT 1680
DB 14620 AAAAATATGACAGTGTGTGTAGAGAGAGATAAAAGTTCGAGAGTAAAGTATTTAT 14679

QY 1681 TTTTAAATGAATTTGATCGAACATGTAGATGATATCTAGCATTAATTTGTTTAAATC 1740
DB 14680 TTTTAAATGAATTTGATCGAACATGTAGATGATATCTAGCATTAATTTGTTTAAATC 14739

QY 1741 ATAATAGTAATTTCTAGCTGGTTTGTATGAATTTAAATATCAATGATAAAATCTATAGTAAA 1800
DB 14740 ATAATAGTAATTTCTAGCTGGTTTGTATGAATTTAAATATCAATGATAAAATCTATAGTAAA 14799

QY 1801 AATAAGATAAATAAATAAATAAATAATTTTATGATTAATAGTTTATTAATAATTA 1860
DB 14800 AATAAGATAAATAAATAAATAAATAATTTTATGATTAATAGTTTATTAATAATTA 14859

QY 1861 AATATCTATACATTTACTAAATATTTTATAGTTTAAAGTTTAAATATTTTGTAGAAAT 1920

Db 14860 AATATCTATACCACTTACTAATACTTTAGTTTAAAGTTAATAATATTTTGTAGAAAT 14919
Qy 1921 TCCAAATCTGCTGTGTAATTTATCAATAAACAATAATTAATAATAACAAGCTAAAGTAAACAAA 1980
Db 14920 TCCAAATCTGCTGTGTAATTTATCAATAAACAATAATTAATAATAACAAGCTAAAGTAAACAAA 14979
Qy 1981 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGCTAATAT 2040
Db 14980 TAATATCAAACTAATAGAAAACAGTAATCTAATGTAAACAAAACATAAATCTAATGCTAATAT 15039
Qy 2041 AACAAAGCGCAAGTCTATCAATTTATATAGTATATTTTCAATCAACATTTCTTATTAAT 2100
Db 15040 AACAAAGCGCAAGTCTATCAATTTATATAGTATATTTTCAATCAACATTTCTTATTAAT 15099
Qy 2101 TTCTAAATAAATCTGTGTAGTTTATTAATCTTAACTCTAAATGGATGACTATTAATTAAGTAA 2160
Db 15100 TTCTAAATAAATCTGTGTAGTTTATTAATCTTAACTCTAAATGGATGACTATTAATTAAGTAA 15159
Qy 2161 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTATTTGTGTTTATCATTTGAT 2220
Db 15160 TTAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTATTTGTGTTTATCATTTGAT 15219
Qy 2221 CTTCATTTGGATTTGATTTACAGTTGGGAAGCTGGGTTCCGAATCGATTAAGCTTGGATCCT 2280
Db 15220 CTTCATTTGGATTTGATTTACAGTTGGGAAGCTGGGTTCCGAATCGATTAAGCTTGGATCCT 15279
Qy 2281 CTAGACCACTTTGTACAAAGAAAGCTGAACGAAACGTAATAATGATATAAATATCAATAT 2340
Db 15280 CTAGACCACTTTGTACAAAGAAAGCTGAACGAAACGTAATAATGATATAAATATCAATAT 15339
Qy 2341 ATTAATTTAGATTTTGGCAATAAACAAGCTACATAATACCTGTAATAACAACATATCCA 2400
Db 15340 ATTAATTTAGATTTTGGCAATAAACAAGCTACATAATACCTGTAATAACAACATATCCA 15399
Qy 2401 GTCACTATGAATCAACTACTTAGATGGTATAGTGACCTGTAGTGCATTAAGTTGGCAGC 2460
Db 15400 GTCACTATGAATCAACTACTTAGATGGTATAGTGACCTGTAGTGCATTAAGTTGGCAGC 15459
Qy 2461 ATCACCCGACGACCTTGGCGGAAATAAATCCTGTGACGGAAGTCACTTCGCAAGATA 2520
Db 15460 ATCACCCGACGACCTTGGCGGAAATAAATCCTGTGACGGAAGTCACTTCGCAAGATA 15519
Qy 2521 AATAAATCCTGGTGCCCTGTGTATACCGGGAAGCCCTGGGCAACTTTTGGCGGAAAATG 2580
Db 15520 AATAAATCCTGGTGCCCTGTGTATACCGGGAAGCCCTGGGCAACTTTTGGCGGAAAATG 15579
Qy 2581 AGACGTTGATCGGATTTACAACTCTTATACCTTTCTCTTACAGTGGTTCGGCTTCATC 2640
Db 15580 AGACGTTGATCGGATTTACAACTCTTATACCTTTCTCTTACAGTGGTTCGGCTTCATC 15639
Qy 2641 TGGATTTTCAGCCTCTATACCTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATC 2700
Db 15640 TGGATTTTCAGCCTCTATACCTTACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATC 15699
Qy 2701 GACCTGCAAGCTGGCTGTGTATTAAGGAGCCTGACATTTATATCCCGAAGACATCAGGT 2760
Db 15700 GACCTGCAAGCTGGCTGTGTATTAAGGAGCCTGACATTTATATCCCGAAGACATCAGGT 15759
Qy 2761 TAAATGGCGTTTGTATGTCATTTTGGCGGTGGCTGAGATCAGCCACTTCTCCCGATAA 2820
Db 15760 TAAATGGCGTTTGTATGTCATTTTGGCGGTGGCTGAGATCAGCCACTTCTCCCGATAA 15819
Qy 2821 CGGAGACCGGCACTGGCCATATCGGTGGTCAATGCGCCAGCTTTTCATCGCCGATAT 2880
Db 15820 CGGAGACCGGCACTGGCCATATCGGTGGTCAATGCGCCAGCTTTTCATCGCCGATAT 15879
Qy 2881 GCACCAACCGGTAAGTTTCAACGGGAGACTTTTATCTGACAGCAGCTGCACTGGCCAGGG 2940
Db 15880 GCACCAACCGGTAAGTTTCAACGGGAGACTTTTATCTGACAGCAGCTGCACTGGCCAGGG 15939
Qy 2941 GGAATCACCAATCCGTCGCGCGGCGTGTCAATTAATATCATCTGTGATCATCCACAAACAGAC 3000
Db 15940 GGAATCACCAATCCGTCGCGCGGCGTGTCAATTAATATCATCTGTGATCATCCACAAACAGAC 15999

Qy 3001 GATAACGGCTCTCTCTTTTATAGGTAAACCTTAAACTGCATTTACACAGTCCCTGTTT 3060
Db 16000 GATAACGGCTCTCTCTTTTATAGGTAAACCTTAAACTGCATTTACACAGTCCCTGTTT 16059
Qy 3061 TCGTCAGCAAAAAGAGCGGTTTCAATTTCAATAAAACGGGCGAGCCTCAGCCATCCCTTCTCTGA 3120
Db 16060 TCGTCAGCAAAAAGAGCGGTTTCAATTTCAATAAAACGGGCGAGCCTCAGCCATCCCTTCTCTGA 16119
Qy 3121 TTTTTCGGCTTTCCAGCGTTCCGGCAGCAGAGCGGCTTCAATCTGCATGGTTGTGCTT 3180
Db 16120 TTTTTCGGCTTTCCAGCGTTCCGGCAGCAGAGCGGCTTCAATCTGCATGGTTGTGCTT 16179
Qy 3181 ACCAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTCAA 3240
Db 16180 ACCAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGTGCTGTCAA 16239
Qy 3241 CTGTCACTGAATAACGCTGCTTCATAGCACACCTCTTTTGTGACATATCTCTGTCTTGTAT 3300
Db 16240 CTGTCACTGAATAACGCTGCTTCATAGCACACCTCTTTTGTGACATATCTCTGTCTTGTAT 16299
Qy 3301 GCAGATGATTTTCAGGACTATGACACTAGCTATATGAATAGGTAGATGTTTTATTTTGT 3360
Db 16300 GCAGATGATTTTCAGGACTATGACACTAGCTATATGAATAGGTAGATGTTTTATTTTGT 16359
Qy 3361 TCACACAAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCA 3420
Db 16360 TCACACAAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTAATACGGCA 16419
Qy 3421 TTGAGGCAATATAGCAGTAGCTGGATACGACGATCCGTTTGTGAGAGAACATTTGGAAG 3480
Db 16420 TTGAGGCAATATAGCAGTAGCTGGATACGACGATCCGTTTGTGAGAGAACATTTGGAAG 16479
Qy 3481 GCTGTCCGTGCACTAAGTTGGCAGCATCACCGAAGAACATTTGGAAGGCTGTCCGTCGA 3540
Db 16480 GCTGTCCGTGCACTAAGTTGGCAGCATCACCGAAGAACATTTGGAAGGCTGTCCGTCGA 16539
Qy 3541 CTACAGGTCACATAATACCTCTAAGTAGTTGATTCATAGTACCTGGATATGTTGTGTTTT 3600
Db 16540 CTACAGGTCACATAATACCTCTAAGTAGTTGATTCATAGTACCTGGATATGTTGTGTTTT 16599
Qy 3601 ACAGTATATGATGTCTGTGTTTTTATGCAAAATCAATCTAATTAATATATGATTTATATC 3660
Db 16600 ACAGTATATGATGTCTGTGTTTTTATGCAAAATCAATCTAATTAATATATGATTTATATC 16659
Qy 3661 ATTTTACGTTTCTCGTTCCAGCTTTTTTGTACAACTTGTCTAGAGTCCCTGCTTAAATGAG 3720
Db 16660 ATTTTACGTTTCTCGTTCCAGCTTTTTTGTACAACTTGTCTAGAGTCCCTGCTTAAATGAG 16719
Qy 3721 ATATGCGAGACGCTATGATCGCATGATTTTGTCTTTCAATTTCTGTGTGCAAGTTGTAA 3780
Db 16720 ATATGCGAGACGCTATGATCGCATGATTTTGTCTTTCAATTTCTGTGTGCAAGTTGTAA 16779
Qy 3781 AAAACCTGAGATGTGTAGCTCAGATCCTTACCGCGGTTTCCGTTCAATCTAATGATA 3840
Db 16780 AAAACCTGAGATGTGTAGCTCAGATCCTTACCGCGGTTTCCGTTCAATCTAATGATA 16839
Qy 3841 TATCACCGGTTACTATCGTATTTTATGAATAATTTCTCCGTTCAATTTACTGATTTGTA 3900
Db 16840 TATCACCGGTTACTATCGTATTTTATGAATAATTTCTCCGTTCAATTTACTGATTTGTA 16899
Qy 3901 CCTACTACTTATATGTAACAATTTAAATGAAAACAATATTTGTGCTGAATAGTTTAA 3960
Db 16900 CCTACTACTTATATGTAACAATTTAAATGAAAACAATATTTGTGCTGAATAGTTTAA 16959
Qy 3961 TAGCGACATCTATGATAGAGCGGCACAAATAACAACATTTCCGTTTATTTATTAACAATC 4020
Db 16960 TAGCGACATCTATGATAGAGCGGCACAAATAACAACATTTCCGTTTATTTATTAACAATC 17019
Qy 4021 CAATTTTAAAAAAGCGGCGAGAACCGGTCAAAACCTTAAAGAGCTGATTAATATAATCTTAT 4080
Db 17020 CAATTTTAAAAAAGCGGCGAGAACCGGTCAAAACCTTAAAGAGCTGATTAATATAATCTTAT 17079

QY 4081 TCAATTTTCAAAAGCCCGGAGGCTAGTACTACGACACACCGGCGGAACATAAA 4140
DB 17080 TCAATTTTCAAAAGCCCGGAGGCTAGTACTACGACACACCGGCGGAACATAAA 17139
QY 4141 CGTTCACTGAAGGGAACATCCGGTTCCTCCGCGCGCATGGGTGAGATTCCTTGAAGTT 4200
DB 17140 CGTTCACTGAAGGGAACATCCGGTTCCTCCGCGCGCATGGGTGAGATTCCTTGAAGTT 17199
QY 4201 GAGTATGGCGTCCGCTTACCGAAAGTTACGGGACCAATCAACCGGTCACGACGG 4260
DB 17200 GAGTATGGCGTCCGCTTACCGAAAGTTACGGGACCAATCAACCGGTCACGACGG 17259
QY 4261 CGGCGGGTAACCGACTTCCTCCGCGGAGAAATATGAGCAATTTTGGTGTATGGG 4320
DB 17260 CGGCGGGTAACCGACTTCCTCCGCGGAGAAATATGAGCAATTTTGGTGTATGGG 17319
QY 4321 CCCCAAATGAAGTCAGGTCACCAACCTTGACAGTACGACAAATCGTTGGCGGGTCCAGG 4380
DB 17320 CCCCAAATGAAGTCAGGTCACCAACCTTGACAGTACGACAAATCGTTGGCGGGTCCAGG 17379
QY 4381 GCGAATTTTGGACAAACATGTCAGGCTCAGGAGACCTGAGGATGCAAGCTAGCTTA 4440
DB 17380 GCGAATTTTGGACAAACATGTCAGGCTCAGGAGACCTGAGGATGCAAGCTAGCTTA 17439
QY 4441 CTAGTGATGCATATCTATAGTGTCACTTAAATCTGC 4477
DB 17440 CTAGTGATGCATATCTATAGTGTCACTTAAATCTGC 17476

RESULT 2
ABQ82142
ID ABQ82142 standard; DNA; 17458 BP.
XX ABQ82142;
AC ABQ82142;
XX
DT 11-DEC-2002 (first entry)
XX
XX Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25.
XX
XX Chimeric nucleic acid construct; recombinational cloning; silencing;
XW recombination site; double stranded RNA; plant; ds.
KW
XX
XX Synthetic.
XX
XX W0200259294-A1.
XX
XX
XX PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU000073.
XX
XX 26-JAN-2001; 2001US-0264067P.
XX
XX 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wesley S, Waterhouse P, Helliwell C;
XX
XX WPI; 2002-682669/73.
XX
XX New vectors comprising operably linked DNA fragments having an origin of
PT replication, a selectable marker and a chimeric DNA construct, useful for
PT silencing target nucleic acids and for producing large amounts of double-
PT stranded RNA.
XX
XX Claim 16; Page 83-93; 104pp; English.
XX
XX The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)
CC selectable marker region capable of being expressed in the recipient cell
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC region capable of being recognized by RNA polymerases of a eukaryotic
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and

CC fourth recombination sites; (iii) 3' transcription terminating and
CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 98.4%; Score 4406.6; DB 6; Length 17458;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4450; Conservative 0; Mismatches 9; Indels 18; Gaps 2;
QY 1 TTTCAATTTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAAGCTCAACGAGAAAGCT 60
DB 13000 TTTCAATTTGGAGAGACACGCTCGAGACAAGTTTGTACAAAAAAGCTCAACGAGAAAGCT 13059
QY 61 AAAATGATATAAATCAATATATTAATTAAGATTTTGCATAAAAAAGCTCAACATCAAT 120
DB 13060 AAAATGATATAAATCAATATATTAATTAAGATTTTGCATAAAAAAGCTCAACATCAAT 13119
QY 121 ACTGTAACCAACACATATCCAGTCACTATGAATCAACTACTAGATGGTATTAGTGACC 180
DB 13120 ACTGTAACCAACACATATCCAGTCACTATGAATCAACTACTAGATGGTATTAGTGACC 13179
QY 181 TGTAGTCACCGACAGACCTTCCAAATGTTCTCCGGTGTATGCTGCAACTAGTCGACCG 240
DB 13180 TGTAGTCACCGACAGACCTTCCAAATGTTCTCCGGTGTATGCTGCAACTAGTCGACCG 13239
QY 241 ACAGCTTCCAAATGTTCTTCTCAACGGAATCGTCGTATCCAGCTACTCGCTATTGTC 300
DB 13240 ACAGCTTCCAAATGTTCTTCTCAACGGAATCGTCGTATCCAGCTACTCGCTATTGTC 13299
QY 301 CTCATATGCGGTATTAAATCATATAAAGAAATAAGAAAAAGGTCGAGACCTCTTTTGTG 360
DB 13300 CTCATATGCGGTATTAAATCATATAAAGAAATAAGAAAAAGGTCGAGACCTCTTTTGTG 13359
QY 361 TGTGCAAAATAAABACATCTACCTATTATATATAGTGTATAGTCTGAAATATCA 420
DB 13360 TGTGCAAAATAAABACATCTACCTATTATATATAGTGTATAGTCTGAAATATCA 13419
QY 421 TCTGCATCAAGAACAAATTTCAAACTCTTTATATTTCTTTTACAGTCTGTTCCGCTTCA 480
DB 13420 TCTGCATCAAGAACAAATTTCAAACTCTTTATATTTCTTTTACAGTCTGTTCCGCTTCA 13479
QY 481 TCTGGAATTTGAGCTCTATATCTTACTTAACGTGATAAGTTTCTGTAATTTCTACTGTA 540
DB 13480 TCTGGAATTTGAGCTCTATATCTTACTTAACGTGATAAGTTTCTGTAATTTCTACTGTA 13539
QY 541 TCGACCTGACAGTCTGCTGTATAGGAGCTGACATTTATATTTCCCGCAACATCAAG 600
DB 13540 TCGACCTGACAGTCTGCTGTATAGGAGCTGACATTTATATTTCCCGCAACATCAAG 13599
QY 601 GTTAATGGCGTTTGTATGTCATTTTTCGCGGTGGTGTAGATCAGCACTTTCTCCCGAT 660
DB 13600 GTTAATGGCGTTTGTATGTCATTTTTCGCGGTGGTGTAGATCAGCACTTTCTCCCGAT 13659
QY 661 AACGGAGACCGGACACATCGGTCATATCGGTGTATCATGCGCCAGCTTTATCCCGAT 720
DB 13660 AACGGAGACCGGACACATCGGTCATATCGGTGTATCATGCGCCAGCTTTATCCCGAT 13719
QY 721 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 780
DB 13720 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 13779

QY 781 GGGGATCAACATCCGTCGCCCGGGCGGTGTCAATAATATACATCTGTGTACATCCAGAAACAG 840
DB 13780 GGGGATCAACATCCGTCGCCCGGGCGGTGTCAATAATATACATCTGTGTACATCCAGAAACAG 13839
QY 841 ACGATAAGCGGTCTCTCTTTTATAGGTGTAAACCTTAAACCTGCAATTCACCAAGTCCCTGT 900
DB 13840 ACGATAAGCGGTCTCTCTTTTATAGGTGTAAACCTTAAACCTGCAATTCACCAAGTCCCTGT 13899
QY 901 TCTGTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCT 960
DB 13900 TCTGTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTCT 13959
QY 961 GATTTTCGGCTTTCAGCGGTCGGGACGAGAGCGGCTTCATTTCTGCATGGTGTGTC 1020
DB 13960 GATTTTCGGCTTTCAGCGGTCGGGACGAGAGCGGCTTCATTTCTGCATGGTGTGTC 14019
QY 1021 TTACAGACCGGAGATATTTGACATCATATATATGCTTTGAGCAACTGATAGCTGTCGCTGTC 1080
DB 14020 TTACAGACCGGAGATATTTGACATCATATATGCTTTGAGCAACTGATAGCTGTCGCTGTC 14079
QY 1081 AACTGTCACTGTAAATACGCTGCTTATAGCAACACCTCTTTTGTGACATCTCGGGTAGTG 1140
DB 14080 AACTGTCACTGTAAATACGCTGCTTATAGCAACACCTCTTTTGTGACATCTCGGGTAGTG 14139
QY 1141 CCGATCAAGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGAC 1200
DB 14140 CCGATCAAGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGAC 14199
QY 1201 ACCAGGATTTATTTCTGCGAAGTGATCTTCGGTCAAGGTATTTATTCGGCGCAAG 1260
DB 14200 ACCAGGATTTATTTCTGCGAAGTGATCTTCGGTCAAGGTATTTATTCGGCGCAAG 14259
QY 1261 TCGGTCGGGTGATGTCGCCAATCTAGTCACACAGCTTACATTAACATCAAGTAGTT 1320
DB 14260 TCGGTCGGGTGATGTCGCCAATCTAGTCACACAGCTTACATTAACATCAAGTAGTT 14319
QY 1321 GATTCATAGTACTGGATATGTTGTGTTTACAGTATTTATGATGCTGTTTTATGCA 1380
DB 14320 GATTCATAGTACTGGATATGTTGTGTTTACAGTATTTATGATGCTGTTTTATGCA 14379
QY 1381 AATCTAATTTAATATATGATATTTATATATTTATATATTTATATATTTATGCA 1440
DB 14380 AATCTAATTTAATATATGATATTTATATATTTATATATTTATATATTTATGCA 14439
QY 1441 CAAAGTGCTCGAGGAATTCGGTACCCAGCTTGGTAAAGGAATTAATTTCTTTT 1500
DB 14440 CAAAGTGCTCGAGGAATTCGGTACCCAGCTTGGTAAAGGAATTAATTTCTTTT 14495
QY 1501 TCCTTTTAGTATAAAATAGTAAAGTGATGTTAATTAGTATGATTAATAATAATAGTTGT 1560
DB 14496 TCCTTTTAGTATAAAATAGTAAAGTGATGTTAATTAGTATGATTAATAATAATAGTTGT 14555
QY 1561 TATAATGTGAAAAATATATTAATAATATATTTGTTTACATTAACACATAGTAATGTAA 1620
DB 14556 TATAATGTGAAAAATATATTAATAATATATTTGTTTACATTAACACATAGTAATGTAA 14615
QY 1621 AAAAATATGACAGTATGTTAAGACGAAGAAGATAAAAGTTGAGAGTAAGTATATAT 1680
DB 14616 AAAAATATGACAGTATGTTAAGACGAAGAAGATAAAAGTTGAGAGTAAGTATATAT 14675
QY 1681 TTTTAAATGAAATTTGATCGAACATGTAGATGATATCTAGCATTAATTTGTTTTAATC 1740
DB 14676 TTTTAAATGAAATTTGATCGAACATGTAGATGATATCTAGCATTAATTTGTTTTAATC 14735
QY 1741 ATAAATAGTAATTTAGCTGGTTGATGCAATTAATATATCAATGATATAAATACTAGTAA 1800
DB 14736 ATAAATAGTAATTTAGCTGGTTGATGCAATTAATATCAATGATATAAATACTAGTAA 14795
QY 1801 AATAAGAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1860
DB 14796 AATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 14855

QY 1861 AATATCTATACATTTACTAATAATTTTAGTTTAAAAAGTTAAATAATTTTGTAGAAAT 1920
DB 14856 AATATCTATACATTTACTAATAATTTTAGTTTAAAAAGTTAAATAATTTTGTAGAAAT 14915
QY 1921 TCCAAATCTGCTGTAAATTTTATCAATAAACAATAATTTAAATTAACAGCTAAAGTAACAAA 1980
DB 14916 TCCAAATCTGCTGTAAATTTTATCAATAAACAATAATTTAAATTAACAGCTAAAGTAACAAA 14975
QY 1981 TAATATCAAACTAATATAGAAACAGTAATCTAATGTAAACAAAATAATCTAATGCTAAAT 2040
DB 14976 TAATATCAAACTAATATAGAAACAGTAATCTAATGTAAACAAAATAATCTAATGCTAAAT 15035
QY 2041 AACAAAGCGCAAGATCTATCAATTTTATATAGTATTTTCAATCAACATTTCTTATTAAT 2100
DB 15036 AACAAAGCGCAAGATCTATCAATTTTATATAGTATTTTCAATCAACATTTCTTATTAAT 15095
QY 2101 TTTCAAAATTAATCTGTAGTTTATTAACCTTCTAAATGGATGACTATTAATTAATGA 2160
DB 15096 TTTCAAAATTAATCTGTAGTTTATTAACCTTCTAAATGGATGACTATTAATTAATGA 15155
QY 2161 TTAGTCGAACATGATTAACAAAGGTAAACATGATAGATCATGTCTTGTGTTTATCAATGAT 2220
DB 15156 TTAGTCGAACATGATTAACAAAGGTAAACATGATAGATCATGTCTTGTGTTTATCAATGAT 15215
QY 2221 CTTTACATTTGGATTTACAGTTGGGAAGCTGGGTTGAAAATCGATAGCTTGGATCTCT 2280
DB 15216 CTTTACATTTGGATTTGATTTACAGTTACTTACCTT-----TAAGCTTGGATCTCT 15261
QY 2281 CTAGACCACTTTGTACAAAGAACCTGACGAGAACGTAABATGATATAAATATCAATAT 2340
DB 15262 CTAGACCACTTTGTACAAAGAACCTGACGAGAACGTAABATGATATAAATATCAATAT 15321
QY 2341 ATTAAATTTAGATTTTGCAATAAAAAACAGACTACATAATCTGTAAACACACATATCCA 2400
DB 15322 ATTAAATTTAGATTTTGCAATAAAAAACAGACTACATAATCTGTAAACACATATCCA 15381
QY 2401 GTCACTATGAATCAACTAGTAGTGTATTTAGTGACCTGTAGTGTGCTTGGCAGC 2460
DB 15382 GTCACTATGAATCAACTAGTAGTGTATTTAGTGACCTGTAGTGTGCTTGGCAGC 15441
QY 2461 ATCCCGGACGACCTTTGCGCGAATAAATACCTGTGCGGAAGATCACTTCGCGAAGATA 2520
DB 15442 ATCCCGGACGACCTTTGCGCGAATAAATACCTGTGCGGAAGATCACTTCGCGAAGATA 15501
QY 2521 AATAAATCTGCTGCTCCCTGTTGATACCGGGAAGCCCTGGGCAACTTTTGGCGAAAAATG 2580
DB 15502 AATAAATCTGCTGCTCCCTGTTGATACCGGGAAGCCCTGGGCAACTTTTGGCGAAAAATG 15561
QY 2581 AGAGTGTGATCGGATTTCAAACTCTTATCTTTCTTCAAGTCTGCTTGGCTTCAATC 2640
DB 15562 AGAGTGTGATCGGATTTCAAACTCTTATCTTTCTTCAAGTCTGCTTGGCTTCAATC 15621
QY 2641 TCGATTTTTCAGGCTCTATACCTTACTTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATC 2700
DB 15622 TCGATTTTTCAGGCTCTATACCTTACTTAAACGCTGATAAAGTTTCTGTAAATTTCTACTGTATC 15681
QY 2701 GACCTGACAGCTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAGAACATCAGGT 2760
DB 15682 GACCTGACAGCTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAGAACATCAGGT 15741
QY 2761 TAAATGGCGTTTGTGATGCTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAA 2820
DB 15742 TAAATGGCGTTTGTGATGCTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAA 15801
QY 2821 CGGAGACCGGACACCTGGGCATATCGGTGGTCTATCATGCGCCAGCTTTTCTATCCCGATAT 2880
DB 15802 CGGAGACCGGACACCTGGGCATATCGGTGGTCTATCATGCGCCAGCTTTTCTATCCCGATAT 15861
QY 2881 GCACCAACCGGTAAGTTTCAACGGAGACTTTTATCTGACAGCAGACGTCGACCTGGCCAGG 2940
DB 15862 GCACCAACCGGTAAGTTTCAACGGAGACTTTTATCTGACAGCAGACGTCGACCTGGCCAGG 15921
QY 2941 GGATCACCATCCGTCGCCCGGGCGGTCTCAATTAATATCACTCTGTATATCCACAAAACAGAC 3000

Db 15922 GGATCACCATCGTCGCGCGCGGTCAATTAATATCACTCTGTATACATCCAAACAGAC 15981
QY 3001 GATAACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTCACAGTCCCTGTC 3060
Db 15982 GATACGGCTCTCTCTTTTATAGGTGTAACCTTAAACTGCAATTCACAGTCCCTGTC 16041
QY 3061 TCGTCAGGAAAGAGCGGTTCAATTTCAATTAACCGGGGAGCTCAGCCATCCCTTCCTGA 3120
Db 16042 TCGTCAGGAAAGAGCGGTTCAATTTCAATTAACCGGGGAGCTCAGCCATCCCTTCCTGA 16101
QY 3121 TTTTCGGCTTTCCAGGTTTCGACGACGACGAGGCTTCAATTCGATGCTGCTGCT 3180
Db 16102 TTTTCGGCTTTCCAGGTTTCGACGACGACGAGGCTTCAATTCGATGCTGCTGCT 16161
QY 3181 ACCAGACCGGAGATATTGACATCATATATGCTTTCAGCAACTGATAGCTGCTGCTGCT 3240
Db 16162 ACCAGACCGGAGATATTGACATCATATATGCTTTCAGCAACTGATAGCTGCTGCTGCT 16221
QY 3241 CTGTACTGTATATGCTGCTTCATAGACACACTCTTTTTCATACACTCTGCTTCTGAT 3300
Db 16222 CTGTACTGTATATGCTGCTTCATAGACACACTCTTTTTCATACACTCTGCTTCTGAT 16281
QY 3301 GCAGATGATTTTCAGGACTATGACACTAGCTATATGATAGTATGATAGTATGAT 3360
Db 16282 GCAGATGATTTTCAGGACTATGACACTAGCTATATGATAGTATGATAGTATGAT 16341
QY 3361 TCACACAAAAGAGGCTGCGACCTCTTTTCTTATCTTTTATGATTTAATACGGCA 3420
Db 16342 TCACACAAAAGAGGCTGCGACCTCTTTTCTTATCTTTTATGATTTAATACGGCA 16401
QY 3421 TTGAGACATAGCGAGTGGCTGGATACGAGATTCGGTTTCAGAGAACATTTGGAG 3480
Db 16402 TTGAGACATAGCGAGTGGCTGGATACGAGATTCGGTTTCAGAGAACATTTGGAG 16461
QY 3481 GCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAGAACATTTGGAGGCTGCTGCTGCA 3540
Db 16462 GCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAGAACATTTGGAGGCTGCTGCTGCA 16521
QY 3541 CTACAGGTCACTAATACATTAAGTATGATGATGATGATGATGATGATGATGATGAT 3600
Db 16522 CTACAGGTCACTAATACATTAAGTATGATGATGATGATGATGATGATGATGATGAT 16581
QY 3601 ACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTAATATGATGATGATGATGAT 3660
Db 16582 ACAGTATATGATGCTGTTTTTATGCAAAATCTAATTTAATATGATGATGATGATGAT 16641
QY 3661 ATTTTACGTTTCGTTTCAGCTTTTGTACAAACTTGTCTAGAGTCCCTGCTTAAAGAG 3720
Db 16642 ATTTTACGTTTCGTTTCAGCTTTTGTACAAACTTGTCTAGAGTCCCTGCTTAAAGAG 16701
QY 3721 ATATGCGAGCGCTATGATCGCATGATATTCCTTCAATTCGTTGTCAGGTTGTA 3780
Db 16702 ATATGCGAGCGCTATGATCGCATGATATTCCTTCAATTCGTTGTCAGGTTGTA 16761
QY 3781 AAAACCTGAGCATGTAGTCTAGATCCCTTACCGCGGTTTCGGTTCAATTTAATGAATA 3840
Db 16762 AAAACCTGAGCATGTAGTCTAGATCCCTTACCGCGGTTTCGGTTCAATTTAATGAATA 16821
QY 3841 TATCACCGGTTATGCTGATTTTATGATTAATATATCTCCGTTCAATTTACTGATGTA 3900
Db 16822 TATCACCGGTTATGCTGATTTTATGATTAATATATCTCCGTTCAATTTACTGATGTA 16881
QY 3901 CCTTACTACTTATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3960
Db 16882 CCTTACTACTTATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 16941
QY 3961 TAGCGCATCTATGATAGCGCCACAAATACAAATTCGGTTTATTTATTTACAAATC 4020
Db 16942 TAGCGCATCTATGATAGCGCCACAAATACAAATTCGGTTTATTTATTTACAAATC 17001
QY 4021 CAATTTTAAAGAGCGGAGACCGGTCAACCTTAAAGACTGATTTACATTAATCTTAT 4080

Db 17002 CAATTTTAAAGAGCGGAGAACCGGTCAAAACCTTAAAGACTGATTACATATAATCTTAT 17061
QY 4081 TCAAAATTTCAAAAGCGCCGAGGCTAGTATCTAGACACACCGAGCGGCGAACTAATAA 4140
Db 17062 TCAAAATTTCAAAAGCGCCGAGGCTAGTATCTAGACACACCGAGCGGCGAACTAATAA 17121
QY 4141 CGTTCACTGAAGGAACTCCGGTTCCCGCGGCGCGCATGGGTGAGATTCCTTGAAGTT 4200
Db 17122 CGTTCACTGAAGGAACTCCGGTTCCCGCGGCGCGCATGGGTGAGATTCCTTGAAGTT 17181
QY 4201 GAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGCACTTCAACCCGCTCCAGCAGG 4260
Db 17182 GAGTATTTGGCGCTCCGCTCTACCGAAAGTTACGGGCACTTCAACCCGCTCCAGCAGG 17241
QY 4261 CGGCGGGTAACCGACATTCGCTGCGCGGAGATTTATGAGCATTTTGTGTATGTGG 4320
Db 17242 CGGCGGGTAACCGACATTCGCTGCGCGGAGATTTATGAGCATTTTGTGTATGTGG 17301
QY 4321 CCCCAATTAAGTGCAGGTCAAACTTGCACAGTACGACAAATCGTTGGGCGGTCACAGG 4380
Db 17302 CCCCAATTAAGTGCAGGTCAAACTTGCACAGTACGACAAATCGTTGGGCGGTCACAGG 17361
QY 4381 GCGAATTTTGGCAACAAATGTCGAGGCTCAGCAGACCTGCGAGCATGCAAGCTAGCTTA 4440
Db 17362 GCGAATTTTGGCAACAAATGTCGAGGCTCAGCAGACCTGCGAGCATGCAAGCTAGCTTA 17421
QY 4441 CTAGTGTAGCATATTTCTATAGTGTCACTAAATCTGC 4477
Db 17422 CTAGTGTAGCATATTTCTATAGTGTCACTAAATCTGC 17458

RESULT 3

ABQ82143
ID ABQ82143 standard; DNA; 17681 BP.

XX ABQ82143;

XX AC

XX DT

XX 11-DEC-2002 (first entry)

XX Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.

XX Chimeric nucleic acid construct; recombinational cloning; silencing;

XX recombination site; double stranded RNA; plant; ds.

XX Synthetic.

XX WO200259294-A1.

XX PD

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-AU000073.

XX 26-JAN-2001; 2001US-0264067P.

XX 29-NOV-2001; 2001US-0333743P.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Wesley S, Waterhouse P, Helliwell C;

XX WPI; 2002-682669/73.

XX New vectors comprising operably linked DNA fragments having an origin of

XX replication, a selectable marker and a chimeric DNA construct, useful for

XX silencing target nucleic acids and for producing large amounts of double-

XX stranded RNA.

XX Claim 17; Page 93-102; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked

XX DNA fragments having: (a) origin of replication allowing replication in a

XX recipient cell, preferably in bacteria such as Escherichia coli; (b)

XX selectable marker region capable of being expressed in the recipient cell

XX ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter

15760 ATAGTAATCTAGCTGGTTGATGAATTAATATCAATGATAAATACTATAGTAAATAAT 15819
1804 AAGATAAATAAATAAATAAATAATTTTTTANGATAATAGTTTATTAATAATAAAT 1863
15820 AAGAATAAATAAATAAATAAATAATTTTTTANGATAATAGTTTATTAATAATAAAT 15879
1864 ATCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1923
15880 ATCTATACCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15939
1924 AATCTGCTGTAAATTAATCAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1983
15940 AATCTGCTGTAAATTAATCAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15999
1984 ATCTAAACATAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGTAAATTAAC 2043
16000 TATCAAACTTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGTAAATTAAC 16059
2044 AAGCGCAGATCTATCAATTTATATAGTATTAATTTCAATCAACATCTTATTAATTTTC 2103
16060 AAGCGCAGATCTATCAATTTATATAGTATTAATTTCAATCAACATCTTATTAATTTTC 16119
2104 TAAATAATACTTGTAGTTTTTAACTTCTAATGGAATGACTATTAATAATAAATAAATAA 2163
16120 TAAATAATACTTGTAGTTTTTAACTTCTAATGGAATGACTATTAATAATAAATAAATAA 16179
2164 GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTTATCATTTGATCTT 2223
16180 GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTTATCATTTGATCTT 16239
2224 ACATTTGGATTCATTAACAGTTCGGAGCTGGGTTCGAAATCGATAAGCTTGGATCTCTTA 2283
16240 ACATTTGGATTCATTAACAGTTCGGAGTTCGGGTTCGAAATCGATAAGCTTGGATCTCTTA 16299
2284 GA----- 2285
16300 GAGAGCTGAGCTGGATGGCAATAATGATTTATTTGACTGATAGTGACCTGTTGCTT 16359
2286 -----CCACTTTGTACAAGAAAGCTGAACG 2310
16360 GCAACAAATGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAGAAAAGCTGAACG 16419
2311 AGAAACGTAAATGATATAAATAATCAATATATTAATAATAGATTTTGCATAAATAAACAAGAC 2370
16420 AGAAACGTAAATGATATAAATAATCAATATATTAATAATAGATTTTGCATAAATAAACAAGAC 16479
2371 TACATAAATACTGTAAACACACATATCCAGTCACTATGAATCAACTCTTAGATGGTAT 2430
16480 TACATAAATACTGTAAACACACATATCCAGTCACTATGAATCAACTCTTAGATGGTAT 16539
2431 TAGTGACCTGTAGTCGACTAAGTTGGCAGCATCAACCGGAGCACTTTGCGCGAATATAT 2490
16540 TAGTGACCTGTAGTCGACTAAGTTGGCAGCATCAACCGGAGCACTTTGCGCGAATATAT 16599
2491 ACCGTGACGGAGATCACTTCGAGATAAATAAATAAATAAATAAATAAATAAATAAATAA 2550
16600 ACCGTGACGGAGATCACTTCGAGATAAATAAATAAATAAATAAATAAATAAATAAATAA 16659
2551 GAAGCCCTGGGCCAACTTTTGGCGGAAAATGAGACGTTGATTCGG-----ATTTCCACAA 2602
16660 GAAGCCCTGGGCCAACTTTTGGCGGAAAATGAGACGTTGATTCGGCACTACCCCAATTTCCACAA 16719
2603 CTCTTATACCTTTCTCTTACAAGTTCGTTGCGCTTCACTCGGATTTTTCAGCTCTATACCTT 2662
16720 CTCTTATACCTTTCTCTTACAAGTTCGTTGCGCTTCACTCGGATTTTTCAGCTCTATACCTT 16779
2663 ACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATPCGACCTGCAGACTGGCTGTGTAT 2722
16780 ACTAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATPCGACCTGCAGACTGGCTGTGTAT 16839
2723 AAGGAGCCTGACATTTATATATCCCCAGAACATCAGGTTAATGGCGTTTGTATGATTCATT 2782

16840 AAGGAGCCTGACATTTATATATCCAGAACATCAGGTTAATGCGTTTGTGATGTCATT 16899
2783 TTCCGCGTGGCTGATCAGACCACTTTCTCCCGATAACCGAGACCGCACACTGGCCCAT 2842
16900 TTCCGCGTGGCTGATCAGACCACTTTCTCCCGATAACCGAGACCGCACACTGGCCCAT 16959
2843 ATCCGTGGTCACTATGCGCCAGCTTTTCATCCCGGATATGACCAACCGGCTAAAGTTTCAG 2902
16960 ATCCGTGGTCACTATGCGCCAGCTTTTCATCCCGGATATGACCAACCGGCTAAAGTTTCAG 17019
2903 GGAGACTTTTATCTGACAGCAGCTGTCATCCGCGAGGGGATCAACATCCGCTGCGCCCGGG 2962
17020 GGAGACTTTTATCTGACAGCAGCTGTCATCCGCGAGGGGATCAACATCCGCTGCGCCCGGG 17079
2963 CGTGTCAATATATCACTCTCTACATCCACAAAACAGAGATAACGGCTCTCTCTTTTATA 3022
17080 CGTGTCAATATATCACTCTCTACATCCACAAAACAGAGATAACGGCTCTCTCTTTTATA 17139
3023 GGTGTAAACCTTTAAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 3082
17140 GGTGTAAACCTTTAAACTGCAATTTCCACAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCA 17199
3083 TTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCG 3142
17200 TTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGCGTTCCG 17259
3143 CACGACAGCAGCGGCTTTCAATCTGATGTTGTTGCTTACAGACCGGAGATATTGACAT 3202
17260 CACGACAGCAGCGGCTTTCAATCTGATGTTGTTGCTTACAGACCGGAGATATTGACAT 17319
3203 CATATATCCCTTTGAGCAACTGATAGCTGCTGCTGCTCAACTGTCACTGTAATAACGCTGCT 3262
17320 CATATATCCCTTTGAGCAACTGATAGCTGCTGCTGCTCAACTGTCACTGTAATAACGCTGCT 17379
3263 CATAGCACACCTCTTTTGGACATCTCTGTTCTGATGTCAGATGATTTTCAGHACTAG 3322
17380 CATAGCACACCTCTTTTGGACATCTCTGTTCTGATGTCAGATGATTTTCAGHACTAG 17439
3323 ACACATAGCGTATATCAATAGGTAGATGTTTATTTTGTTCACACAAAAGAGGCTCGCA 3382
17440 ACACATAGCGTATATCAATAGGTAGATGTTTATTTTGTTCACACAAAAGAGGCTCGCA 17499
3383 CCTCTTTTCTTATTTCTTTTATGATTTAAATACGGCAATGAGGCAATAGCGAGTAGCG 3442
17500 CCTCTTTTCTTATTTCTTTTATGATTTAAATACGGCAATGAGGCAATAGCGAGTAGCG 17559
3443 TGGATACGACGATTCGCTTTGAGAGACATTTGGAAGCTGTCGGTCGACATAGTTGCG 3502
17560 TGGATACGACGATTCGCTTTGAGAGACATTTGGAAGCTGTCGGTCGACATAGTTGCG 17619
3503 AGCATCACCGCAAGAACATTTGGAAGCTGTCGGTCGACATAGTTGCAATACCATCT 3562
17620 AGCATCACCGCAAGAACATTTGGAAGCTGTCGGTCGACATAGTTGCAATACCATCT 17679
3563 AAGTAGTTGATTCATAGTACGATGATATGTTGTTTACAGTATATAGTACTGTTT 3622
17680 AAGTAGTTGATTCATAGTACGATGATATGTTGTTTACAGTATATAGTACTGTTT 17739
3623 TTATCGAAATCTAATTTAATATATATGATTTATATATATATATATATATATATATATAT 3682
17740 TTATCGAAATCTAATTTAATATATATGATTTATATATATATATATATATATATATATAT 17799
3683 TTTTGTACAAACTTG----- 3698
17800 TTTTGTACAAAGTTGGCATTAATAAAGCATTGCTCATCAATTTGTTGCAACGAACAG 17859
3699 -----TCTAGAG 3705
17860 GTCACATATCAGTCAAAAATAAATAATCAATTTTGGGCGCCGAGATCCATGCTAGCTCTAGAG 17919
3706 TCCTGCTTTAATGAGATATGCGAGCGCTATGATGCGATGATATTGCTTTCAATTCG 3765
17920 TCCTGCTTTAATGAGATATGCGAGCGCTATGATGCGATGATATTGCTTTCAATTCG 17979

Dd 16266 ATGTCAAAAGAGGTGTCCTATGAA--GCAGCGTATTACAGTGACAGTTCGACAGCGACA 16210
Qy 501 ACTTACTAAACGTGATAAAGTTTCGTAAATTTCTACTGTATCGACCTCGACAGCTGGCTGT 560
Dd 16209 GCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGTGTAAGCACAAACAT 16150
Qy 561 GTATAAGGAGGCTCAGCATTTATATTCGCCAGACATCAGGTTAATGGCGTTTGTGATG 620
Dd 16149 GCAGAAATGAAGCCCGTGTCTCGCTGCC--GAACGCTGGAAGCGGAAATCAGGAAG 16093
Qy 621 CATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGATTAACGGAGACCGGCACACTGG 680
Dd 16092 GATGCTGAGGTGCGCCCGGTTTATTGAAATGAACGGCTCTTTTGTGACGGAACAGGG- 16034
Qy 681 CCAATATCGGTGTCATCATGCGCCAGCTTTCATCCCGATATGACACCGCGGTAAGTT 740
Dd 16033 -----ACTGGTGAATGTCAGTTTAAAGTTTACACCTATAAAGAGAGAGCGGTTATCGTC 15979
Qy 741 CACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCCGTCGCC 800
Dd 15978 TGTGTTGTGATGTCAGAGTGATATTATGACACGCCCGGCGACGGATGGTGATCCCCC 15919
Qy 801 CGGGCGTGTCAATATATCCTCTGTACATCCAAAACAGACGATAACGCTCTCTCTTT 860
Dd 15918 TGGCCAGTGCACTGCTGTGTCAGATAAAGTCTCCCGTGAACTTTACCGCGTGGTGCA 15859
Qy 861 TATAGGTGTAACCTTAACTGCATTTACCC-----AGTCCCTGTTCTCGTCAGCAAAA 914
Dd 15858 TCGGGGATGAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTA 15799
Qy 915 GAGCGGTCATTTCAATTAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCCGGTTTC 974
Dd 15798 TCGGGGAAGAGTGGCTGATCTCAGCCACCGGGAATGACATCAAAACGCCATTAAC 15739
Qy 975 CAGCGTTC---GGCAGCGAGACGACGGGCTTCACTCTGATGGTGTGCTTACGACACCG 1031
Dd 15738 TGATGTTCTCGGGGAATATAAATGTCAAGGCTCCCTATACACAG-----CGAGTCTG 15688
Qy 1032 GAGATATTCACATCATATATGCTTCGAGCAACTGATAGTGTGCTGTCACACTGTCAC 1091
Dd 15687 CAGGTCGATACAGTAAATTAAGAACTTTATCAGGTTAGTAGTATAGAGGCTGAA 15628
Qy 1092 TAATAGCTGTCTTCAAGACACCTCTTTTGACATACCTTCGGGTAGTG---CGATCA 1147
Dd 15627 AATCCAGATGAAGCCGACGACTGTGAAGAGAAAGATATAAGAGTTGTGAATCCGATCA 15568
Qy 1148 AGTCTCATTTTCGCCAAAAGTTGGCCAGGCTTCCCGTATCAACAGGACACACGCA 1207
Dd 15567 ACGTCTCATTTTGGCCAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACGCA 15508
Qy 1208 TTTATTTATCTCGGAAGTATCTCCGTCAAGATATTATTTCGGCGCAAAAGTGGCTG 1267
Dd 15507 TTTATTTATCTCGGAAGTATCTCCGTCAAGATATTATTTCGGCGCAAAAGTGGCTG 15448
Qy 1268 GGTATGCTGCCAACTTAGTTCGATACAGTCACTAATACCATCTAAGTAGTGTATCAT 1327
Dd 15447 GGTATGCTGCCAACTTAGTTCGATACAGTCACTAATACCATCTAAGTAGTGTATCAT 15388
Qy 1328 AGTACGCTGATGTTGTTTACAGTATATGATGCTGTTTATTTATGCAAAATCTAA 1387
Dd 15387 AGTACGCTGATGTTGTTTACAGTATATGATGCTGTTTATTTATGCAAAATCTAA 15328
Qy 1388 TTTAATATATTGATATTATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTACAAAGTG 1447
Dd 15327 TTTAATATATTGATATTATATCATTTTACGTTTCTCGTTTCAGCTTCTTGTACAAAGTG 15268
Qy 1448 GTCTCGGAATTCGGTACCCGAGCTTGGTAAAGAAATATATTTCTTTTCTTTTCTTTT 1507
Dd 15267 GTCTAGAGGA--TCCAGCTTAAAGTAAAGTAACTG--TAATCAATCCAAATGTAAGATCA 15212
Qy 1508 AGTATAAATAGTTAGTGATGTTAATAGTATGATTTAATATATAGTTGTTAATTT 1567
Dd 15211 ATGATAACAAATGACATGATCTATCATGTTTACCTGTTTATTTCATGTTCCGACTAATTC 15152

Qy 1568 GTGAAAAATAAATTATATAATATCTTTACATAAAACACATAGTAATGTAAAAAATA 1627
Dd 15151 TTTAATTTAATAGTCAATCCATTTAGAGAGTTAATAAAACTCAAGTATTTATTAGAAATTA 15092
Qy 1628 TGACAAGTGATGTGTAGAGACGAAGATAAAGTTGAGAGTAAGTATATTTATTTTAAAT 1687
Dd 15091 ATAAGATGTTGATTTGAAATAATCTATATATAAATGATAGATCTTGGCGTTGTATAT 15032
Qy 1688 GAATTTGATCGAATGATGATATATCTAGCATTAATTTGTTTATCATATATAG 1747
Dd 15031 TAGCATTAGATTTATGTTTGTTCATTAGATTTACTGTTTCTATTAGTTTGTATTTTGG 14972
Qy 1748 TAAATTTAGCTGGTTTGTATGAATTAATAATCAATGATAAAATCTATAGTAAAAATBAGA 1807
Dd 14971 TTAATTTAGCTGGTTTATTAATTTTATTTCTTTTATTGATTAATAATCAAGCAGATTGGAATTT 14912
Qy 1808 ATAATAAATTAATAATATTTTATTAGTATTAATAGTATTAATAATAATATCT 1867
Dd 14911 CTAACAAAATATTTAATACTTTTAACTAAATAATTTAGTAATGGTATAGATATTTAAT 14852
Qy 1868 ATACCATTTACTAAATATTTTATGTTTAAAGTTAATAATATTTTGTAGAAATTTCCAATC 1927
Dd 14851 TATATAATAAATCTAATCAATAAATAATATTTTAAATTTATTATTCTTTATTTTAA 14792
Qy 1928 TGCTTGTAAATTTATCAATAAAACAAATAATTAATAACAAAGCTAAAGTAAACAATAATC 1987
Dd 14791 CTATAGTATTTTATCATTTGATATTTAATTTCAATCAACCCAGCTAGAAATTTACTATTATGAT 14732
Qy 1988 AAACATAATAGAAACAGTAACTCTAATGTAACAAACATAATCTAATGCTTAATAATAACAAG 2047
Dd 14731 AAAACAAATATTAATGCTAGTATATATCATCTTACATGTTTCAATCAATTTCAATTAACAA 14672
Qy 2048 CGCAGATCTCATTTTATATATAGTATTTTCAATCAACATCTCTAATAATTTCTAAA 2107
Dd 14671 TATCTTACTCTCACTTTTATCTTCTGCTTACACATCACATTTGTCATATTTTATTTTAC 14612
Qy 2108 TAATACTTTGTAGTTTATTAACCTCTAAATGGATGACTATTAATAATGAATTAGTCTG 2167
Dd 14611 ATTACTATGTTGTTTATGTAACAAATATATTATAAATTTATTTTTCACAAATTAACAA 14552
Qy 2168 AACATGAATAACAAGGTAAACATGATAGTATCATGTCATGTCGTTATCATTTGATTTACAT 2227
Dd 14551 CTATATTTATTAATTCATCTAATTAATTAACATCACCTTTAATCTTATTAACAAAGAAATA 14492
Qy 2228 TTGGATTCATTCACGTTGGGAAGCTGGGTTGAAATCGAATAGCTTGGATCTCTAGACC 2287
Dd 14491 AGAAATAATTTATTTCCCTTACAGTTGGTACCGAAT-----TCCTCGAGACC 14446
Qy 2288 ACTTTGTACAGAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATTAAT 2347
Dd 14445 ACTTTGTACAGAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATTAAT 14386
Qy 2348 TAGATTTTGCATAAABAAACAGACTATAAATCTGTAACACACATATCCAGTCACCTA 2407
Dd 14385 TAGATTTTGCATAAABAAACAGACTATAAATCTGTAACACACATATCCAGTCACCTA 14326
Qy 2408 TGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCCGACTAAGTTGCGACATCAACC 2467
Dd 14325 TGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCCGACTAAGTTGCGACATCAACC 14266
Qy 2468 GACGCACTTTGGCGGATTAATACTCTGTGACGGAAGATCACTTTCGAGAAATAAATAAT 2527
Dd 14265 GACGCACTTTGGCGGATTAATACTCTGTGACGGAAGATCACTTTCGAGAAATAAATAAT 14206
Qy 2528 CCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAATTTTGGCGAAATAGACAGCTT 2587
Dd 14205 CCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAATTTTGGCGAAATAGACAGCTT 14146
Qy 2588 GATCGGATTTCAAACTCTTATACTTTTCTCTTACAAGTCTTCCGCTTCATCTGGATTT 2647
Dd 14145 GATCGS-----CACTACCGAAGTATCTCAAAAGAGGTGTGCTATGAACGACGCTATTAC 14090

QY 2648 TCAGCTCTTACTTACTAAACGTCATAAAGTTTCTGTAAATTTCTACTGTATCGACTGC 2707
Db 14089 AGTGACAGTTGACAGCGACGATACAGTTGCTGCTAAGGCATATATGATGTCAATATCTCC 14030
QY 2708 AGACTGG-----CTGTGTATAAGGAGGCTGACATTTATATATCCCCAGAACATCAG 2758
Db 14029 GGTCTGGTAAGACACAACCATGACAGATGAAGCCCGTCTGTCGTGCC---GAAGCTGG 13973
QY 2759 GTTAATGGGTTTTGTATGATCAATTTCCGGGFGGTGATGATCAGCACTTCTTCCCGCAT 2818
Db 13972 AAAGCGAAATCAGGAAGGATGCTGAGTGGCGCGGTTTATTGAAATGAACGGCTCT 13913
QY 2819 AACGAGACCGGACACACTGGCCATATCGTGTCTATCATGCGCCAGCTTTCATCCCGAT 2878
Db 13912 TTTGTGTGACGAAACAGGGA-----CTGTGAAATGCGATTTAAGTTTACACTATAA 13859
QY 2879 ATGCACACCGGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTCGACTGGCCAG 2938
Db 13858 AAGAGAGAGCCGTTATCGTCTGTTGTGGATGACAGAGTGATATTTATGACACGCCGG 13799
QY 2939 GGGGATCACCATCCGTCGCGCGGGGTGTAATAATATCACTCTGTACATCCAAACAG 2998
Db 13798 GCGAGGATGATGATCCCGCTGCCAGTCACGCTCTGCTGTGATGATGATGATGATGATG 13739
QY 2999 AGGATAAGCGCTCTCTTTTATAGTGTAAACCTTAAACTGATTTACAC-----AGT 3052
Db 13738 ACTTACCCGGTGTGCATATCGGGATGAAAGTGGCCCATGATGACACCGATATGCG 13679
QY 3053 CCCTGTCTCTGTCAGCAAAAGCCGTTTCATTTCAATAAACCGGCGACCTCAGCCATCC 3112
Db 13678 CAGTGTGCGGTCTCGGTTATCGGGAAGAGTGGCTGATCTCAGCCACCGCGAAATGA 13619
QY 3113 CTTCTGTATTTCCGTTTCCAGCGTTC---GGCAGCAGACGACGGGCTTCTATCTGCA 3169
Db 13618 CATCAAAAACGCCATTAACCTGATGTTCTGGGGAATATAATGTGAGGCTCCCTTATACA 13559
QY 3170 TGG---TTGTGTTTACAGACCGGAGATATTGACATCATATATGCTTGAGCAACTGATA 3226
Db 13558 CAGCCAGTCTGAGGTCGATACAGTAGAATATACAGAACTTTATCAGTTAGTAGTA 13499
QY 3227 GCTGTCGCTGTAACCTGTCTGATGATGATTTTCAGGACTATGACACTGATGATGATG 3286
Db 13498 TAGAGCTGAAATCCAGATGAAGCCGACGACTTGTAAAGAAAAAGTATAAGAGTTGTG 13439
QY 3287 CTTCTCTTCTGATGAGATGATTTTCAGGACTATGACACTGATGATGATGATGATGATG 3346
Db 13438 AATTTGTTCTGATGAGATGATTTTCAGGACTATGACACTGATGATGATGATGATGATG 13379
QY 3347 ATGTTTTTATTTTGTACACAAAAAGAGGCTCGACCTCTTTTCTTTTCTTTTCTTTTAT 3406
Db 13378 ATGTTTTTATTTTGTACACAAAAAGAGGCTCGACCTCTTTTCTTTTCTTTTCTTTTAT 13319
QY 3407 GATTTAATACGGATTTGAGACAAATAGCGATAGGCTGGATGATGATGATGATGATGATG 3466
Db 13318 GATTTAATACGGATTTGAGACAAATAGCGATAGGCTGGATGATGATGATGATGATGATG 13259
QY 3467 AGAACATTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3526
Db 13258 AGAACATTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13199
QY 3527 AGGCTGTCGCTGACTACAGTCACTAATACCTAATGATGATGATGATGATGATGATGATG 3586
Db 13198 AGGCTGTCGCTGACTACAGTCACTAATACCTAATGATGATGATGATGATGATGATGATG 13139
QY 3587 ATATGTTGTTTACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATG 3646
Db 13138 ATATGTTGTTTACAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13079
QY 3647 TTGATATTTATCATTTTACGTTTCTCGTTTCTCGTTTCTCGTTTCTCGTTTCTCGTTTCT 3705
Db 13078 TTGATATTTATCATTTTACGTTTCTCGTTTCTCGTTTCTCGTTTCTCGTTTCTCGTTTCT 13020

RESULT 6

ABQ82141/C

ID ABQ82141 standard; DNA; 17476 BP.

XX AC ABQ82141;

XX AC ABQ82141;

DT 11-DEC-2002 (first entry)

XX

XX

DE Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.

XX

XX

KW Chimeric nucleic acid construct; recombinational cloning; silencing;

KW recombination site; double stranded RNA; plant; ds.

XX

OS Synthetic.

XX

PN WO200259294-A1.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-AU0000073.

XX

XX 26-JAN-2001; 2001US-0264067P.

PR 29-NOV-2001; 2001US-0333743P.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX

PI Wesley S, Waterhouse P, Helliwell C;

XX

XX WPI; 2002-682669/73.

DR

XX

PT New vectors comprising operably linked DNA fragments having an origin of

PT replication, a selectable marker and a chimeric DNA construct, useful for

PT silencing target nucleic acids and for producing large amounts of double-

PT stranded RNA.

XX

PS Claim 15; Page 74-83; 104pp; English.

XX

CC The present invention describes a vector (I) comprising operably linked

CC DNA fragments having: (a) origin of replication allowing replication in a

CC recipient cell, preferably in bacteria such as Escherichia coli; (b)

CC selectable marker region capable of being expressed in the recipient cell

CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter

CC region capable of being recognized by RNA polymerases of a eukaryotic

CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and

CC fourth recombination sites; (iii) 3' transcription terminating and

CC polyadenylation region functional in the eukaryotic cell. The first and

CC fourth recombination sites, or the second and third recombination sites

CC are capable of reacting with a same recombination site, and preferably

CC are identical. The first and second recombination sites, or the third and

CC fourth recombination sites, do not recombine with each other or with a

CC same recombination site. The vector is useful for producing large amounts

CC of double-stranded RNA which can be used for silencing target nucleic

CC acid sequences. The vectors can also be used to convert a DNA fragment

CC into an inverted repeat structure. Plants transformed with a vector from

CC the present invention can be used in a conventional breeding scheme to

CC produce more plants with the same characteristics or to introduce a

CC chimeric gene for reduction of the phenotypic expression of nucleic

CC acids. The present sequence represents an acceptor vector nucleotide

CC sequence from the present invention

XX

SQ Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 28.4%; Score 1273; DB 6; Length 17476;

Best Local Similarity 62.1%; Pred. No. 2.1e-172;

Matches 2316; Conservative 0; Mismatches 1325; Indels 88; Gaps 16;

QY 21 CTCGACAGAGTTTGTACAAAAAGCTGACAGAAACGTTAAATGATATAATATCAAT 80

Db 16704 CTCACAGAGTTTGTACAAAAAGCTGACAGAAACGTTAAATGATATAATATCAAT 16645

QY 81 ATATTAAATAGATTGTCATATAAAAAACAGACTACATATACTGTAAAAACACAAATATC 140

Db 16644 ATATTAAATAGATTGTCATATAAAAAACAGACTACATATACTGTAAAAACACAAATATC 16585

141 CAGTCACATGAACTCACTTAGATGGTATTAGTACCTGTAGTCGACGACGCTT 200
16584 CAGTCACATGAACTCACTTAGATGGTATTAGTACCTGTAGTCGACGACGCTT 16525
201 CCAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACGACGCTTCCAAATGTTCTT 260
16524 CCAATGTTCTTCGGGTGATGTCGCAACTTAGTCGACGACGCTTCCAAATGTTCTT 16465
261 CTCAAACGGAATCGTCGTATCCAGCTTACTGCTATTGTCCTCAATGCGGTATTAAATCA 320
16464 CTCAAACGGAATCGTCGTATCCAGCTTACTGCTATTGTCCTCAATGCGGTATTAAATCA 16405
321 TAAAAAGAAATAAGAAAAAGAGTGGAGCTCTTTTGTGTGCAAAATAAAAAACATC 380
16404 TAAAAAGAAATAAGAAAAAGAGTGGAGCTCTTTTGTGTGCAAAATAAAAAACATC 16345
381 TACCTATTCAATACGCTAGTCATAGTCCTGAAATCATCTGCAATCAAGAACCAATTC 440
16344 TACCTATTCAATACGCTAGTCATAGTCCTGAAATCATCTGCAATCAAGAACCAAGT 16285
441 ACAACTCTTACTTCTCTTACAAGTCGTTGCGCTTCATCTGGATTCTCAGCCTCTAT 500
16284 ATGTCAAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGCA 16228
501 ACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGT 560
16227 GCTATCAGTTGCTCAAGGCATATATGATGCTCAATATCTCCGGTCTGGTAAGCACAACT 16168
561 GTATAGGAGGCTGACATTTATATPCCCGAGAACATCAGGTTAATGGCGTTTTTGATGT 620
16167 GCAGAATGAAGCCGTCGTCTGGTGCC---GAAACGCTGAAAGCGGAAATCAGGAAG 16111
621 CATTTTCGGGTGGCTGAGATCAGCACATCTTCCCGATTAACGAGACCGGACACTGG 680
16110 GATGGCTGAGTGGCCCGGTTTATTGAAATGAACGGCTCTTTTCTGTCGAGAAAGGG- 16052
681 CCATATCGGTGGTCATCATCGCGCAGCTTTCATPCCCGGATATGCACACCGGGTAAAGTT 740
16051 -----ACTGGTGAATGCAGTTTAAGTTTACACCTATAAAGAGAGCGGTATCGTC 15997
741 CACGGAGACTTTATCTGACAGACAGTGCACCTGGCCGAGGGGATCAACATCCGTCGCC 800
15996 TGTGTTGTGATGTPACAGAGTGATATTATTGACACGCGCCGCGGACGGATGGTGAATCC 15937
801 CGGGCTGTCAATAATATCACTCTGTACATPCCACAAACAGACGATTAACGGCTCTCTCTT 860
15936 TGSCCAGTGACGTCTGCTGTGATAAAGTCTCCGCTGNACTTTACCGGTGGTGATA 15877
861 TAPAGGTAAACCTTAAACTGCAATTCACC-----AGTCCCTGTTCTGTCGACGAA 914
15876 TCGGGATGAAAGCTGGCGCATGATGACCAACCGATATGGCCAGTGTGCGGTCTCGGTTA 15817
915 GAGCCGTTCATTTCAATAACGGCGGACCTCAGCCATCCCTCTGATTTTCGGCTTTC 974
15816 TCGGGGAAGAGTGGGTGATCTCAGCACCGCGGAAATGATCAAAAACGCCATTAAAC 15757
975 CAGCGTTC---GGCAGCAGACGAGCGGCTTCATCTGCAATGTTGTGCTTACGACCG 1031
15756 TGATGTTCTGGGAATAAATGTACGGCTCCCTTATACAG-----CCAGTCTG 15706
1032 GAGATATGACATATATGCTTGTAGCAACTGATAGTGTGCTGCTGCTCACTGCTCACTG 1091
15705 CAGCTCGATACAGTAGAAATACAGAACTTTATCAGTTTAGTAGTATAGAGGCTGAA 15646
1092 TAATACGCTGTTCAATAGCACCTCTTTTGTACATCTTCGGGTAGTG---CCGATCA 1147
15645 AATCCAGATGAAGCCGAAACGACTTGTGAAGAAAGTATAGAGTTGTGAAATCCGATCA 15586
1148 ACGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGACACACGAG 1207
15585 ACGTCTCATTTTCGCCAAAAGTTGGCCAGGGCTTCCCGGTATCAACAGGACACACGAG 15526

1208 TTTATTATTCTGCAAGTGTATCTTCGTCACAGGTATTTATTTCGGGCAAGTGGCTCG 1267
15525 TTTATTATTCTGCAAGTGTATCTTCGTCACAGGTATTTATTTCGGGCAAGTGGCTCG 15466
1268 GGTGATGCTGCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGTATTCAT 1327
15465 GGTGATGCTGCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTGTATTCAT 15406
1328 AGTCAGCTGATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAA 1387
15405 AGTCAGCTGATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAA 15346
1388 TTTAATATATTGATTTATATCATTTTACGTTTCTCGTTGAGCTTCTGTCACAAAGT 1447
15345 TTTAATATATTGATTTATATCATTTTACGTTTCTCGTTGAGCTTCTGTCACAAAGT 15286
1448 GTCTCGAGGAATTCGGTACCCGCTTGTGAAGGAA-----TAAATATTTTCTT 1497
15285 GTCTAGAGGATCCAGCTTATCGATTTTCGAAACCCAGCTTCCCACTGTAATCAATCCAA 15226
1498 TTTTCCTTTTAGTATAAAAATAGTTAAGTGATGTTAAATTAGTATGATTAATAATATAGT 1557
15225 TGTAGATCAATGATAACAAATGACATGATCTATCATGTTACCTGTTTATTCATGTT 15166
1558 TGTATAATGTCGAAAAAATAATTTATATAATATGTTTACATAAAACACATAGTAATG 1617
15165 GACTAATTCATTTAATTAATAGTCAATCCATTTAGAGTTAATAAACTACAGATTTAT 15106
1618 TAAAAAATATCACAAGTGATGTAAGACGAAGAGATAAAGTTGAGAGTAAGTATAT 1677
15105 TTAGAAATTAATAGAAATGTTGATTTGAAATTAATTAATTAATTAATGATAGTCTGGC 15046
1678 TATTTTAAATGAATTTGATCGAAACATGTAAGATGATATCTAGCAATTAATTTGTTTA 1737
15045 TTTGTTATATTAGCATTAGATTATGTTTGTGTACATTAGATTACTGTTTCTATTAGTTG 14986
1738 ATCAATAATAGTAATTTCTAGCTGGTTTGATGAATTAATAATCAATGATAAAATACATAGT 1797
14985 ATATTATTGTTACTTTAGCTTTGTTTAAATTTTGTTTTATGATAAATACAGCAG 14926
1798 AAAAAATGAATAAATAAATAAATAATTTTTTTTATGATTAATAGTTTATATATAA 1857
14925 ATTGGAATTTCTACAAATAATTTATTAACITTTTAAACTTAAATAATTTAGTAATGGTAT 14866
1858 TTAATAATCTATPACCATTAATAATTTTGTGTTTAAAGTTTAAATAATTTTGTGTTAG 1917
14865 GATAATTAATTAATAAATAAATAATTAATCAATAAATAAATAATTTTAAATTTATTTAT 14806
1918 AATTCCAATCTGCTGTTGATTTTATCAATAAACAATAATTAATAAACAAGCTTAAAGTAA 1977
14805 CTTATTTTCTATAGTATTTTATCATTTGATTAATTTAATTCATCAACACGCTAGAAATTA 14746
1978 AATAATATCAAACTAATAAAGAACAGTATCTAATGTAAACAAACATAATCTTAATGCTAA 2037
14745 TATTATGATTAACAACAAATTAATTAATGCTAGTATATCATCTTACATGTTTCGATCAATTC 14686
2038 TATAACAAAGCGCAGATCTATCATTTTATATAGTATTAATTTTCAATCAACATCTTAT 2097
14685 TTAATAAATAATATCTTACTCTCACTTTTATCTTCTCGCTTACACATCTCTGTCAT 14626
2098 AATTTCTAATAATACTTCTGATGTTTATTAACCTTCTTAATGGATGACATTAATTAAT 2157
14625 ATTTTCTTACATTTACATGTTGTTTATGTAACAATATATTTTAAATTTTATTTTTCACA 14566
2158 GAATTAGTCGAACATGAATAAACAAGGTAAACATGATGATCATGTCATTTGTTTATCAT 2217
14565 ATTATACAACTATATTTATTAATCACTAATTAACATCACTTAATTAATTTTATACTA 14506
2218 GATCTTACATTTGGATGATTAACAGTTGGGAAGCTGGGTTCCGAATTCGATTAAGCTTGGAT 2277
14505 AAAGGAAAAAAGAAAAATAATTTATTT-----TCCTTACCAGCTGGGTACCGAAT 14456
2278 CCTCTAGACCACTTTGTACAGAAAGCTGAACGAGNAACGTAAATGATATAAATATCAA 2337

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 3; Length 4470;
Best Local Similarity 99.8%; Pred. No. 5.1e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATAAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAATATGATATAAATATCAATATATT 161

QY 86 AAATTAGATTTTGCATAAAAACAGACTACATATACTGTAAACACACATATCCAGTC 145
DB 162 AAATTAGATTTTGCATAAAAACAGACTACATATACTGTAAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGAGCGCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTCGACGAGCGCTTCCAAA 281

QY 206 TGTCTTCGGGTGATGCTGCCAACTAGTCGACGAGCGCTTCCAAATGTTCTCTCAA 265
DB 282 TGTCTTCGGGTGATGCTGCCAACTAGTCGACGAGCGCTTCCAAATGTTCTCTCAA 341

QY 266 ACGGAATGCTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 325
DB 342 ACGGAATGCTGTATCCAGCCTACTCGCTATTGTCTCAATGCCGTATTAAATCATATAAA 401

QY 326 AGAATTAAGAAAAAGAGTGGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385
DB 402 AGAATTAAGAAAAAGAGTGGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 461

QY 386 ATTCATATACGTAGTGTATGATGCTGAAATCATCTGCATCAAGAAACAATTTCAACAC 445
DB 462 ATTCATATACGTAGTGTATGATGCTGAAATCATCTGCATCAAGAAACAATTTCAACAC 521

QY 446 TCTTATACCTTTTCTTACAGTTCGCTTCGGCTTCATCTCGANTTTTCAGCCTCTATACCTTA 505
DB 522 TCTTATACCTTTTCTTACAGTTCGCTTCGGCTTCATCTCGANTTTTCAGCCTCTATACCTTA 581

QY 506 CTAACCGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTATTA 565
DB 582 CTAACCGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTATTA 641

QY 566 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGGCGTTTGTATGTCATT 625
DB 642 AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGGCGTTTGTATGTCATT 701

QY 626 TCGCGTGGCTGAGTACGACCTCTTCCCGATACGAGACCGGACACTGGGCCATA 685
DB 702 TCGCGTGGCTGAGTACGACCTCTTCCCGATACGAGACCGGACACTGGGCCATA 761

QY 686 TCGGTGGTATCATATGCGCCAGCTTTTCATCCCCGATATGCACACCGGGTAAAGTTCCAGG 745
DB 762 TCGGTGGTATCATATGCGCCAGCTTTTCATCCCCGATATGCACACCGGGTAAAGTTCCAGG 821

QY 746 GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATACCATTCGCTGCCCGGGC 805
DB 822 GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATACCATTCGCTGCCCGGGC 881

806 GTGTCATATATATCACTCTGTACATCCACAAAACAGACGATAAAGGCTCTCTCTTTTATAG 865
882 GTGTCATATATATCACTCTGTACATCCACAAAACAGACGATAAAGGCTCTCTCTTTTATAG 941
866 GTGTAACACCTTAAATGTCATTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCAT 925
942 GTGTAACACCTTAAATGTCATTTCCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTTCAT 1001
926 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTCCAGCGTTCGGC 985
1002 TTCAATAAACCGGGCGACCTCAGCCATCCCTCTCTGATTTTCCGCTTCCAGCGTTCGGC 1061
986 ACGCAGACGACGGGCTTTCATTTCTGCACTGGTTGTCTTACCAGACCGGAGATATTGACATC 1045
1062 ACGCAGACGACGGGCTTTCATTTCTGCACTGGTTGTCTTACCAGACCGGAGATATTGACATC 1121
1046 ATATATGCTTTAGCAAACTGATAGCTGTCTGTCTCAACTGTCTGTAATACGCTGCTTC 1105
1122 ATATATGCTTTAGCAAACTGATAGCTGTCTGTCTCAACTGTCTGTAATACGCTGCTTC 1181
1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
1182 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1213

RESULT 8
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
AC ABZ58767;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR201 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
XX Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 26B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence

XX SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
Query Match 24.8%; Score 1108.8; DB 7; Length 4470;
Best Local Similarity 99.8%; Pred. No. 5.1e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTTAAATGATATATAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAAGCTGAACGAGAAACGTTAAATGATATATAATATCAATATATT 161

QY 86 AAATTAGATTTCATATAAACAACACACTACATAATCTGTAACACACATATCCAGTC 145
DB 162 AAATTAGATTTCATATAAACAACACACTACATAATCTGTAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 281

QY 206 TTTTCTCGGGTGATGCTGCGAAGTGTAGTCGACGAGCGCTTCCAAATGTTCTCTCAA 265
DB 282 TTTTCTCGGGTGATGCTGCGAAGTGTAGTCGACGAGCGCTTCCAAATGTTCTCTCAA 341

QY 266 ACGGAATCGTGTATCCAGCGCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
DB 342 ACGGAATCGTGTATCCAGCGCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 401

QY 326 AGAAATAAGAAAAGAGTGGAGCGCTCTTTTGTGTGACAAATATAAAAAATCTACCT 385
DB 402 AGAAATAAGAAAAGAGTGGAGCGCTCTTTTGTGTGACAAATATAAAAAATCTACCT 461

QY 386 ATTCAATACGCTAGTGTCTATAGTCTGGAATCATCTGCATCAAGAAATTTTCAACAC 445
DB 462 ATTCAATACGCTAGTGTCTATAGTCTGGAATCATCTGCATCAAGAAATTTTCAACAC 521

QY 446 TCTTATACCTTTTCTTACAAAGTCGTTTCGGCTTCATCTGGAATTTTCAGCTCTATATCTTA 505
DB 522 TCTTATACCTTTTCTTACAAAGTCGTTTCGGCTTCATCTGGAATTTTCAGCTCTATATCTTA 581

QY 506 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACACTGGCTGTGTATA 565
DB 582 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACACTGGCTGTGTATA 641

QY 566 AGGAGCGCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 625
DB 642 AGGAGCGCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 701

QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACTGGGCGATA 685
DB 702 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACTGGGCGATA 761

QY 686 TCGGTGTGATCATGCGGAGCTTTCATCCCGATATGCACACCGGTTAAAGTTCAAGG 745
DB 762 TCGGTGTGATCATGCGGAGCTTTCATCCCGATATGCACACCGGTTAAAGTTCAAGG 821

QY 746 GAGACTTTATCTGACAGCAGACGTCGACTGCGCAGGGGGATCACATTCGCTCGCCGGGC 805
DB 822 GAGACTTTATCTGACAGCAGACGTCGACTGCGCAGGGGGATCACATTCGCTCGCCGGGC 881

QY 806 GTGTCAATAATATACCTCTGTATATCCAAACAGAGCATACCGCTCTCTTTTATAG 865
DB 882 GTGTCAATAATATACCTCTGTATATCCAAACAGAGCATACCGCTCTCTTTTATAG 941

QY 866 GTGTAAACCTTAACTGCATTTACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCAT 925
DB 942 GTGTAAACCTTAACTGCATTTACAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCAT 1001

QY 926 TTCAATAAACCGGGGAGCTCAGCGATCCCTTCTCGATTTTTCGCTTTTCCAGCGTTCGGC 985
DB 1002 TTCAATAAACCGGGGAGCTCAGCGATCCCTTCTCGATTTTTCGCTTTTCCAGCGTTCGGC 1061

QY 986 ACGCAGACGAGCGGCTTCATTTCTGATGGTTGTGCTTACAGACGGGAGATTTTGACATC 1045

DB 1062 ACGCAGACGAGCGGCTTTCATTTCTGCTGTTGTGCTTACCAGACCGGAGATATTGACATC 1121
QY 1046 ATATATGCTTGTAGCACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 1105
DB 1122 ATATATGCTTGTAGCACTGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 1181
QY 1106 ATAGCACACCTCTTTTGTGACATATCTTCGGGTA 1137
DB 1182 ATAGCACACCTCTTTTGTGACATATCTTCGGGTA 1213

RESULT 9
ADA50329
ID ADA50329 standard; DNA; 4892 BP.
XX ADA50329;
AC ADA50329;
DT 20-NOV-2003 (first entry)
XX Plasmid vector pMK2010 DNA sequence.
DE site-specific recombination; array construction; reporter gene fusion;
KW mutagenesis; protein production; protein characterisation;
KW plasmid pMK2010; ds.
XX Synthetic.
OS
XX WO2003064623-A2.
PN
XX 07-AUG-2003.
PD
XX 31-JAN-2003; 2003WO-US003176.
PF
XX 31-JAN-2002; 2002US-0354063P.
PR
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
PA
XX Kahn ML, House BL, Mortimer MW;
PI WPI; 2003-679497/64.
DR
XX Moving an insert nucleic acid between vectors using site-specific
PT recombination in vivo, useful for studying the biology of the organism,
PT including array construction, reporter gene fusions, mutagenesis and
PT protein production.
XX Claim 41; Page 47-51; 52pp; English.
PS
XX The invention comprises a method for moving an insert nucleic acid
CC molecule between vectors, the method involves moving an insert nucleic
CC acid from one vector to another using site-specific recombination. The
CC method of the invention is useful for studying the biology of an
CC organism, including array construction, reporter gene fusions,
CC mutagenesis, protein production and characterisation. The present DNA
CC sequence represents the plasmid vector pMK2010 of the invention.
XX
SQ Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;
Query Match 24.8%; Score 1108.8; DB 8; Length 4892;
Best Local Similarity 99.8%; Pred. No. 5.1e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTTAAATGATATATAATATCAATATATT 85
DB 102 GCCAACTTTGTACAAAAAAGCTGAACGAGAAACGTTAAATGATATATAATATCAATATATT 161

QY 86 AAATTAGATTTCATATAAACAACACACTACATAATCTGTAACACACATATCCAGTC 145
DB 162 AAATTAGATTTCATATAAACAACACACTACATAATCTGTAACACACATATCCAGTC 221

QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 205
DB 222 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGAGCGCTTCCAAA 281

QY 206 TGTTCCTCGGTGATGCTCCCAACTTAGTCGACCGACGCTTCGAAATGTTCTTCTCAA 265
Db 282 TGTTCCTCGGTGATGCTCCCAACTTAGTCGACCGACGCTTCGAAATGTTCTTCTCAA 341
QY 266 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATGCGGTATTAATCATATAAA 325
Db 342 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCCTCAATGCGGTATTAATCATATAAA 401
QY 326 AGAATAAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAATCAATCACT 385
Db 402 AGAATAAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAATCAATCACT 461
QY 386 ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAATTTCAAC 445
Db 462 ATTCAATACGCTAGTGTCTATAGTCTGAAATCATCTGCATCAAGAAATTTCAAC 521
QY 446 TCTTATACCTTTCTCTTCAAGTCGTTCCGCTTCATCTGATTTTCAGGCTCTTATCTTA 505
Db 522 TCTTATACCTTTCTCTTCAAGTCGTTCCGCTTCATCTGATTTTCAGGCTCTTATCTTA 581
QY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGGTGTATA 565
Db 582 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGGTGTATA 641
QY 566 AGGGAGCCTGACATTTATATCCCGAGAACATCAGGTAAATGCGGTTTGTATGTCATTT 625
Db 642 AGGGAGCCTGACATTTATATCCCGAGAACATCAGGTAAATGCGGTTTGTATGTCATTT 701
QY 626 TCGCGTGGTGTAGATCAGCACTTCTTCCCGATTAACGGAGACCGGCACCTGGCCATA 685
Db 702 TCGCGTGGTGTAGATCAGCACTTCTTCCCGATTAACGGAGACCGGCACCTGGCCATA 761
QY 686 TCGGTGTGATCATGCGCAGCTTTTATCCCGATATGACACACCGGGTAAAGTTCAAGG 745
Db 762 TCGGTGTGATCATGCGCAGCTTTTATCCCGATATGACACACCGGGTAAAGTTCAAGG 821
QY 746 GAGACTTTATCTGACAGCAGCTGCACTGCGCAGGGGATACCATTCGTCGCCCGGGC 805
Db 822 GAGACTTTATCTGACAGCAGCTGCACTGCGCAGGGGATACCATTCGTCGCCCGGGC 881
QY 806 GTGTCAATAATATCACTCTGTATATCCCAAAACAGACGATAACGGCTCTCTCTTTATAG 865
Db 882 GTGTCAATAATATCACTCTGTATATCCCAAAACAGACGATAACGGCTCTCTCTTTATAG 941
QY 866 GTGTAAACCTTAACTGATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCA 925
Db 942 GTGTAAACCTTAACTGATTTTACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCA 1001
QY 926 TTCAATAAACCGGGGACCTCAGCATCCCTTCTGATTTTCCGCTTTCCAGGTTCCGGC 985
Db 1002 TTCAATAAACCGGGGACCTCAGCATCCCTTCTGATTTTCCGCTTTCCAGGTTCCGGC 1061
QY 986 ACGCAGACGAGCGGCTTCTATTCATGATGTTGCTTACAGACCGGAGATATGACATC 1045
Db 1062 ACGCAGACGAGCGGCTTCTATTCATGATGTTGCTTACAGACCGGAGATATGACATC 1121
QY 1046 ATATATGCTGTGCAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db 1122 ATATATGCTGTGCAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
QY 1106 ATAGCACACCTCTTTTGGACATCTTCCGGTA 1137
Db 1182 ATAGCACACCTCTTTTGGACATCTTCCGGTA 1213

RESULT 10
ID AAC55525
XX AAC55525 standard; DNA; 4939 BP.
AC AAC55525;
XX 11-JAN-2001 (first entry)

XX DE Donor plasmid pDONR205 nucleotide sequence.
XX KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX KW mutant; recombinational cloning; entry vector; destination vector;
XX KW gene product targeting; fusion tag cleavage; ds.
XX OS Bacteriophage lambda.
OS Synthetic.
XX WO200052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US005432.
XX PR 02-MAR-1999; 99US-0122389P.
XX PR 23-MAR-1999; 99US-0126049P.
XX PR 28-MAY-1999; 99US-0136744P.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX DR WPI; 2000-543948/49.
XX PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX Example 10; Fig 53; 459pp; English.
XX CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 3; Length 4939;
Best Local Similarity 99.8%; Pred. No. 5.1e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAAGCTAAAATGATATAATATATATTT 85
Db 3636 GCCAACTTTGTACAAAAAAGCTGAACGAGAAAGCTAAAATGATATAATATATATTT 3695
QY 86 AAATTAGATTTTGCATATAAAAAACAGACTACATATATCTGTAAACACATATCCAGTC 145
Db 3696 AAATTAGATTTTGCATATAAAAAACAGACTACATATATCTGTAAACACATATCCAGTC 3755
QY 146 ACTATGAATCAACTACTAGTGTATTTAGTACCTGTAGTCACCGACGACGCTTCCAAA 205
Db 3756 ACTATGAATCAACTACTAGTGTATTTAGTACCTGTAGTACCGACGACGCTTCCAAA 3815

QY 206 TGTCTCTGGGTGATGCTGCGCACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 265
DB |||||
QY 3816 TGTCTCTGGGTGATGCTGCGCACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 3875
DB |||||
QY 266 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCCTCAATCGGTATTAAATCATAAAA 325
DB |||||
QY 3876 ACGGAATCGTCTGATCCAGCCTACTCGCTATTGTCCTCAATCGGTATTAAATCATAAAA 3935
DB |||||
QY 326 AGAATTAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGTCAGCAAAATAAAAAATCTACT 385
DB |||||
QY 3936 AGAATTAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGTCAGCAAAATAAAAAATCTACT 3995
DB |||||
QY 386 ATTCTATACGCTAGTGTCTATAGTCTGGAATCATCTGCATCAAGAACAAATTCACAC 445
DB |||||
QY 3996 ATTCTATACGCTAGTGTCTATAGTCTGGAATCATCTGCATCAAGAACAAATTCACAC 4055
DB |||||
QY 446 TCTTATACCTTTCTCTTACAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTTA 505
DB |||||
QY 4056 TCTTATACCTTTCTCTTACAAGTCGTTCCGGCTTCATCTGGATTTTCAGCCTCTATACCTTA 4115
DB |||||
QY 506 CTAAAGCTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGCGACGTGGTGTGTATA 565
DB |||||
QY 4116 CTAAAGCTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGCGACGTGGTGTGTATA 4175
DB |||||
QY 566 AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGCGGTTTTTGTATGTCATT 625
DB |||||
QY 4176 AGGAGCCTGACATTTATATTCGCCAGAACATCAGGTTAATGCGGTTTTTGTATGTCATT 4235
DB |||||
QY 626 TCGCGTGTGAGATCAGCACTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATA 685
DB |||||
QY 4236 TCGCGTGTGAGATCAGCACTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATA 4295
DB |||||
QY 686 TCGGTGTCATCATGCGCAGCTTTCATCCCGATATGACACACCGGTAAGTTCAACGG 745
DB |||||
QY 4296 TCGGTGTCATCATGCGCAGCTTTCATCCCGATATGACACACCGGTAAGTTCAACGG 4355
DB |||||
QY 746 GAGACTTTATCTGACAGACAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGGC 805
DB |||||
QY 4356 GAGACTTTATCTGACAGACAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCCGGGC 4415
DB |||||
QY 806 GTGTCAATTAATCATCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTTATAG 865
DB |||||
QY 4416 GTGTCAATTAATCATCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTTATAG 4475
DB |||||
QY 866 GTGTAAACCTTAACCTGCAATTCACAGTCCCTGTTCTGTCAAGAAAAGAGCGGTCAT 925
DB |||||
QY 4476 GTGTAAACCTTAACCTGCAATTCACAGTCCCTGTTCTGTCAAGAAAAGAGCGGTCAT 4535
DB |||||
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCCAGCGTTCCGC 985
DB |||||
QY 4536 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGGCTTTCCAGCGTTCCGC 4595
DB |||||
QY 986 ACCGACAGCAGCGGCTTCATCTGCATGGTGTGCTTACAGACCGGAGATTTGCAATC 1045
DB |||||
QY 4596 ACCGACAGCAGCGGCTTCATCTGCATGGTGTGCTTACAGACCGGAGATTTGCAATC 4655
DB |||||
QY 1046 ATATATGCTTGAAGCACTGATAGTCTGCTGCTGCTCACTGCTACTGTAATACGCTGCTC 1105
DB |||||
QY 4656 ATATATGCTTGAAGCACTGATAGTCTGCTGCTGCTCACTGCTACTGTAATACGCTGCTC 4715
DB |||||
QY 1106 ATAGCACACCTCTTTTGAACATACTTCGGGTA 1137
DB |||||
QY 4716 ATAGCACACCTCTTTTGAACATACTTCGGGTA 4747
DB |||||

RESULT 11

AAC55632/c

ID AAC55632 standard; DNA; 5584 BP.

XX AC

AC AAC55632;

XX AC

DT 11-JAN-2001 (first entry)

XX

Donor plasmid pDONR207 nucleotide sequence.
Bacteriophage lambda; att; recombination site; attB; attP; attL; attR; attL;
mutant; recombinational cloning; entry vector; destination vector;
gene product targeting; fusion tag cleavage; ds.
Bacteriophage lambda.
Synthetic.
WO200052027-A1.
08-SEP-2000.
02-MAR-2000; 2000WO-US005432.
02-MAR-1999; 99US-0122389P.
23-MAR-1999; 99US-0126049P.
28-MAY-1999; 99US-0136744P.
(LIFE-) LIFE TECHNOLOGIES INC.
Hartley JL, Brasch MA, Temple GF, Chao D;
WPI; 2000-543948/49.
Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides.
Disclosure; Fig 97; 459pp; English.
The present invention describes isolated nucleic acid molecules (I)
encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
nucleotide sequence. Also described are: (1) an isolated nucleic acid
molecule (II) comprising one or more att recombination sites comprising
at least one mutation in its core region that increases the specificity
of interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (I), (II), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is used
in the exemplification of the present invention
Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;
Query Match 24.8%; Score 1108.8; DB 3; Length 5584;
Best Local Similarity 99.8%; Pred. No. 5e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GACAAGTTTGTTCACAAAAAGCTGAACGAGAAACGTAATAATGATATATAATATATATATT 85
DB 5483 GCCAAGTTTGTTCACAAAAAGCTGAACGAGAAACGTAATAATGATATATAATATATATT 5424
QY 86 AAATTAGATTTTGCATTAATAAACAGACTACATAAATCTGTAATAACACACATATCCAGTC 145
DB 5423 AAATTAGATTTTGCATTAATAAACAGACTACATAAATCTGTAATAACACACATATCCAGTC 5364
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCAGCGACAGCCTTCCAAA 205
DB 5363 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCAGCGACAGCCTTCCAAA 5304
QY 206 TGTTCCTGGGTGATGCTGCGCACTTAGTCGACCGACAGCCTTCCAAATGTTCTCTCAA 265

Db 5303 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCTTCAAATGTTCTTCTCAA 5244
Qy 266 ACGGAATCGTGTATCCAGCGCTACTCGGTATGTTCTCAATGCGGTATTAATCATATAAA 325
Db 5243 ACGGATCGTGTATCCAGCGCTACTCGGTATGTTCTCAATGCGGTATTAATCATATAAA 5184
Qy 326 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAATCATCTACT 385
Db 5183 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAATCATCTACT 5124
Qy 386 ATTCAATACGCTAGTGTGATAGTCTGAAATATCTGCAATCAAGAAACAAATTTTCAACAAC 445
Db 5123 ATTCAATACGCTAGTGTGATAGTCTGAAATATCTGCAATCAAGAAACAAATTTTCAACAAC 5064
Qy 446 TCTTATACCTTTCTCTTACAGCTGCTCGGCTTCACTGGAATTTTTCAGCTCTATACATTA 505
Db 5063 TCTTATACCTTTCTCTTACAGCTGCTCGGCTTCACTGGAATTTTTCAGCTCTATACATTA 5004
Qy 506 CTAAACGCTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGCGACTGGCTGTGTATA 565
Db 5003 CTAAACGCTGATAAAGTTCTGTAAATTTCTACTGTATCGACCTGCGACTGGCTGTGTATA 4944
Qy 566 AGGGAGCTGACATTTATATTTCCCAAGACATCAGGTAAATGCGGTTTTTGTATGTCATTT 625
Db 4943 AGGGAGCTGACATTTATATTTCCCAAGACATCAGGTAAATGCGGTTTTTGTATGTCATTT 4884
Qy 626 TCGCGTGTGCTGAGATPAGCCACTTCTTCCCGATTAACGAGACCGGCACTGGCCATA 685
Db 4883 TCGCGTGTGCTGAGATPAGCCACTTCTTCCCGATTAACGAGACCGGCACTGGCCATA 4824
Qy 686 TCGGTGCTCATATGCGGAGCTTTTCATCCCGATATGACACACCGGTAAGTTTCAACG 745
Db 4823 TCGGTGCTCATATGCGGAGCTTTTCATCCCGATATGACACACCGGTAAGTTTCAACG 4764
Qy 746 GAGACTTTATCTGACAGCAGAGTGCACCTGGCCAGGGGGATCACCATCGTGGCCCGGCG 805
Db 4763 GAGACTTTATCTGACAGCAGAGTGCACCTGGCCAGGGGGATCACCATCGTGGCCCGGCG 4704
Qy 806 GTGTCAATATATCATCTGTATACATCAACAAACAGACGATACGCGCTCTCTTTTATAG 865
Db 4703 GTGTCAATATATCATCTGTATACATCAACAAACAGACGATACGCGCTCTCTTTTATAG 4644
Qy 866 GTGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 925
Db 4643 GTGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 4584
Qy 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTCCGG 985
Db 4583 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCCGCTTTTCCAGCGTTCCGG 4524
Qy 986 ACCGACAGCGGGCTTCACTTCCGATGTTGCTTACAGACCGGAGATATTGACATC 1045
Db 4523 ACCGACAGCGGGCTTCACTTCCGATGTTGCTTACAGACCGGAGATATTGACATC 4464
Qy 1046 ATATATGCTTGTAGCACTGATAGTGTGCTGCTGCACTGCTCACTGTAATACGCTGCTTC 1105
Db 4463 ATATATGCTTGTAGCACTGATAGTGTGCTGCTGCACTGCTCACTGTAATACGCTGCTTC 4404
Qy 1106 ATAGCACACCTCTTTTGTACATCTTCCGGTA 1137
Db 4403 ATAGCACACCTCTTTTGTACATCTTCCGGTA 4372

RESULT 12

ABZ58766/C

ID ABZ58766 standard; DNA; 5584 BP.

XX AC ABZ58766;

XX DT 01-MAY-2003 (first entry)

XX DE Donor plasmid pDONR207 nucleotide sequence.

XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW Nucleic acid isolation; ds.
XX OS Synthetic.
XX PN WO200295055-A2.
XX PD 28-NOV-2002.
XX PF 21-MAY-2002; 2002WO-US015947.
XX PR 21-MAY-2001; 2001US-0291973P.
XX PA (INVI-) INVITROGEN CORP.
XX BR Brach MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX WI WPI; 2003-129436/12.
XX CC The invention relates to inserting a population of nucleic acids into a second target molecule for nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the donor plasmid pDONR207 nucleotide sequence
XX SQ Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;

Query Match 24.8%; Score 1108.8; DB 7; Length 5584;
Best Local Similarity 99.8%; Pred. No. 5e-149;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 GCAAGTGTGACAAAAGCTGAACGAGAAAGTAAATGATATAATATCAATATATT 85
Db 5483 GCAAGTGTGACAAAAGCTGAACGAGAAAGTAAATGATATAATATCAATATATT 5424
Qy 86 AAATTAGATTTTGCATAAAAAACAGACTACATACTGTATAAAACACATATCCAGTC 145
Db 5423 AAATTAGATTTTGCATAAAAAACAGACTACATACTGTATAAAACACATATCCAGTC 5364
Qy 146 ACTATGAATCACTACTTAGATGGTATAGTACCTGTAGTCGACGAGCGCTTCCAA 205
Db 5363 ACTATGAATCACTACTTAGATGGTATAGTACCTGTAGTCGACGAGCGCTTCCAA 5304
Qy 206 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCAA 265
Db 5303 TGTTCCTTCGGGTGATGCTGCCAACTTAGTCGACGAGCGCTTCCAAATGTTCTTCAA 5244
Qy 266 ACGGAATCGTGTATCCAGCTTACTCGCTTATTTGCTCAATCGGCTTAAATCATATAAA 325
Db 5243 ACGGAATCGTGTATCCAGCTTACTCGCTTATTTGCTCAATCGGCTTAAATCATATAAA 5184
Qy 326 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAATCATCTACT 385
Db 5183 AGAAATAGAAAAAGAGTGCAGGCTCTTTTGTGTGACAAATATAAAATCATCTACT 5124
Qy 386 ATTCAATACGCTAGTGTGATAGTCTGAAATATCTGCAATCAAGAAACAAATTTTCAACAAC 445
Db 5123 ATTCAATACGCTAGTGTGATAGTCTGAAATATCTGCAATCAAGAAACAAATTTTCAACAAC 5064

QY 446 TCTTATACCTTTCTCTTACAAAGTCGTTGCGCTTCATCTGGAATTTTTCAGCCTCTATATCTTA 505
Db 5063 TCTTATACCTTTCTCTTACAAAGTCGTTGCGCTTCATCTGGAATTTTTCAGCCTCTATATCTTA 5004
QY 506 CTAACAGTGTATAAGTTTCTGTAATTTCTACTGTATCGACCTCGACAGCTGGCTGTGTATA 565
Db 5003 CTAACAGTGTATAAGTTTCTGTAATTTCTACTGTATCGACCTCGACAGCTGGCTGTGTATA 4944
QY 566 AGGAGCCTGACATTTATATATCCCCAGAACATCAGGTTAAATGCGTTTGTGATGTCATTT 625
Db 4943 AGGAGCCTGACATTTATATATCCCCAGAACATCAGGTTAAATGCGTTTGTGATGTCATTT 4884
QY 626 TCGCGTGGCTGAGATCAGACCACTTCTTCCCGATACAGGACCGGACACTGGCCATA 685
Db 4883 TCGCGTGGCTGAGATCAGACCACTTCTTCCCGATACAGGACCGGACACTGGCCATA 4824
QY 686 TCGGTGTGATCATCGCCGACGTTTCATCCCGATATGACACCGGGTAAAGTTCAACGG 745
Db 4823 TCGGTGTGATCATCGCCGACGTTTCATCCCGATATGACACCGGGTAAAGTTCAACGG 4764
QY 746 GAGACTTTATCTGACAGACAGCTGCACTGCGCAGGGGGATACCATTCGTCGCGCGGC 805
Db 4763 GAGACTTTATCTGACAGACAGCTGCACTGCGCAGGGGGATACCATTCGTCGCGCGGC 4704
QY 806 GTGTCAATATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTTATAG 865
Db 4703 GTGTCAATATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGCATTTTCAACGATCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCA 925
Db 4643 GTGTAAACCTTAACTGCATTTTCAACGATCCCTGTTCTCGTCAGCAAAAGAGCGGTTTCA 4584
QY 926 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTCGCTTTCAGAGGTTTCGGC 985
Db 4583 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCAGAGGTTTCGGC 4524
QY 986 ACGCAGACGCGGCTTCATTTCTCATGTTGTCCTTACAGACCGGAGATATTGACATC 1045
Db 4523 ACGCAGACGCGGCTTCATTTCTCATGTTGTCCTTACAGACCGGAGATATTGACATC 4464
QY 1046 ATATATGCTTGTAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC 1105
Db 4463 ATATATGCTTGTAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC 4404
QY 1106 ATAGCAGACCTCTTTTGTACATCTTCGGTA 1137
Db 4403 ATAGCAGACCTCTTTTGTACATCTTCGGTA 4372

RESULT 13

ID AB258768 standard; DNA; 4428 BP.

XX AC AB258768;

XX AC AB258768;

DT 01-MAY-2003 (first entry)

DE Destination plasmid pDONR212 nucleotide sequence.

XX Nucleic acid insertion; recombination; nucleic acid selection;

KW Nucleic acid isolation; ds.

XX Synthetic.

XX WO200295055-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US015947.

XX 21-MAY-2001; 2001US-0291973P.

XX (INV-) INVITROGEN CORP.

XX
PI
XX
DR

Brasch MA, Cheo D, Li X, Esposito D, Byrd DN;

WPI; 2003-129436/12.

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

Disclosure; Fig 27B-C; 273pp; English.

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212 nucleotide sequence

SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;

Query Match 24.6%; Score 1102.4; DB 7; Length 4428;

Best Local Similarity 99.5%; Pred. No. 4.1e-148;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAACTTTGTACAAAAAGCTGAACGAGAAAGCTAAATATGATATAATATCAATATAT 85

Db 939 GCCAATTTGTACAAAAAGCTGATATCGAAGTAAATATGATATAATATCAATATAT 998

QY 86 AAATTAGATTTTGCATPAAAAAAGACACTACATAATATCTGTAACACAAATATCCAGTC 145

Db 999 AAATTAGATTTTGCATPAAAAAAGACACTACATAATATCTGTAACACAAATATCCAGTC 1058

QY 146 ACTATGAATCACTACTTAGATGGTATTAGTACCTGTAGTCAGCGAGCGCTTCCAA 205

Db 1059 ACTATGAATCACTACTTAGATGGTATTAGTACCTGTAGTCAGCGAGCGCTTCCAA 1118

QY 206 TGTCTCTCGGTTGATGCTGCCAATTTAGTCGACGACGCTTCCAAATGTTCTTCTCAA 265

Db 1119 TGTCTCTCGGTTGATGCTGCCAATTTAGTCGACGACGCTTCCAAATGTTCTTCTCAA 1178

QY 266 ACGGAATGCTGATCCAGCTACTCGCTATTGTCCTCAATGCGGTTAAATCAATAA 325

Db 1179 ACGGAATGCTGATCCAGCTACTCGCTATTGTCCTCAATGCGGTTAAATCAATAA 1238

QY 326 AGAATAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGACAAATATAAAACATCTACCT 385

Db 1239 AGAATAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGACAAATATAAAACATCTACCT 1298

QY 386 ATTATATAGCTAGTGTATAGTCTCTGAAATATCATCTGCATCAAGAACAAATTTCAAC 445

Db 1299 ATTATATAGCTAGTGTATAGTCTCTGAAATATCATCTGCATCAAGAACAAATTTCAAC 1358

QY 446 TCTTATACCTTTCTCTTACAAAGTCGTTGCGCTTCATCTGGAATTTTTCAGCCTCTATATCTTA 505

Db 1359 TCTTATACCTTTCTCTTACAAAGTCGTTGCGCTTCATCTGGAATTTTTCAGCCTCTATATCTTA 1418

QY 506 CTAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGCTGTGTATA 565

Db 1419 CTAACGTTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGCTGTGTATA 1478

QY 566 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAAATGCGGTTTGTATGTCATTT 625

Db 1479 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAAATGCGGTTTGTATGTCATTT 1538

QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGACACTGGCCATA 685

Db 1539 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATACGAGACCGGACACTGGCCATA 1598

930	GTGTAAACCTTAAATGCAATTTACCAAGTCCCTGTCTTCGTACGAAAAAGACCGTTCAAT	989
Db		
926	TTCAATAAACCGGGGACCTCAGCCATCCCTTCCTGATTTTCGGCTTTCAGAGGTTTCGGC	985
QY		
990	TTCAATAAACCGGGGACCTCAGCCATCCCTTCCTGATTTTCGGCTTTCAGAGGTTTCGGC	1049
Db		
986	ACGCAGACGACGGGCTTCATCTTCGATGTTGTGCTTACAGACCGGAGATATGACATC	1045
QY		
1050	ACGCAGACGACGGGCTTCATCTTCGATGTTGTGCTTACCGACCGGAGATATGACATC	1109
Db		
1046	ATATATGCGCTTGAGCAACTGATAGCTGTGCGCTCTCAACTGTCTGTAATACGCTCGTTC	1105
QY		
1110	ATATATGCGCTTGAGCAACTGATAGCTGTGCGCTGTCAACTGTCTGATATACGCTCGTTC	1169
Db		
1106	ATAGCACACCTCTTTTGGACATACCTTCGGGTA	1137
QY		
1170	ATAGCACACCTCTTTTGGACATACCTTCGGGTA	1201
Db		

RESIST 15

RESULT IS
ABZ58770

ABZ58770
ID ABZ58770 standard: DNA: 4627 BP.

XX
GT
01/0679W

AC ABZ58770;

XX
XXXXXXXXXXXX

DT 01-MAY-2003 (first entry)

XX
XX

DE Destination

KW Nucleic acid

KW nucleic acid isolation; ds.

XXI

OS Synthetic.

XX	
DW	XXXXXXX
XX	XXXXXXXX

PN WO200295055-A2.
yy

28-NOV-2002.
21-MAY-2002; 2002WO-US015947.
21-MAY-2001; 2001US-0291973P.
(INVI-) INVITROGEN CORP.
Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
WFI; 2003-129436/12.
Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

Sequence 4627 BP: 1262 A: 1126 C: 990 G: 1249 T: 0 U: 0 Other: 0

Query Match

Query Match 24.6%; Score 1102.4; DB 7; Length 4627;

Best Local Similarity 99.5%; Pred. No. 4.1e-148;

26	QY	26	GACAAAGTTGTACAAAAAGCTGACGAGAAACGTAATAATGATATATAATATCAATATATT	85
90	Db	90	GCCAACTTTGTACAAAAAGCTGATATCGAAACGTAAATGATATAATAATATCAATATATT	149
86	QY	86	AAATTTAGATTTTGTCAATAAAAAACAGACTACATAAATCTGTAAAAACAAACATATCCAGTC	145
150	Db	150	AAATTTAGATTTTGTCAATAAAAAACAGACTACATAAATCTGTAAAAACAAACATATCCAGTC	209
146	QY	146	ACTATGAATCAACTACTTTAGATGGTATTAGTACCTCTGTAGTCGACCGACAGCCTTCCAAA	205
210	Db	210	ACTATGAATCAACTACTTTAGATGGTATTAGTACCTCTGTAGTCGACCGACAGCCTTCCAAA	269
206	QY	206	TGCTCTTTGGGGTGATGCTGCCAACTTTAGTCGACCGACAGCCTTCCAAAATGTTCTCTCAA	265
270	Db	270	TGTTCTTTGGGGTGATGCTGCCAACTTTAGTCGACCGACAGCCTTCCAAAATGTTCTCTCAA	329
266	QY	266	ACGGAATCGTCTGATCCAGCTTACTCGGTATTGTCTTAATGCCGTATTAAATCATATAAA	325
330	Db	330	ACGGAATCGTCTGATCCAGCTTACTCGGTATTGTCTTAATGCCGTATTAAATCATATAAA	389
326	QY	326	AGAAATAGAAAAGAGGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAACATCTACCT	385
390	Db	390	AGAAATAGAAAAGAGGGTGCGAGCCTCTTTTGTGTGACAAAAATAAAAAACATCTACCT	449
386	QY	386	ATTCTATATACGCTAGTGTCTATAGTCTCTGAAAAATCATCTGCATCAAGAACAAATTCACAAC	445
450	Db	450	ATTCTATATACGCTAGTGTCTATAGTCTCTGAAAAATCATCTGCATCAAGAACAAATTCACAAC	509
446	QY	446	TCCTTATACHTTTCTCTTACAAGTCGTTCCGGCTTCATCTCGATTTTCAGCCTCTATACTTTA	505
510	Db	510	TCCTTATACHTTTCTCTTACAAGTCGTTCCGGCTTCATCTCGATTTTCAGCCTCTATACTTTA	569
506	QY	506	CTAAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA	565
570	Db	570	CTAAAACGTGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA	629
566	QY	566	AGGGAGCCTGCACATTTATATCTCCAGAACATCAGGTTAATGGCGTTTTTGATGTCAATTT	625
630	Db	630	AGGGAGCCTGCACATTTATATCTCCAGAACATCAGGTTAATGGCGTTTTTGATGTCAATTT	689
626	QY	626	TGCGGTGTGCTGAGATCAGCCACTTCTCCCGATAACGGAGACGGGCACACTGGCCATA	685
690	Db	690	TGCGGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACGGGCACACTGGCCATA	749
686	QY	686	TGGTGGTGCATCATGCGCCAGCTTTTCATCCCGGATATGACCAACCGGGTAAAGTTCAACGG	745
750	Db	750	TGGTGGTGCATCATGCGCCAGCTTTTCATCCCGGATATGACCAACCGGGTAAAGTTCAACGG	809
746	QY	746	GAGACTTTATCTGACAGCAGAGTGTCACCTGGCCAGGGGATCAACATCGCTGCCCGGGC	805
810	Db	810	GAGACTTTATCTGACAGCAGAGTGTCACCTGGCCAGGGGATCAACATCGCTGCCCGGGC	869
806	QY	806	GTGTCAATAATATCACTCTGTACATCCCAAAAACAGACGATAGCGGTCTCTCTTTTATAG	865
870	Db	870	GTGTCAATAATATCACTCTGTACATCCCAAAAACAGACGATAGCGGTCTCTCTTTTATAG	929
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Job time : 1064.31 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 1193.76 Seconds
(without alignments)
16988.923 Million cell updates/sec

Title: US-10-055-001B-24_COPY_13000_17476

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4477	100.0	17476	15	US-10-055-001A-24
2	4477	100.0	17476	15	US-10-385-546-7
3	4406.6	98.4	17458	15	US-10-055-001A-25
4	4262	95.2	17681	15	US-10-055-001A-26
5	4112.4	91.9	17862	15	US-10-055-001A-23
6	3234.8	72.3	18691	15	US-10-055-001A-13
7	1277.8	28.5	17458	15	US-10-055-001A-25
8	1273	28.4	17476	15	US-10-055-001A-24
9	1273	28.4	17476	15	US-10-385-546-7
10	1108.8	24.8	4470	15	US-10-151-690-21
11	1108.8	24.8	4892	16	US-10-357-268-1
12	1108.8	24.8	5584	15	US-10-151-690-61
13	1102.4	24.6	4428	15	US-10-151-690-62
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18	780	17.4	786	15	US-10-385-521-9
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ALIGNMENTS

RESULT 1

US-10-055-001A-24
; Sequence 24, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24

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Gaps	0						
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US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match 100.0%; Score 4477; DB 15; Length 17476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCAATTTGGAGAGGACACGCTCGAGACAAGTTTGTGTAACAAAAGCTGAACGAAACGTT 60
DB 13000 TTTTCAATTTGGAGAGGACACGCTCGAGACAAGTTTGTGTAACAAAAGCTGAACGAAACGTT 13059
QY 61 AAAATGATATAAATATCAATATATTAATTTAGATTTTGCATATAAAGACACACTACATAAT 120
DB 13060 AAAATGATATAAATATCAATATATTAATTTAGATTTTGCATATAAAGACACACTACATAAT 13119
QY 121 ACTGTAAAAACACACATATCCAGTCACTATGAATCACTACTTAGATGGTATTAGTGACC 180
DB 13120 ACTGTAAAAACACACATATCCAGTCACTATGAATCACTACTTAGATGGTATTAGTGACC 13179
QY 181 TGTAGTGCAGGACAGGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG 240
DB 13180 TGTAGTGCAGGACAGGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG 13239
QY 241 ACAGCCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCCTTACCTCGCTATTGTC 300
DB 13240 ACAGCCTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCCTTACCTCGCTATTGTC 13299
QY 301 CTCAATGCCGTATTAATCAATAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTGTG 360
DB 13300 CTCAATGCCGTATTAATCAATAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTGTG 13359
QY 361 TGTGACAAAATAAAGACATCTACTATTATATACGCTAGTGTATGCTCTGAAATCA 420
DB 13360 TGTGACAAAATAAAGACATCTACTATTATATACGCTAGTGTATGCTCTGAAATCA 13419
QY 421 TCTGCATCAAGAACAAATTTCCAACTCTTATCTTTTCTCTTCAAGTCTGTCGGCTTCA 480
DB 13420 TCTGCATCAAGAACAAATTTCCAACTCTTATCTTTTCTTCAAGTCTGTCGGCTTCA 13479
QY 481 TCTGGATTTTCAGCCTCTATCTTATCTAAACGTTGATAAGGTTCTGTAAATTTCTACTGTA 540
DB 13480 TCTGGATTTTTCAGCCTCTATCTTATCTAAACGTTGATAAGGTTCTGTAAATTTCTACTGTA 13539
QY 541 TCGACCTGACAGCTGGCTGTATTAAGGAGCCTTGACATTTATATCCCCAGAACATCAG 600
DB 13540 TCGACCTGACAGCTGGCTGTATTAAGGAGCCTTGACATTTATATCCCCAGAACATCAG 13599
QY 601 GTTAATGGCCTTTTGTATGTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGCAT 660
DB 13600 GTTAATGGCCTTTTGTATGTCATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGCAT 13659
QY 661 AACGGAGACCGGACACTGCGCATATCGGTGTCATCATGCGGACGCTTTCATCCCGCAT 720
DB 13660 AACGGAGACCGGACACTGCGCATATCGGTGTCATCATGCGGACGCTTTCATCCCGCAT 14759
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Db 13660 AACGGAGACCGGACACTGCGCATATCGGTGTCATCATGCGGACGCTTTCATCCCGCAT 13719
QY 721 ATGCACACACCGGTAAGTTTCAACGGAGACTTTATCTGACAGACAGCTGCACTGGCCAG 780
Db 13720 ATGCACACACCGGTAAGTTTCAACGGAGACTTTATCTGACAGACAGCTGCACTGGCCAG 13779
QY 781 GGGGATCAACATCCGTCGCGCGCGGCGTGCATATATATCACTCTGTACATCCACAAACAG 840
Db 13780 GGGGATCAACATCCGTCGCGCGGCGTGCATATATATCACTCTGTACATCCACAAACAG 13839
QY 841 ACGATAACCGCTCTCTCTTTTATAGTGTAAACCTTAACTCACTTCACTTCACTAGTCCCTGT 900
Db 13840 ACGATAACCGCTCTCTCTTTTATAGTGTAAACCTTAACTCACTTCACTAGTCCCTGT 13899
QY 901 TCTCGTCAGCAAAAGAGCGCTTCAITTTCAATAAAGCGGCGACCTCAGCCATCCCTTCT 960
Db 13900 TCTCGTCAGCAAAAGAGCGCTTCAITTTCAATAAAGCGGCGACCTCAGCCATCCCTTCT 13959
QY 961 GATTTTCCGCTTTCAGCGTTCGGACAGCAGAGCGGCTTCACTCTGCTAGTGGTGTGC 1020
Db 13960 GATTTTCCGCTTTCAGCGTTCGGACAGCAGAGCGGCTTCACTCTGCTAGTGGTGTGC 14019
QY 1021 TTACACAGACCGGAGATATTGACATCATATATATGCTTTGACCAACTGATAGCTGCTGTC 1080
Db 14020 TTACACAGACCGGAGATATTGACATCATATATGCTTTGACCAACTGATAGCTGCTGTC 14079
QY 1081 AACTGTCACTGTAAATACGCTGCTTCATAGCAACCTCTTTTGTGACATACCTTCGGGTAGT 1140
Db 14080 AACTGTCACTGTAAATACGCTGCTTCATAGCAACCTCTTTTGTGACATACCTTCGGGTAGT 14139
QY 1141 CCGATCAACGCTCTCATTTTCGCCAAAGTTGCCGCCAGGCTTCCCGGTATCAACAGGAC 1200
Db 14140 CCGATCAACGCTCTCATTTTCGCCAAAGTTGCCGCCAGGCTTCCCGGTATCAACAGGAC 14199
QY 1201 ACCAGATTTATTTATTTTCGGAAGTATCTTCCGTCACAGGTATTTATTTCCGCGCAAG 1260
Db 14200 ACCAGATTTATTTATTTTCGGAAGTATCTTCCGTCACAGGTATTTATTTCCGCGCAAG 14259
QY 1261 TCGCTCGGTGATGCTGCCAACTTAGTGCATACAGGTCACTAATACCATCTAAGTAGTT 1320
Db 14260 TCGCTCGGTGATGCTGCCAACTTAGTGCATACAGGTCACTAATACCATCTAAGTAGTT 14319
QY 1321 GATTCATAGTACTGATATGTTGTTTACAGTATTTATGATGTTAGTCTGTTTATGCA 1380
Db 14320 GATTCATAGTACTGATATGTTGTTTACAGTATTTATGATGTTAGTCTGTTTATGCA 14379
QY 1381 AATCTAAATTAATATATGATATTTATATCACTTTTACGTTTCTCGTTCAGCTTCTTGT 1440
Db 14380 AATCTAAATTAATATATGATATTTATATCACTTTTACGTTTCTCGTTCAGCTTCTTGT 14439
QY 1441 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAATAATATTTTCTTTT 1500
Db 14440 CAAAGTGTCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAATAATATTTTCTTTT 14499
QY 1501 TCTTTTGTAGTAATAATAGTTAAGTGATTTAATAGTATGATTAATAATAATATAGTTGT 1560
Db 14500 TCTTTTGTAGTAATAATAGTTAAGTGATTTAATAGTATGATTAATAATAATATAGTTGT 14559
QY 1561 TATAATGTGAAAAAATAATTTTATAAATAATATGTTTACATAAACAACATAGTAATGAA 1620
Db 14560 TATAATGTGAAAAAATAATTTTATAAATAATATGTTTACATAAACAACATAGTAATGAA 14619
QY 1621 AAAATATGACAGTGTGTCAGACGAGAGTAAGTGTGAGCTAGTATATAT 1680
Db 14620 AAAATATGACAGTGTGTCAGACGAGAGTAAGTGTGAGCTAGTATATAT 14679
QY 1681 TTTTAAATGAATTTGATCGAAACATGTAAGTATGATGATTAATAATTTGTTTAAATC 1740
Db 14680 TTTTAAATGAATTTGATCGAAACATGTAAGTATGATGATTAATAATTTGTTTAAATC 14739
QY 1741 ATAAATAGTAATTTCTAGCTGGTGTGATTAATAATCAATGATAAAACTATAGTAAA 1800
Db 14740 ATAAATAGTAATTTCTAGCTGGTGTGATTAATAATCAATGATAAAACTATAGTAAA 14799
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16960	Db		TAGCGACATCTATGATAGAGCGCCAATTAACAAACATTCGGTCTTTATTATTACAATC	17019
4021	QY		CAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGATTACATAAATCTTAT	4080
17020	Db		CAATTTTAAAAAAGCGGAGAACCGGTCAAACCTTAAAGACTGATTACATAATCTTAT	17079
4081	QY		TCAATTTTAAAAAGGCCCCAGGGGCTAGTATCTACGACACACCGAGCGCGCAACTAATAA	4140
17080	Db		TCAATTTTAAAAAGGCCCCAGGGGCTAGTATCTACGACACACCGAGCGCGCAACTAATAA	17139
4141	QY		CGTTCACCTGAAGGAACCTCGGTTCCCGCGGCGGCGCATGGGTGAGATTCTTTGAAGTT	4200
17140	Db		CGTTCACCTGAAGGAACCTCGGTTCCCGCGGCGGCGCATGGGTGAGATTCTTTGAAGTT	17199
4201	QY		GAGTATTGGCCGTCGCTCTACCGAAAGTTACGGGCACCAATTCACCCGGTCCAGCACGG	4260
17200	Db		GAGTATTGGCCGTCGCTCTACCGAAAGTTACGGGCACCAATTCACCCGGTCCAGCACGG	17259
4261	QY		CGGCGCGGTTAACCGACTTGTGCCCCGAGAAATATGCAGCAATTTTTTGGTGATGTGGG	4320
17260	Db		CGGCGCGGTTAACCGACTTGTGCCCCGAGAAATATGCAGCAATTTTTTGGTGATGTGGG	17319
4321	QY		CCCCAAATGNAAGTGCAGGTCACAACTTGACGTGACGTAGCAGCAAAATCGTTGGGCGGTCGAGG	4380
17320	Db		CCCCAAATGNAAGTGCAGGTCACAACTTGACGTGACGTAGCAGCAAAATCGTTGGGCGGTCGAGG	17379
4381	QY		GCGAATTTTCCGACAACTGTTCGAGGCTCAGCAGAGACCTGCGAGGCATGCAAGCTAGCTTA	4440
17380	Db		GCGAATTTTCCGACAACTGTTCGAGGCTCAGCAGAGACCTGCGAGGCATGCAAGCTAGCTTA	17439
4441	QY		CTAGTGATGCATATTTCTATAGTGTCACTTAAATCTGCG	4477
17440	Db		CTAGTGATGCATATTTCTATAGTGTCACTTAAATCTGCG	17476

RESULT 3

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US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

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Db	13120	ACTGTAACACACACATATCCAGTCACATATGAATCAACTACTTATGATGGTATTAGTGACC	13179
Qy	181	TGTAGTCGACCGACAGCCCTTCAAATGTTCTTTCCGGGTGATGCTGCCAACTAGTCTGACGCG	240
Db	13180	TGTAGTCGACCGACAGCCCTTCAAATGTTCTTTCCGGGTGATGCTGCCAACTAGTCTGACGCG	13239
Qy	241	ACAGCCCTTCAAATGTTCTTCTCAACGGAATTCGTCGTATCCAGCCTACTCGCTATTGTC	300
Db	13240	ACAGCCCTTCAAATGTTCTTCTCAACGGAATTCGTCGTATCCAGCCTACTCGCTATTGTC	13299
Qy	301	CTCAATGCCGTATTAAATCATATAAAGAAATTAAGAAAAAGAGGTCGAGCCCTCTTTTGTG	360
Db	13300	CTCAATGCCGTATTAAATCATATAAAGAAATTAAGAAAAAGAGGTCGAGCCCTCTTTTGTG	13359
Qy	361	TGTGACAAATAAACAATCTACTTATTCATATATACGTTAGTGTCAATAGTCCTGAAAAATCA	420
Db	13360	TGTGACAAATAAACAATCTACTTATTCATATACGTTAGTGTCAATAGTCCTGAAAAATCA	13419
Qy	421	TCTGCAATCAAGAACAAATTTCAACAATCTTATATCTTTCTCTTACAAGTCGTTCCGCTTCA	480
Db	13420	TCTGCAATCAAGAACAAATTTCAACAATCTTATATCTTTCTCTTACAAGTCGTTCCGCTTCA	13479
Qy	481	TCTGGATTTTCAGCCTCTATACTATAAACGTGATAAAGTTTCTGTAAATTTCTACTGTA	540
Db	13480	TCTGGATTTTCAGCCTCTATACTATAAACGTGATAAAGTTTCTGTAAATTTCTACTGTA	13539
Qy	541	TCCAGCTGCAGACTGGCTGTATTAAGGAGCGCTCACATTTATATTTCCCGCAGACATCAG	600
Db	13540	TCCAGCTGCAGACTGGCTGTATTAAGGAGCGCTCACATTTATATTTCCCGCAGACATCAG	13599
Qy	601	GTTAATGGCGTTTTTGATGTCAATTTTCGGCGTGGCTGAGATCAGCACTTCTTCCCGAT	660
Db	13600	GTTAATGGCGTTTTTGATGTCAATTTTCGGCGTGGCTGAGATCAGCACTTCTTCCCGAT	13659
Qy	661	AA CGGAGACGGGACACTGGCCCATTCGCTGGTGTATCATCGCCGAGCTTTCAATCCCGAT	720
Db	13660	AA CGGAGACGGGACACTGGCCCATTCGCTGGTGTATCATCGCCGAGCTTTCAATCCCGAT	13719
Qy	721	ATGCACACCGGGTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGCATGGCCAG	780
Db	13720	ATGCACACCGGGTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGCATGGCCAG	13779
Qy	781	GGGGATCACATCCGTCGCCCGGGCGGTGCATATATATCATCTGTATCATCCACAAAACAG	840
Db	13780	GGGGATCACATCCGTCGCCCGGGCGGTGCATATATATCATCTGTATCATCCACAAAACAG	13839
Qy	841	ACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACAGATCCCTGT	900
Db	13840	ACGATAACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACAGATCCCTGT	13899
Qy	901	TCTCGTCAGCAAAAGAGCCGTTCAATTTCAATTAACCGGCGACCTCAGCCATCCCTTCCT	960
Db	13900	TCTCGTCAGCAAAAGAGCCGTTCAATTTCAATTAACCGGCGACCTCAGCCATCCCTTCCT	13959
Qy	961	GATTTTCCGCTTTCCAGCGTTTCGGCAGCAGACGCGGCTTCATCTTCGATGGTTGTC	1020
Db	13960	GATTTTCCGCTTTCCAGCGTTTCGGCAGCAGACGCGGCTTCATCTTCGATGGTTGTC	14019
Qy	1021	TTACCGACCGGAGATATTGACATCATATATGCCCTTGAGCAACTGATAGCTGTGCGCTGC	1080
Db	14020	TTACCGACCGGAGATATTGACATCATATATGCCCTTGAGCAACTGATAGCTGTGCGCTGC	14079
Qy	1081	AACGTGCATGTAATACGTGCTTCATAGCACACCTCTTTTGTGACATACTTCGGGTAGTG	1140
Db	14080	AACGTGCATGTAATACGTGCTTCATAGCACACCTCTTTTGTGACATACTTCGGGTAGTG	14139
Qy	1141	CCGATCAACGTCTCATTTTTCGCCAAAAGTTGGCCACAGGCTTCCCGGTATCAACAGGGAC	1200
Db	14140	CCGATCAACGTCTCATTTTTCGCCAAAAGTTGGCCACAGGCTTCCCGGTATCAACAGGGAC	14199
Qy	1201	ACCAGGATTTATTTATCTCGGAAGTGATCTTCCGTCACAGGATTTTATTCGGGCAAG	1260
Db	14200	ACCAGGATTTATTTATCTCGGAAGTGATCTTCCGTCACAGGATTTTATTCGGGCAAG	14259

15880 AGATTTCCTGTAATTTCTACTGTAATGACCTGACAGCTGCTGTGTATAGGAGGAGCTGAC 15939
2736 ATTATATATCCCGAGAACATCAGGTTAAATGGGCTTTTGTGATGTCATTTTCGGGGGGCTG 2795
15940 ATTATATATCCCGAGAACATCAGGTTAAATGGGCTTTTGTGATGTCATTTTCGGGGGGCTG 15999
2796 AGATCAGCACATCTTCTCCCGGATAAAGGAGACCGGCACACTGGCCATATCGGGTGCATC 2855
16000 AGATCAGCACATCTTCTCCCGGATAAAGGAGACCGGCACACTGGCCATATCGGGTGCATC 16059
2856 ATCGCGCAGCTTTCATCCCGATATGACACCGGGTAAAGTTTCAAGGAGACTTTATCT 2915
16060 ATCGCGCAGCTTTCATCCCGATATGACACCGGGTAAAGTTTCAAGGAGACTTTATCT 16119
2916 GACAGCAGAGCTGACATGGCCAGGGGATACCATCGCTGCGCCGGCGGTGTCAATTAATA 2975
16120 GACAGCAGAGCTGACATGGCCAGGGGATACCATCGCTGCGCCGGCGGTGTCAATTAATA 16179
2976 TCACTCTGTACATCCCAACAGACGATACCGCTCTCTTTTATAGGTGTAACCTTA 3035
16180 TCACTCTGTACATCCCAACAGACGATACCGCTCTCTTTTATAGGTGTAACCTTA 16239
3036 AACTGCATTTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCAATTTCAATAAACCG 3095
16240 AACTGCATTTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCAATTTCAATAAACCG 16299
3096 GGGGACCTCAGCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCCGACGAGACG 3155
16300 GGGGACCTCAGCATCCCTCTCTGATTTTCCGCTTTCCAGCGTTCCGACGAGACG 16359
3156 GGCTTCATCTGATGCTGCTGCTTACAGACCGGAGATATGACATCATATATGCTTG 3215
16360 GGCTTCATCTGATGCTGCTGCTTACAGACCGGAGATATGACATCATATATGCTTG 16419
3216 AGCAACTGATAGCTGCTGCTGCTCAACTGTCATGTAATACGCTGCTTCATAGCAACCTC 3275
16420 AGCAACTGATAGCTGCTGCTGCTCAACTGTCATGTAATACGCTGCTTCATAGCAACCTC 16479
3276 TTTTGTGACATCTCTGCTTGTGATGAGATGATTTTCCAGGACTATGACACTAGCGTATA 3335
16480 TTTTGTGACATCTCTGCTTGTGATGAGATGATTTTCCAGGACTATGACACTAGCGTATA 16539
3336 TGAATAGGTAGATGTTTTTATTTTGTGTCACAAAGAGAGGCTCGCACCTCTTTTCTTA 3395
16540 TGAATAGGTAGATGTTTTTATTTTGTGTCACAAAGAGAGGCTCGCACCTCTTTTCTTA 16599
3396 TTTCTTTTATGATTTAATACGCAATTCAGGACCAATAGCGAGTAGGCTGGATACGAGAT 3455
16600 TTTCTTTTATGATTTAATACGCAATTCAGGACCAATAGCGAGTAGGCTGGATACGAGAT 16659
3456 TCCGTTTGAAGAACATTTGGAAGGCTGTCGGTCACTAAGTTGGCAGCATCACCGAA 3515
16660 TCCGTTTGAAGAACATTTGGAAGGCTGTCGGTCACTAAGTTGGCAGCATCACCGAA 16719
3516 GAAATTTGGAAGGCTGTCGGTCACTAAGTTGGCAGCATCACCGAA 3575
16720 GAAATTTGGAAGGCTGTCGGTCACTAAGTTGGCAGCATCACCGAA 16779
3576 ATAGTACTGATATGTTGCTTTTACAGTATATGATGCTGTTTTTATGCAAAATCT 3635
16780 ATAGTACTGATATGTTGCTTTTACAGTATATGATGCTGTTTTTATGCAAAATCT 16839
3636 AATTATATATATGATTTTATATCATTTTACGTTTCTGTTTACGTTTGTGACAAAC 3695
16840 AATTATATATATGATTTTATATCATTTTACGTTTCTGTTTACGTTTGTGACAAAC 16899
3696 TTGCTAGAGCTCCTGCTTTTATAGATATGAGACGCTATGATCGCATGATATTTGCT 3755
16900 TTGCTAGAGCTCCTGCTTTTATAGATATGAGACGCTATGATCGCATGATATTTGCT 16959
3756 TTCAATTTCTGTCGAGTTGTAAAGAACCTGACATGCTAGCTCAGATCCCTTACCGC 3815

16960 TTCAATTTCTGTCGAGCTTTGTAAAGAACCTGAGCATGTGTAGCTCAGATCTTACCGC 17019
3816 CGGTTTCGGTTTCATTTCAATGAATATATCACCGTTACTATCGTATTTTATGAATAATA 3875
17020 CGGTTTCGGTTTCATTTCAATGAATATATCACCGTTACTATCGTATTTTATGAATAATA 17079
3876 TTCTCCGTTTCAATTTTACTGATTTGATCCCTACTACTTATATGTACAAATTTAAATGAAAA 3935
17080 TTCTCCGTTTCAATTTTACTGATTTGATCCCTACTACTTATGTACAAATTTAAATGAAAA 17139
3936 CAATATATTTGCTGCAATAGGTTTATAGCGACATCTATGTAGAGCGGCAATTAACAA 3995
17140 CAATATATTTGCTGCAATAGGTTTATAGCGACATCTATGTAGAGCGGCAATTAACAA 17199
3996 CAATTTGCGTTTATTTATTTACAAATCCAAATTTTAAAGAACCGGCAACCGTCAAACT 4055
17200 CAATTTGCGTTTATTTATTTACAAATCCAAATTTTAAAGAACCGGCAACCGTCAAACT 17259
4056 AAAAGACTGATTTACATAAATCTTTTCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTAC 4115
17260 AAAAGACTGATTTACATAAATCTTTTCAAAATTTCAAAAGGCCCCAGGGGCTAGTATCTAC 17319
4116 GACACACGAGCGGCGAACTAATTAACGTTTCACTGAAGGAACTCCGTTCCCGCGCGG 4175
17320 GACACACGAGCGGCGAACTAATTAACGTTTCACTGAAGGAACTCCGTTCCCGCGCGG 17379
4176 CGCATGGGTGAGATTTCTTGAAGTTGAGTATTTGGCGCTCTACCGAAAGTTACGGG 4235
17380 CGCATGGGTGAGATTTCTTGAAGTTGAGTATTTGGCGCTCTACCGAAAGTTACGGG 17439
4236 CACCATTTCAACCGGTTCCAGCACGCGCGCGGTTAACCGACTTGTCTGCCCGCGAGATTA 17499
4296 GCAGCATTTTCTTGGTATGTTGGCCCCCAATGAAGTCAAGTCAAACTTTGACAGTGA 4355
17500 GCAGCATTTTCTTGGTATGTTGGCCCCCAATGAAGTCAAGTCAAACTTTGACAGTGA 17559
4356 CGACAAATCTTTGGGCGGTTCCAGGCGCAATTTTTCGCAAACTGTGAGGCTCAGCAGG 4415
17560 CGACAAATCTTTGGGCGGTTCCAGGCGCAATTTTTCGCAAACTGTGAGGCTCAGCAGG 17619
4416 ACCTGAGCGCATGCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTCACTAAATCT 4475
17620 ACCTGAGCGCATGCAAGCTAGCTTACTAGTATGATATTTCTATAGTGTCACTAAATCT 17679
4476 GC 4477
17680 GC 17681

RESULT 5

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US2003004983A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match	91.9%;	Score 4112.4;	DB 15;	Length 17862;	
Best Local Similarity	93.8%;	Pred. No. 0;			
Matches 4446;	Conservative 0;	Mismatches 6;	Indels 290;	Gaps 4;	
QY	26	GACAAAGTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAATATATT	85		
Db	13121	GCCAACTTTGTACAAAAAGCTGAACAGAAACGTAATAATGATATAATATCAATATATT	13180		
QY	86	AAATAGATTTTGCATAAAAAACAGACTACATAATATCTGTAAAAACACACATATCCAGTC	145		
Db	13181	AAATAGATTTTGCATAAAAAACAGACTACATAATATCTGTAAAAACACACATATCCAGTC	13240		
QY	146	ACTATGAATCAACTACTTAGATGATTAAGTGAACCTGAGTCGACGACAGCCCTTCCAAA	205		
Db	13241	ACTATGAATCAACTACTTAGATGATTAAGTGAACCTGAGTCGACGACAGCCCTTCCAAA	13300		
QY	206	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACAGCCCTTCCAAATGTTCTTCTCAA	265		
Db	13301	TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACAGCCCTTCCAAATGTTCTTCTCAA	13360		
QY	266	ACGGAATCGTGTATCCAGCCCTACTCGCTATTTGCTCTCAATGCCGTATTAATCATRAAA	325		
Db	13361	ACGGAATCGTGTATCCAGCCCTACTCGCTATTTGCTCTCAATGCCGTATTAATCATRAAA	13420		
QY	326	AGAAATAGAAAAGAGGTGCGAGCCCTCTTTTCTGTGACAAAAATAAAACATCTACT	385		
Db	13421	AGAAATAGAAAAGAGGTGCGAGCCCTCTTTTCTGTGACAAAAATAAAACATCTACT	13480		
QY	386	ATTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGAAACAAATTCACAAAC	445		
Db	13481	ATTATATACGCTAGTGTATAGTCTGAAATCATCTGCATCAAGAAACAAATTCACAAAC	13540		
QY	446	TCTTATACCTTTCTCTTACAAAGTCTGCGCTTCTGATCTGGAATTTTTCAGCTCTTACTTA	505		
Db	13541	TCTTATACCTTTCTCTTACAAAGTCTGCGCTTCTGATCTGGAATTTTTCAGCTCTTACTTA	13600		
QY	506	CTAAAGCTGATAAAGTTCTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA	565		
Db	13601	CTAAAGCTGATAAAGTTCTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA	13660		
QY	566	AGGAGCCCTGACATTTATATTCCTCCAGAACATCAGAGTAAATGCGGTTTGTATGTCATTT	625		
Db	13661	AGGAGCCCTGACATTTATATTCCTCCAGAACATCAGAGTAAATGCGGTTTGTATGTCATTT	13720		
QY	626	TCCGGTGGCTGAGATCAGCCACTTCTCCCGATACGAGACCGGACACACTGGGCCATA	685		
Db	13721	TCCGGTGGCTGAGATCAGCCACTTCTCCCGATACGAGACCGGACACACTGGGCCATA	13780		
QY	686	TCCGTGTGTATCATGCGCCAGCTTTTCATCCCGATATGCAACCCCGGTAAAGTTCAACGG	745		
Db	13781	TCCGTGTGTATCATGCGCCAGCTTTTCATCCCGATATGCAACCCCGGTAAAGTTCAACGG	13840		
QY	746	GAGACTTTATCTGACAGACAGTGCTACTGGCAGGGGGATCACCCTCGTCGCCCGGGC	805		
Db	13841	GAGACTTTATCTGACAGACAGTGCTACTGGCAGGGGGATCACCCTCGTCGCCCGGGC	13900		
QY	806	GTGTCAATATATCACTCTGTACATCCACAAAACAGAGATAACCGCTCTCTCTTTTATAG	865		
Db	13901	GTGTCAATATATCACTCTGTACATCCACAAAACAGAGATAACCGCTCTCTCTTTTATAG	13960		
QY	866	GTGTAAACCTTAAACTGCAATTCACAGTCCCTGTTCTCGTACGAAAAAGAGCGGTTTCAT	925		
Db	13961	GTGTAAACCTTAAACTGCAATTCACAGTCCCTGTTCTCGTACGAAAAAGAGCGGTTTCAT	14020		
QY	926	TTCAATAAACCGGGGAGCTCAGGCATCCCTTCTGATTTTCCGCTTCCAGCGTTCCGGC	985		
Db	14021	TTCAATAAACCGGGGAGCTCAGGCATCCCTTCTGATTTTCCGCTTCCAGCGTTCCGGC	14080		
QY	986	ACGACAGACGGGCTTCAATCTGATGTTGTCTTACAGACGGGAGATTTGACATC	1045		
Db	14081	ACGACAGACGGGCTTCAATCTGATGTTGTCTTACAGACGGGAGATTTGACATC	14140		

QY	1046	ATATATGCCCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC	1105		
Db	14141	ATATATGCCCTTGAGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAAATACGCTGCTTC	14200		
QY	1106	ATAGCACACCTCTTTTGGACATATCTTCGGGTAGTGGCGATCAACAGCTCTCAATTTTCGCCAA	1165		
Db	14201	ATAGCACACCTCTTTTGGACATATCTTCGGGTAGTGGCGATCAACAGCTCTCAATTTTCGCCAA	14260		
QY	1166	AAAGTTGGCCCGCCAGGCTTCCCGGTATCAACAGGGAACCCAGGATTTATTTATCTGCGAAG	1225		
Db	14261	AAAGTTGGCCCGCCAGGCTTCCCGGTATCAACAGGGAACCCAGGATTTATTTATCTGCGAAG	14320		
QY	1226	TGATCTTCCTGTCACAGGTATTTATTCGGCGAAGTGGCTGGGTGATGCTGCCAATCTTA	1285		
Db	14321	TGATCTTCCTGTCACAGGTATTTATTCGGCGAAGTGGCTGGGTGATGCTGCCAATCTTA	14380		
QY	1286	GTCGACTACAGGTCACTAATACCACTTAAAGTAGTGTGATTCATAGTGAATGTTGT	1345		
Db	14381	GTCGACTACAGGTCACTAATACCACTTAAAGTAGTGTGATTCATAGTGAATGTTGT	14440		
QY	1346	GTTTTACAGTATTAATGATGCTGTTTTTATGCAAAATCTAAATTAATATTTGATATTT	1405		
Db	14441	GTTTTACAGTATTAATGATGCTGTTTTTATGCAAAATCTAAATTAATATTTGATATTT	14500		
QY	1406	ATATCATTTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTGG-----	1448		
Db	14501	ATATCATTTTACGTTTCTCGTTCAGCTTCTTGTACAAAGTGGCAATTAAGAAGCAT	14560		
QY	1449	-----	1448		
Db	14561	TGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCAGTCAAAATAAAATCATTTATTCG	14620		
QY	1449	-----TCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATAATTTATTT	1493		
Db	14621	CATCCAGCTGCAAGCTCTCGAGGAATTCGGTACCCAGCTTGGTAAAGAAATAATTTATTT	14680		
QY	1494	TCTTTTTCCTTTTAGTATATAAATAGTTAAAGTGATTAATTAGTATGATTAATAATAATA	1553		
Db	14681	TCTTTTTCCTTTTAGTATATAAATAGTTAAAGTGATTAATTAGTATGATTAATAATAATA	14740		
QY	1554	TAGTTGTTATATTTGTGAAAAATAATTTATAAATATATTTGTTTACATAAAACAATAGT	1613		
Db	14741	TAGTTGTTATATTTGTGAAAAATAATTTATAAATATATTTGTTTACATAAAACAATAGT	14800		
QY	1614	AATGTAAAAAATAATGACAGTGATGTAACGACGAGAGATAAAGTTGAGAGTAAGT	1673		
Db	14801	AATGTAAAAAATAATGACAGTGATGTAACGACGAGAGATAAAGTTGAGAGTAAGT	14860		
QY	1674	ATATTATTTTAAATGAATTTGATCGAACATGTAAGATGATATATAGCATTAATATTTGT	1733		
Db	14861	ATATTATTTTAAATGAATTTGATCGAACATGTAAGATGATATATAGCATTAATATTTGT	14920		
QY	1734	TTTAAATCAATAATAGTAATTTCTAGCTGGTTTGAATTAATAATCAATGAATAATACTA	1793		
Db	14921	TTTAAATCAATAATAGTAATTTCTAGCTGGTTTGAATTAATAATCAATGAATAATACTA	14980		
QY	1794	TAGTAAAAATAAGATAAATAAATAAATAATTTTTTTTATGATTAATAGTTTATTTAT	1853		
Db	14981	TAGTAAAAATAAGATAAATAAATAAATAATTTTTTTTATGATTAATAGTTTATTTAT	15040		
QY	1854	ATAATTAATAATCTATACCAATTTACTAAATATTTTAGTTTAAAGTTTAAATAATTTTGT	1913		
Db	15041	ATAATTAATAATCTATACCAATTTACTAAATATTTTAGTTTAAAGTTTAAATAATTTTGT	15100		
QY	1914	TAGAAATTCCTGCTGTAATTTATCAATAAACAATAATTAATAACAGCTAAAG	1973		
Db	15101	TAGAAATTCCTGCTGTAATTTATCAATAAACAATAATTAATAACAGCTAAAG	15160		
QY	1974	TAAACAATAATATCAAACTTAATAGAACAGTAATCTAAATGTAACAAAAACAATAATCTAATG	2033		
Db	15161	TAAACAATAATATCAAACTTAATAGAACAGTAATCTAAATGTAACAAAAACAATAATCTAATG	15220		
QY	2034	CTAATATAACAAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATCTCT	2093		

Db ||||| 15221 CTAATATAACAAAGCGAGATCTATCATTTATATATAGTATTTTCAATCAACATCT 15280
QY TATTAATTTCTAAATAAATCTGTAGTTTATTAACCTTCTAAATGAGTATGACTAATAAT 2153
Db TATTAATTTCTAAATAAATCTGTAGTTTATTAACCTTCTAAATGAGTATGACTAATAAT 15340
QY AAATGAAATAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTGTGTTAT 2213
Db AAATGAAATAGTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTGTGTTAT 15400
QY CATTGATCTTACATTTGGATTGATTAACAGTTCGGAAGCTGGGTTCGAATTCGATAGCTT 2273
Db CATTGATCTTACATTTGGATTGATTAACAGTTCGGAAGCTGGGTTCGAATTCGATAGCTT 15460
QY GGATCCTCTPAGA----- 2285
Db GGATCCTCTAGAGAGCTGCAGCTGGATGGCAAAATATGATTTTATTTTGAATGATGTA 15520
QY -----CCACTTTGTACAGA 2300
Db COTGTTCTGTTGCAACAAATGTGATAGCAATGCTTTCTTATATATGCTTTTGTACAGA 15580
QY AAGCTGAAACGAGAAAAGCTAAATATGATATAAATATCAATATATTAATAGATTTTGCATA 2360
Db AAGCTGAAACGAGAAAAGCTAAATATGATATAAATATCAATATATTAATAGATTTTGCATA 15640
QY AAAAAAGACTACATTAATCTGTAAACACACATATCCAGTCACATGAATCAACTACT 2420
Db AAAAAAGACTACATTAATCTGTAAACACACATATCCAGTCACATGAATCAACTACT 15700
QY TAGATGGTATAGTGACCTGTAGTCCAGTAAGTTGGCAGCATCACCCGAGCACTTTGCG 2480
Db TAGATGGTATAGTGACCTGTAGTCCAGTAAGTTGGCAGCATCACCCGAGCACTTTGCG 15760
QY CCGAATAAATPACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCTGTGTCCCTG 2540
Db CCGAATAAATPACCTGTGACGGAAGATCACTTCGAGAAATAAATAAATCTGTGTCCCTG 15820
QY TTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAATAAGACGTTGATCGG----- 2593
Db TTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAATAAGACGTTGATCGG----- 15880
QY -ATTTCACAACTCTTATACCTTTCTCTTCAAGTCTGTGGCTTCACTGTGATTTTCAGC 2652
Db CAATTCACAACTCTTATACCTTTCTCTTCAAGTCTGTGGCTTCACTGTGATTTTCAGC 15940
QY CTTCTATCTTACTAAACGATGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACT 2712
Db CTTCTATCTTACTAAACGATGATAAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACT 15941
QY GCGTGTGATAAGGGGACCTGACATTTATATTTCCAGACATCAGGTTAATCGCGTTTT 2772
Db GCGTGTGATAAGGGGACCTGACATTTATATTTCCAGACATCAGGTTAATCGCGTTTT 16060
QY TGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCA 2832
Db TGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGAGACCGGCA 16120
QY CACTGGCCATATCGGTGGTCAATGATGCGCAGCTTTTCATCCCGGATATGACCAACCGGCT 2892
Db CACTGGCCATATCGGTGGTCAATGATGCGCAGCTTTTCATCCCGGATATGACCAACCGGCT 16180
QY AAGGTTACCGGAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGATCACCATCC 2952
Db AAGGTTACCGGAGACTTTATCTGACAGCAGCTGACCTGGCCAGGGGATCACCATCC 16240
QY GTCCCGGGGCTGTCAATATATACCTCTGTACATCCAAAAACAGACGATTAACGGCTCT 3012
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QY CTTCTTTATAGGTGTAACCTTAACTGCAATTCACCGTCCCTGTTCTCGTACGAAAA 3072
Db CTTCTTTATAGGTGTAACCTTAACTGCAATTCACCGTCCCTGTTCTCGTACGAAAA

Db 16301 CTCCTTTATAGGTGTAACCTTAACTGCAATTCACCGTCCCTGTTCTCGTACGAAAA 16360
QY GAGCGCTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCGCTTTC 3132
Db GAGCGCTTCATTTCAATAAACCGGCGACCTCAGCCATCCCTTCTCTGATTTTCGCTTTC 16420
QY CAGGTTTCGGCAGCAGACGAGCGCTTCATTTCTGCAATGTTGTGCTTACAGACCGGAG 3192
Db CAGGTTTCGGCAGCAGACGAGCGCTTCATTTCTGCAATGTTGTGCTTACAGACCGGAG 16480
QY ATATTGACATCATATATATGCTTTGAGCAACTGATAGCTGTCCGTGCAACTGCTCACTG 3252
Db ATATTGACATCATATATATGCTTTGAGCAACTGATAGCTGTCCGTGCAACTGCTCACTG 16540
QY TAGCTGCTTCATAGCACACCTCTTTTGGACATACTTCTGTTGATGACAGATGATTTT 3312
Db TAGCTGCTTCATAGCACACCTCTTTTGGACATACTTCTGTTGATGACAGATGATTTT 16600
QY CAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTATTTTGTCTCACAAAAAA 3372
Db CAGGACTATGACACTAGCGTATATGAATAGGTAGATGTTTATTTTGTCTCACAAAAAA 16660
QY GAGGCTCGACCTCTTTTCTTTATTTCTTTTATGATTAATAACGCAATTGAGGCAATA 3432
Db GAGGCTCGACCTCTTTTCTTTATTTCTTTTATGATTAATAACGCAATTGAGGCAATA 16720
QY GCGAGTAGCTGGATACACGATTCCTGTTGAGAGAACATTTGGAAGCTGTCCGTGCGA 3492
Db GCGAGTAGCTGGATACACGATTCCTGTTGAGAGAACATTTGGAAGCTGTCCGTGCGA 16780
QY CTAAGTTGGCAGCACTACCCGGAAGAACATTTGGAAGCTGTCCGTGCGACTACAGTCACT 3552
Db CTAAGTTGGCAGCACTACCCGGAAGAACATTTGGAAGCTGTCCGTGCGACTACAGTCACT 16840
QY AATAACAATCAAGTAGTATGATTCATAGTACATGATGATGTTGTGTTTACAGTATATGT 3612
Db AATAACAATCAAGTAGTATGATTCATAGTACATGATGATGTTGTGTTTACAGTATATGT 16900
QY AGCTGTGTTTATCGAAAACTCAATTTAATAATATGATATTTATATCATTTTACGTTTC 3672
Db AGCTGTGTTTATCGAAAACTCAATTTAATAATATGATATTTATATCATTTTACGTTTC 16960
QY TCGTTTCAGCTTTTGTACAAACTTTG----- 3698
Db TCGTTTCAGCTTTTGTACAAAGTTGGCATTATAAAAAAGCATTTCTCATCAATTTGTTG 17020
QY ----- 3699
Db CAAAGAACAGGTCACTATCAGTCAAAAAATAAATCAATTTTGGGCGCGAGATCCATGCT 17080
QY ---TCTAGAGTCTCTCTTTAATGAGATATGCGAGACGCTATGATCGCATGATTTTGTCT 3755
Db AGCTCTAGAGTCTCTCTTTAATGAGATATGCGAGACGCTATGATCGCATGATTTTGTCT 17140
QY TTCAATTCCTGTTGTCACGCTTGTAAACCTGAGCATGTGTAGCTCAGATCTTACCGC 3815
Db TTCAATTCCTGTTGTCACGCTTGTAAACCTGAGCATGTGTAGCTCAGATCTTACCGC 17200
QY CGGTTTCGGTTCATTTCTAATGAATATATCACCCTTTCTATCTGTTTATGAAATATA 3875
Db CGGTTTCGGTTCATTTCTAATGAATATATCACCCTTTCTATCTGTTTATGAAATATA 17260
QY TTCTCCGTTCAATTTTACTGATTTGATCCCTTACTTATATGATGATTAATAATGAAAA 3935
Db TTCTCCGTTCAATTTTACTGATTTGATCCCTTACTTATATGATGATTAATAATGAAAA 17320
QY CAATATATTTGCTGATAGGTTTATGAGCAATCTATGATGAGCGCCACATTAACAAA 3995
Db CAATATATTTGCTGATAGGTTTATGAGCAATCTATGATGAGCGCCACATTAACAAA 17380
QY CAATTCGGTTTATTTATTTACAAATCCAAATTTTAAAAAAGCGGCAACCGCTCAACCT 4055
Db CAATTCGGTTTATTTATTTACAAATCCAAATTTTAAAAAAGCGGCAACCGCTCAACCT 17440

QY 4056 AAAAGACTGATTACATAAATCTTATCAAAATTTCAAAGGCGCCAGGGCTAGTATCTAC 4115
Db |||||
QY 17441 AAAAGACTGATTACATAAATCTTATCAAAATTTCAAAGGCGCCAGGGCTAGTATCTAC 17500
Db |||||
QY 4116 GACACACCGAGCGGCGAACTAATAAGCTTCACTGAAGGAACTCCGGTTTCCCGCGCGG 4175
Db |||||
QY 17501 GACACACCGAGCGGCGAACTAATAAGCTTCACTGAAGGAACTCCGGTTTCCCGCGCGG 17560
Db |||||
QY 4176 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGGCGCTCGCTCTACCGAAAGTTACGGG 4235
Db |||||
QY 17561 CGCATGGGTGAGATTCCTTGAAGTTGAGTATGGCGCTCGCTCTACCGAAAGTTACGGG 17620
Db |||||
QY 4236 CACCATTCACCGGTCGACGCGCGCGGTAACCGACTTGTCTGCCCGGAGAAATAT 4295
Db |||||
QY 17621 CACCATTCACCGGTCGACGCGCGGTAACCGACTTGTCTGCCCGGAGAAATAT 17680
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QY 4296 GCAGCAATTTTTTGGTGTATGTGGGCGCCCAAAATGAAGTCAGGTCAAACTTGCACAGTGA 4355
Db |||||
QY 17681 GCAGCAATTTTTTGGTGTATGTGGGCGCCCAAAATGAAGTCAGGTCAAACTTGCACAGTGA 17740
Db |||||
QY 4356 CGACAAATCGTTGGCGGGTCCAGGGCGGAATTTTGGACACATGTCGAGGCTCAGCAGG 4415
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QY 17741 CGACAAATCGTTGGCGGGTCCAGGGCGGAATTTTGGACACATGTCGAGGCTCAGCAGG 17800
Db |||||
QY 4416 ACCTGCAGGCGATCAAGCTAGCTTACTAGTAGTGATGATATCTATAGTGTCACTAAATCT 4475
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QY 17801 ACCTGCAGGCGATCAAGCTAGCTTACTAGTAGTGATGATATCTATAGTGTCACTAAATCT 17860
Db |||||
QY 4476 GC 4477
Db |||||
QY 17861 GC 17862
Db |||||

RESULT 6

US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Hellwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18691
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(9985)
; OTHER INFORMATION: spectinomycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10706)..(11324)
; OTHER INFORMATION: right T-DNA border fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11674)..(13019)
; OTHER INFORMATION: CMV35S promoter fragment
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17690)..(17659)
; OTHER INFORMATION: attP1 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (17610)..(16855)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16551)..(16319)
; OTHER INFORMATION: attP2 recombination site (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14660)..(16258)
; OTHER INFORMATION: pdk2 intron 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15062)..(15661)
; OTHER INFORMATION: chloramphenicol resistance gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14387)..(14619)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13675)..(13980)
; OTHER INFORMATION: ccdB selection marker (complement)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13048)..(13279)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
; US-10-055-001A-13

Query Match 72.3%; Score 3234.8; DB 15; Length 18691;
Best Local Similarity 79.5%; Pred. No. 0;
Matches 4429; Conservative 0; Mismatches 22; Indels 1121; Gaps 6;
QY 26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAAGCTGATAATATGATAATATCAATATAT 85
Db 13121 GCCAACTTTGTACAAAAAAGCTGAAACGAGAAAGCTGATAATATGATAATATCAATATAT 13180
QY 86 AAATTAGATTTTCCATAAAAAACAGACTACATAATACTGTAAACACACATATCCAGTC 145
Db 13181 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAACACACATATCCAGTC 13240
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACGCGCTTCCAAA 205
Db 13241 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACGCGCTTCCAAA 13300
QY 206 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCGCTTCCAAATGTTCTTCTCAA 265
Db 13301 TGTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGCGCTTCCAAATGTTCTTCTCAA 13360
QY 266 ACGGAATCGTCGTATCGAGCCTACTCGCTATTGCTCAATGCGGTATTAATCATAAAA 325
Db 13361 ACGGAATCGTCGTATCGAGCCTACTCGCTATTGCTCAATGCGGTATTAATCATAAAA 13420
QY 326 AGAATTAAGAAAAAGAGGTGCGAGCGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 385

Db	13421	AGAAATAAGAAAAGAGGTGCGAGGCTCTTTTGTGTGACAAAATAAAAAATACCT	13480	Db	14501	ATAATCATTTTACGTTTCTCGTTACGCTTTCTTGTAAGAGTTGGCAATTAAGAAGCAT	14560
Qy	386	ATTCAATACGCTAGTGTCTAGTCTGTAATCAATCTGATCAAGAAACAATTTTCAAC	445	Qy	1449	-----	1448
Db	13481	ATTCAATACGCTAGTGTCTAGTCTGTAATCAATCTGATCAAGAAACAATTTTCAAC	13540	Db	14561	TGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTTATTC	14620
Qy	446	TCTTATACATTTTCTCTTACAAAGTCTGTCGGCTTCATCTGGAATTTTCAAGCTCTATACCTA	505	Qy	1449	-----TCTCGAGGAATTCGGTACCCAGCTTGGTAAAGGAAATAATTAATTT	1493
Db	13541	TCTTATACATTTTCTCTTACAAAGTCTGTCGGCTTCATCTGGAATTTTCAAGCTCTATACCTA	13600	Db	14621	CATCCAGCTGCGAGCTCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAATAATTAATTT	14679
Qy	506	CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGTGTGTATA	13660	Qy	1494	TCTTTTTCCTTTTAGTATAAAATAGTTAAGTGTGTAAATTAGTATGATTAATAATAA	1553
Db	13601	CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGTGTGTATA	13660	Db	14680	TCTTTTTCCTTTTAGTATAAAATAGTTAAGTGTGTAAATTAGTATGATTAATAATAA	14739
Qy	566	AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTGTGATGTCATTT	625	Qy	1554	TAGTTGTTTATTAATTTGTAAGAAATAATTAATAATAATTTGTTTACATAAAACAACATAGT	1613
Db	13661	AGGAGCCTGACATTTATATATCCCAAGAACATCAGGTTAATGCGGTTTGTGATGTCATTT	13720	Db	14740	TAGTTGTTTATTAATTTGTAAGAAATAATTAATAATAATTTGTTTACATAAAACAACATAGT	14799
Qy	626	TGCGGTGCTGAGATCAGCACTTCTTCCCGATTAACGGAGACCCGGACACCTGGCCATA	685	Qy	1614	RATGTAAAAAATATGACAAGTGTGTAAAGCAAGAAAGATAAAAGTTGAGAGTAAGT	1673
Db	13721	TGCGGTGCTGAGATCAGCACTTCTTCCCGATTAACGGAGACCCGGACACCTGGCCATA	13780	Db	14800	AATGTAAAAAATATGACAAGTGTGTAAAGCAAGAAAGATAAAAGTTGAGAGTAAGT	14859
Qy	686	TGCGGTGCTGATGCGCAGCTTTCATCCCGATATGACCAACCCGGTAAAGTTCAACGG	745	Qy	1674	ATATTATTTTAAATGAAATTTGATCGAACATGTAAAGATGATATACATAGCAATTA	1726
Db	13781	TGCGGTGCTGATGCGCAGCTTTCATCCCGATATGACCAACCCGGTAAAGTTCAACGG	13840	Db	14860	ATATTATTTTAAATGAAATTTGATCGAACATGTAAAGATGATATACATAGCAATTA	14919
Qy	746	GAGATTTTATCTGACAGCAGCTGACCTGCGCAGGGGGATCACCATCCGTGCGCCGGGC	805	Qy	1727	-----	1726
Db	13841	GAGATTTTATCTGACAGCAGCTGACCTGCGCAGGGGGATCACCATCCGTGCGCCGGGC	13900	Db	14920	CAACTTTCAACCAATAAGAAATAAGATCACTACCGGGCGTATTTTGTAGTTATCCAGATT	14979
Qy	806	GTGTCAATATATCATCTGTATCATCCCAAAACAGAGGATTAACGGCTCTCTTTTATAG	865	Qy	1727	-----	1726
Db	13901	GTGTCAATATATCATCTGTATCATCCCAAAACAGAGGATTAACGGCTCTCTTTTATAG	13960	Db	14980	TTTCAAGGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCGTTGATAT	15039
Qy	866	GTGTAAACCTTTAACTGATTTTCAACAGTCCCTGTTCTCGTACAGAAAAGAGCGTTTAT	925	Qy	1727	-----	1726
Db	13961	GTGTAAACCTTTAACTGATTTTCAACAGTCCCTGTTCTCGTACAGAAAAGAGCGTTTAT	14020	Db	15040	ATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCACTAGTGTGTCAATGACCTA	15099
Qy	926	TTCAATAAACCGGCGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCAGCGTTTCGGC	985	Qy	1727	-----	1726
Db	14021	TTCAATAAACCGGCGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCAGCGTTTCGGC	14080	Db	15100	TAAACAGACCGTTTCACTGCTGATATTAAGCGCTTTTAAAGACCGTAAGAAAAAAGCA	15159
Qy	986	ACGACAGACGCGGCTTCACTCTGATGTTGCTTTACAGACCGGAGATATGACATC	1045	Qy	1727	-----	1726
Db	14081	ACGACAGACGCGGCTTCACTCTGATGTTGCTTTACAGACCGGAGATATGACATC	14140	Db	15160	CAAGTTTATCCGGCTTTTATTTACATTTCTGCGCGCTGATGAATGCTCATCCCGAAT	15219
Qy	1046	ATATATGCTTGAGCAACTGATAGTCTGCTGCTCAACTGCTCACTGTAATACGCTGCTTC	1105	Qy	1727	-----	1726
Db	14141	ATATATGCTTGAGCAACTGATAGTCTGCTGCTCAACTGCTCACTGTAATACGCTGCTTC	14200	Db	15220	CGGTATGGCAATGAAGACCGGTGAGCTGGTGATATGGGATAGTGTTCACCCCTTGTACAC	15279
Qy	1106	ATAGCACACCTCTTTTGAATACCTGCGGTAGTGGCGATCAAGCTCTCAATTTTCGCCAA	1165	Qy	1727	-----	1726
Db	14201	ATAGCACACCTCTTTTGAATACCTGCGGTAGTGGCGATCAAGCTCTCAATTTTCGCCAA	14260	Db	15280	CGTTTTCATGACAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAACGACGATTT	15339
Qy	1166	AAGTTGCGCAGGCTTCCCGGTATCAACAGGACACAGGATTTATTTATCTGCGAAG	1225	Qy	1727	-----	1726
Db	14261	AAGTTGCGCAGGCTTCCCGGTATCAACAGGACACAGGATTTATTTATCTGCGAAG	14320	Db	15340	CGGACGATTTCTACACATATTTCCGACAGATGTGGCGTGTACGGTGAACCTGCGCTA	15399
Qy	1226	TGATCTTCCGTCACAGGTATTTATTCGGCGCAAGTGGTGGGTGATGCTGCCAATTA	1285	Qy	1727	-----	1726
Db	14321	TGATCTTCCGTCACAGGTATTTATTCGGCGCAAGTGGTGGGTGATGCTGCCAATTA	14380	Db	15400	TTTCCCTAAAGGGTTTATTGAGAAATATGTTTTCGTCTCAGCCAATCCCTGGGTGATTT	15459
Qy	1286	GTCGACTACAGGTCACTAATACCATCTAAGTAGTGTATCTAGTGTGATGATGATGATGTTGT	1345	Qy	1727	-----	1726
Db	14381	GTCGACTACAGGTCACTAATACCATCTAAGTAGTGTATCTAGTGTGATGATGATGATGTTGT	14440	Db	15460	CACCAAGTTTGAATTAACGTGGCCAAATATGGACAACTTCTTCGCCCGCTTTTCCACAT	15519
Qy	1346	GTTTTACAGTATATGATGATCTGTTTATGCAAAATCTAATTAATATATTCATATTT	1405	Qy	1727	-----	1726
Db	14441	GTTTTACAGTATATGATGATCTGTTTATGCAAAATCTAATTAATATATTCATATTT	14500	Db	15520	GGGCAAAATATTAACGCAAGCGCAAGGTGCTGTATGCCCTGGCGATTCAGTTCATCA	15579
Qy	1406	ATATCATTTTACGTTTCTCGTTCAGCTTCTTGTAACAAAGTGG	1448	Qy	1727	-----	1726
		-----		Db	15580	TGCCGTGTGATGGCTTCCATGTCGGCAGAAATGCTTAATGAATTAACACAGTACTGCGA	15639

QY	1727	-----	1726
Db	15640	TGAGTGCAGGGCGGGCGGTAAATCGCGTGGATCCGGCTTACTTAAAGCCAGATAACAGTA	15639
QY	1727	-----	1743
Db	15700	TGCGTATTTGGCGCGTGAATTTTGGCGTATAAGATATATATACTAGTATGTGGGCCCATTA	15759
QY	1744	ATAGTAATTTCTAGCTGGTTTGGATGAATTAATAATCAATGATAAAACTATAGTAAAAAT	1803
Db	15760	ATAGTAATTTCTAGCTGGTTTGGATGAATTAATAATCAATGATAAAACTATAGTAAAAAT	15819
QY	1804	AAGAATAAAATAAAATTAATAATTTTTTTTATGATTAATAGTCTTTATTATATAATTAAT	1863
Db	15820	AAGAATAAAATAAAATTAATAATTTTTTTTATGATTAATAGTCTTTATTATATAATTAAT	15879
QY	1864	ATCTATACCCNTACTAAATATTTTATGTTTAAAGTTAATAAATATTTTGTAGAAATTC	1923
Db	15880	ATCTATACCCNTACTAAATATTTTATGTTTAAAGTTAATAAATATTTTGTAGAAATTC	15939
QY	1924	AATCTGCTTGTAAATTTATCAATAAAACAAATATTAATAACAAGCTAAAGTAACAAATAA	1983
Db	15940	AATCTGCTTGTAAATTTATCAATAAAACAAATATTAATAACAAGCTAAAGTAACAAATAA	15999
QY	1984	TATCAAACTAATPAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTTAATTAAC	2043
Db	16000	TATCAAACTAATPAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTTAATTAAC	16059
QY	2044	AAAGCGAAGATCTATCATTTTATATAGTATTTTCAATCAACATCTCTATTATTAATTC	2103
Db	16060	AAAGCGAAGATCTATCATTTTATATAGTATTTTCAATCAACATCTCTATTATTAATTC	16119
QY	2104	TAAATAAATCTTGTTAGTTTTATTAACCTCTAAATGGATTACATTAATTAATTAATGAATTA	2163
Db	16120	TAAATAAATCTTGTTAGTTTTATTAACCTCTAAATGGATTACATTAATTAATTAATGAATTA	16179
QY	2164	GTCGAAACATGAATAAACAGGTAACATGATAGATCATGTCAATGTGTATCATTTGATCTT	2223
Db	16180	GTCGAAACATGAATAAACAGGTAACATGATAGATCATGTCAATGTGTATCATTTGATCTT	16239
QY	2224	ACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTTGGATCCCTCTA	2283
Db	16240	ACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTTGGATCCCTCTA	16299
QY	2284	GA-----	2285
Db	16300	GAGAGCTGCAGCTGGATGGCAATAATGATTTTATTTTGATGATAGTGACCTGTTCGTT	16359
QY	2286	-----	2310
Db	16360	GCAACAAATTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGAACG	16419
QY	2311	AGAAACGTAAAAATGATATAAATATCAATATTAATTAATAGATTTTGCATAAAAACAGAC	2370
Db	16420	AGAAACGTAAAAATGATATAAATATCAATATTAATTAATAGATTTTGCATAAAAACAGAC	16479
QY	2371	TACATTAATCTGTPAAACACACATATCCAGTGCATATGAATCAACTACTTAGATGGTAT	2430
Db	16480	TACATTAATCTGTPAAACACACATATCCAGTGCATATGAATCAACTACTTAGATGGTAT	16539
QY	2431	TAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTTGGCCGCGAATAAT	2490
Db	16540	TAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTTGGCCGCGAATAAT	16599
QY	2491	ACCTGTGACGGAAGATCAGCTTCGACAGATTAATAAATCCTGGTGTCCCTGTTGATACGG	2550
Db	16600	ACCTGTGACGGAAGATCAGCTTCGACAGATTAATAAATCCTGGTGTCCCTGTTGATACGG	16659
QY	2551	GAAGCCCTGGCCCAACTTTTGGCCAAAATAGACGTTGATCGG-----	ATTTCAAA
Db	16660	GAAGCCCTGGCCCAACTTTTGGCCAAAATAGACGTTGATCGG-----	16719

Qy	2603	CCTTTATACCTTTTCTCTTAACAAGTCGTTCCGGCTTCACTCIGGAATTTTAGCCCTCTAFACTT	2662
Db	16720	CCTTTATACCTTTTCTCTTAACAAGTCGTTCCGGCTTCACTCIGGAATTTTAGCCCTCTATACTT	16779
Qy	2663	ACTAAACGTGATAAAGATTCTCTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTAT	2722
Db	16780	ACTAAACGTGATAAAGATTCTCTAAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTAT	16839
Qy	2723	AAGGAGCCTGCACATTTATATATCCCGAGAACAATCAGGTTAATGGCGTTTTTGATGTCAATT	2782
Db	16840	AAGGAGCCTGCACATTTATATATCCCGAGAACAATCAGGTTAATGGCGTTTTTGATGTCAATT	16899
Qy	2783	TTCGCGGTGGCTGAGATCAGCACATTTCTTCCCAGATAAACGAGACCGGCACACTGGCCCAT	2842
Db	16900	TTCGCGGTGGCTGAGATCAGCACATTTCTTCCCAGATAAACGAGACCGGCACACTGGCCCAT	16959
Qy	2843	ATCGGTGGTCAATCATCGGCCAGCTTTCATCCCGGATATGCAACCAGCGGTAAAGTTCAAG	2902
Db	16960	ATCGGTGGTCAATCATCGGCCAGCTTTCATCCCGGATATGCAACCAGCGGTAAAGTTCAAG	17019
Qy	2903	GGAGACTTTATCTGACAGCAGACGTGCACCTGGCCAGGGGGATCAACATCCGTCGCCCGGG	2962
Db	17020	GGAGACTTTATCTGACAGCAGACGTGCATGSCCAGGGGGATCAACATCCGTCGCCCGGG	17079
Qy	2963	CGTGTCAATAAATATCACTCTGTACATCCAACAACAGACGATAAACGGCTCTCTCTTTTATA	3022
Db	17080	CGTGTCAATAAATATCACTCTGTACATCCAACAACAGACGATAAACGGCTCTCTCTTTTATA	17139
Qy	3023	GGTGTAAACCTTAAACTGCAATTTACACAGTCCCTGTTCTCGTCAGCAAAAAGACGGTTCA	3082
Db	17140	GGTGTAAACCTTAAACTGCAATTTACACAGTCCCTGTTCTCGTCAGCAAAAAGACGGTTCA	17199
Qy	3083	TTTTCAATAAACCCGGCGGACCTCAGCCATCCCTTCTGTATTTTCCGCTTTTCCAGCGTTCCG	3142
Db	17200	TTTTCAATAAACCCGGCGGACCTCAGCCATCCCTTCTGTATTTTCCGCTTTTCCAGCGTTCCG	17259
Qy	3143	CACGCAGACACCGGGCTTCAATCTGCAATGGTGTGCTTACCAGACCGGAGATATTGACAT	3202
Db	17260	CACGCAGACACCGGGCTTCAATCTGCAATGGTGTGCTTACCAGACCGGAGATATTGACAT	17319
Qy	3203	CATATATGCCTTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTT	3262
Db	17320	CATATATGCCTTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTT	17379
Qy	3263	CATAGCACACCTCTTTTGGACATCTCTGTTCTTGATGCAGATGATTTTCCAGGACTATG	3322
Db	17380	CATAGCACACCTCTTTTGGACATCTCTGTTCTTGATGCAGATGATTTTCCAGGACTATG	17439
Qy	3323	ACA CTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTGTCACAAAAAGAGGCTCGCA	3382
Db	17440	ACA CTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTGTCACAAAAAGAGGCTCGCA	17499
Qy	3383	CCTCTTTTCTTATTTCTTTTATGATTTAATACGCCATTTAGGACAAATAGCGAGTAGGC	3442
Db	17500	CCTCTTTTCTTATTTCTTTTATGATTTAATACGCCATTTAGGACAAATAGCGAGTAGGC	17559
Qy	3443	TGGATACGACGATTCGGTTTGGAGAACAATTTGGAAAGCTGTTCGCTCGACTAAGTTGSC	3502
Db	17560	TGGATACGACGATTCGGTTTGGAGAACAATTTGGAAAGCTGTTCGCTCGACTAAGTTGSC	17619
Qy	3503	AGCATCACCCGAGAAACATTTGGAAAGCTGTTCGCTCGACTAAGTTGSC	3562
Db	17620	AGCATCACCCGAGAAACATTTGGAAAGCTGTTCGCTCGACTAAGTTGSC	17679
Qy	3563	AAGTAGTTGATTCATAGTGACTGGATATGTTGTTTTACAGTAAATATGTAAGTCTGTTTT	3622
Db	17680	AAGTAGTTGATTCATAGTGACTGGATATGTTGTTTTACAGTAAATATGTAAGTCTGTTTT	17739
Qy	3623	TTATCCAAAATCTAATTTAATATATGATTTATATATCATTTTACGTTTCTCGTTCAGCT	3682
Db	17740	TTATCCAAAATCTAATTTAATATATGATTTATATATCATTTTACGTTTCTCGTTCAGCT	17799
Qy	3683	TTTTTGTACAAACTTG-----	3698

17800	Db		TTTTGTGACAAAGTTGGCATTATAAAAAAGCATGCTCATCAATTTGTTGCAACGACAG	17859
3699	Qy	-----	-----TCTAGAG	3705
17860	Db		GTCACTATCAGTCABAAATAAAATCATTTATTTGGGGCCGAGATCCATGCTAGCTCTAGAG	17919
3706	Qy		TCTGTCTTTAATCAGATATGCGAGACGCTATGATCGCATGATATTTGCTTTTCAATCTCG	3765
17920	Db		TCTGTCTTTAATCAGATATGCGAGACGCTATGATCGCATGATATTTGCTTTTCAATCTCG	17979
3766	Qy		TTGTGCACGTTGTAAAAAACCTCAGCATGTGTAGCTCAGATCCTTACCCCGGTTTCGGT	3825
17980	Db		TTGTGCACGTTGTAAAAAACCTCAGCATGTGTAGCTCAGATCCTTACCCCGGTTTCGGT	18039
3826	Qy		TCATTTCTAATGAATATACACCGGTTACTATCGTATTTTATGAATAAATTTCTCCGGTTC	3885
18040	Db		TCATTTCTAATGAATATACACCGGTTACTATCGTATTTTATGAATAAATTTCTCCGGTTC	18099
3886	Qy		AAATTACTGATTTGTAACCTACTACTATATGTACAATATTAATAATGAAAAACAATATTTG	3945
18100	Db		AAATTACTGATTTGTAACCTACTACTATATGTACAATATTAATAATGAAAAACAATATTTG	18159
3946	Qy		TGCTGAATAGTTTTATAGACATCTATGATAGAGCGCCAAATPAACAACAAATTCGGTT	4005
18160	Db		TGCTGAATAGTTTTATAGACATCTATGATAGAGCGCCAAATPAACAACAAATTCGGTT	18219
4006	Qy		TTATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGA	4065
18220	Db		TTATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGA	18279
4066	Qy		TTACATAAATCTTATTCAAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGACACCCGA	4125
18280	Db		TTACATAAATCTTATTCAAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGACACCCGA	18339
4126	Qy		GCGGGAACATAACGTTCTACTGAAGGAACTCCGGTTCCCGCCGCGCGCATGGGTG	4185
18340	Db		GCGGGAACATAACGTTCTACTGAAGGAACTCCGGTTCCCGCCGCGCGCATGGGTG	18399
4186	Qy		AGATTCTTTGAAGTTGAGTATGGCCGTCGCTCTACCGAAGTTACGGGACCAATTCAA	4245
18400	Db		AGATTCTTTGAAGTTGAGTATGGCCGTCGCTCTACCGAAGTTACGGGACCAATTCAA	18459
4246	Qy		CCCGTCCAGACACGCGCGCGGTAAACGACTTGCTGCCCGAGAAATTTATCGACATTTT	4305
18460	Db		CCCGTCCAGACACGCGCGCGGTAAACGACTTGCTGCCCGAGAAATTTATCGACATTTT	18519
4306	Qy		TTTGTGTATGTGGGCCCAATGAAGTGCAGGTCAAAACCTTTGACAGTGCAGCAATTCG	4365
18520	Db		TTTGTGTATGTGGGCCCAATGAAGTGCAGGTCAAAACCTTTGACAGTGCAGCAATTCG	18579
4366	Qy		TTGGCGGGTCCAGGGCGAATTTTCGGCAACAATCTCGAGGCTCAGCAGGACCTTCGAGC	4425
18580	Db		TTGGCGGGTCCAGGGCGAATTTTCGGCAACAATCTCGAGGCTCAGCAGGACCTTCGAGC	18639
4426	Qy		ATGCAAGCTAGCTTACTAGTGTGATATTTCTATAGTGTCACTTAAATCTGC	4477
18640	Db		ATGCAAGCTAGCTTACTAGTGTGATATTTCTATAGTGTCACTTAAATCTGC	18691

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RESULT 7
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing
; efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055, 001A
; CURRENT FILING DATE: 2002-06-11
;

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

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Query Match	28.5%;	Score 1277.8;	DB 15;	Length 17458;
Best Local Similarity	62.4%;	Pred. No. 1e-183;		
Matches 2321;	Conservative	0;	Mismatches 1312;	Indels 86; Gaps 17;
QY	21	CTCGAGACAAGTTGTTGACAAAAAGCTGAACGAGAAACGTAAATAATGATATAAAATATCAAT	80	
Db	16686	CTCTAGACAAGTTGTTGACAAAAAGCTGAACGAGAAACGTAAATAATGATATAAAATATCAAT	16627	
QY	81	ATATTAAATTAGATTTTGCATAAAAAAGAGACTCAATAAATCTGTTAAAAACAAACATATC	140	
Db	16626	ATATTAAATTAGATTTTGCATAAAAAAGAGACTCAATAAATCTGTTAAAAACAAACATATC	16567	
QY	141	CAGTCATATGAATCAACTACTTAGATCGGTATTTAGTGACCTGTAGTCGACGACAGCGCTT	200	
Db	16566	CAGTCATATGAATCAACTACTTAGATCGGTATTTAGTGACCTGTAGTCGACGACAGCGCTT	16507	
QY	201	CCAAATGTTCTTCGGGTGATGCTGCCAACTAGTCGACGACAGCGCTTCCAAATGTTCTT	260	
Db	16506	CCAAATGTTCTTCGGGTGATGCTGCCAACTAGTCGACGACAGCGCTTCCAAATGTTCTT	16447	
QY	261	CTCAACGGGAATCGTCGTATCCAGGCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA	320	
Db	16446	CTCAACGGGAATCGTCGTATCCAGGCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA	16387	
QY	321	TAAAAAGAAATAGAAAAAGAGGTGGAGCGCTCTTTTTGTGTGACAAAAATAAAAAATC	380	
Db	16386	TAAAAAGAAATAGAAAAAGAGGTGGAGCGCTCTTTTTGTGTGACAAAAATAAAAAATC	16327	
QY	381	TACCTATTCAATACGCTAGTGTCTAGTCCTGAAATATCATCTGCATCAAGAAACAAATTC	440	
Db	16326	TACCTATTCAATACGCTAGTGTCTAGTCCTGAAATATCATCTGCATCAAGAAACAAAGT	16267	
QY	441	ACAACTCTTATATCTTTCTCTTACAAAGTCGTGGGCTTCATCTGATTTTCAGCCTCTAT	500	
Db	16266	ATGTCAAAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGACA	16210	
QY	501	ACTTACTAAACGATGAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGT	560	
Db	16209	GCTATCATGTCTCAAGGCATATATGATGCAATATCTCCGGTCTGGTAAAGCAACCAT	16150	
QY	561	GTATAAGGAGGCTGACATTTATATCCCCAGAAACATCAGGTTAATGGCGTTTTTGATGT	620	
Db	16149	GCAGAAATGAAGCCGTCGTCTGGTGCC---GAAACGCTGAAAGCGGAAATCAGAAAGG	16093	
QY	621	CATTTTCGGGTGGCTGAGATCAGCACCTTCTTCCCGGATACGAGAGACCGCACACTGG	680	
Db	16092	GATGGCTGAGGTGCGCCCGGTTTATTGAATGAACCGCTCTTTTGTCTGACGAGAACAGG-	16034	
QY	681	CCATATCGGTGCTCATCATGGCCAGGTTTCATCCCGGATATGCACCCGGGTAAAGTT	740	
Db	16033	-----ACTGGTGAATGCAGTTTAAGGTTTACACCTATATAAGAGAGAGCCGTTATCGTC	15979	
QY	741	CACGGGACACTTTATCTGACAGCAGCGTGCACTGGCCAGGGGGATCACCATCCGTCGCC	800	
Db	15978	TGTTTGTGGATGTCAGAGTGATATTATGACACGCCCGGGCGACGGATGGTGATCCCC	15919	
QY	801	CGGGCGGTGCAATAATATCATCTGTGTACATCCCAAAACAGACGATAACGGCTCTCTTT	860	
Db	15918	TGCCAGTGCACGTCTGCTGCATAAAGTCTCCGTGAACCTTACCCTGGGTGGTCATA	15859	
QY	861	TATAGGTGAAACCTTAACTGCAATTTACG-----AGTCCCTGTTCTTCGTACAGAAA	914	
Db	15858	TGGGGATCAAGCTGGCGCATGATGATACCAACCGATATGGCCAGTGTGCCCGTTCGGTTA	15799	

QY 915 GAGCGTTTCATTTCAATAAACCAGGCGGACCTCAGCCATCCCTTCTGTATTTTCGCTTTC 974
Db 15798 TCGGGGAAGAGTGGCTGATCTCAGCCACCGCGAAATGACATCAAAACGCCATTAACC 15739
QY 975 CAGCGTTTC- --GGCAGCGAGACGAGCGGCTTCATTCTGCATGGTGTGCTTACCAGACCG 1031
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QY 1032 GAGATATTGACATCATATATGCTTGTAGCAACTGATAGTGTGCTGTCAACTGTCACTG 1091
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QY 1092 TAAATGCTGCTTTCATAGCACACCTCTTTTGACATACCTCGGAGTG- ---CGATCA 1147
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QY 1148 AGCTCTCATTTTCGCCAAAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACCGA 1207
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QY 1388 TTTAATATATGATATTTATATATTTATAGTTTCTGTTCTGCTTCTGTTCTGTTTACAAAGT 1447
Db 15327 TTTAATATATGATATTTATATTTATAGTTTCTGTTCTGTTCTGTTTCTGTTTACAAAGT 15268
QY 1448 GTCTCAGGAATTCGGTACCCAGCTTGGTAAGGAAATTAATTTATTTCTTTTCTTTT 1507
Db 15267 GTCTCAGGA- -TCCAGCTTAAGTAAAGTAACTG- -TAATCAATCAATGTAAGATCA 15212
QY 1508 AGTATAAATAGTAAAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAAT 1567
Db 15211 ATGATAACAAATGACATGATCATCATGTTTACCTGTTTATTCATGTTTCGACTAATCA 15152
QY 1568 GTGAAAAATATTTAATAATATTTGTTTACATATAACACATAGTAAATGTAABAAATA 1627
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QY 1628 TGCAAGTGTATGTAAGACGAAGATAAAAAGTTGAGAGTAAAGTATATTTTAAAT 1687
Db 15091 ATAAGAAATGTTGATTGAAATATACTATATAAATGATAGATCTTGGCTTTGTTATAT 15032
QY 1688 GAAATTTGATCGAAATGTAAGATGATAATAGTAAATATTTGTTTAACTAATAG 1747
Db 15031 TAGCAATTAGATATGTTTGTATCAATTAGATTAATCTGTTTCTATTTAGTATTTATG 14972
QY 1748 TAATTTAGCTGTTTGTAGTAATTAATATCAATGATAAATACTATAGTAAATAAAGA 1807
Db 14971 TTACTTTAGCTGTTATTTAATATTTTGTATTGATAAATTAACACAGATTTGGAATTT 14912
QY 1808 ATAATAAATTAATAATATTTTATGATTAATAGTTTATTTATATAATAATAATCT 1867
Db 14911 CTAACAAAATATTTATTAACCTTTAABACTAAAATTTAGTAAATGATAGATTTAAT 14852
QY 1868 ATACCAATTAATAATATTTAGTTTAAAGTAAATAATTTGTTAGAAAATCCAAATC 1927
Db 14851 TATATAATAACTATTAATCATATAAAAAATAATTTAATTTAATTTATTTATTTTATTTA 14792
QY 1928 TGCTTGAATTTATCAATAAACAATAATTAATAAAGTAAAGTAAAGTAAAGTAAAGTAAATC 1987
Db 14791 CTATAGTATTTTATCATTTGATATTTAATTTCAACACAGCTAGAAATTTATTTATGATT 14732

QY 1988 AAACCTAATAGAAAACAGTAATCTAATGTACAAAACATAAATCTAATGTAAATAAACAAAG 2047
Db 14731 AAAACAAATTAATAGTGTATATCATCTTACATGTTTCGATCAAAATTCATTAATAATAA 14672
QY 2048 CGAAGATCTATCATTTTATATATAGTATTTTCAATCAACATTTCTTATTAATTTCTTAAA 2107
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Db 14611 ATTACTATGTTTGTATGTAACAAATATATTTAATAATTTATTTTTCACAAATTAACAA 14552
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QY 2288 ACTTTGTACAAGAAAGCTGAAACGAGAAACGTAATAATGATATAATAATCAATATATTAAT 2347
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QY 2348 TAGATTTTGCATAAAAAACAGACTACATACTATCTGTGTAACACACACATATCCAGTCACTA 2407
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QY 2468 GACGCACTTTTGGCCGAATAAATACTGTGACGGAAGATCACTTCGCAAGATAAATAAT 2527
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QY 2708 AGACTGG- -----CTGTGTATAGGAGCCTGCATTTATATTTCCCGAAGACATCAG 2758
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QY 2759 GTTAATGGCGTTTGTATGTCATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGGAT 2818
Db 13972 AAAGCGAAAAATCAGGAAGGATGGCTGAGGTGCGCCCGGTTTATTTGAAATGAACGGCTCT 13913
QY 2819 AACGGAGAACGGCACACTCGGCCATATCGGTGTGTCATCATGCGGCAGCTTTCATCCCGGAT 2878
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QY 2879 ATGCACACCGGGTAAAGTTTCAGGGAAGCTTTATCTGACAGCAGACGTCGACTGGCCAG 2938
Db 13858 AAGAGAGACCGGTATTCGTTCTGTTGTGGAATGTAACAGATGATTTATTTGACACGCCCGG 13799
QY 2939 GGGGATCAACCATCCGTCGCGCCGGCGTGTCAATAATATCACTCTGTACATCCCAAAACAG 2998
Db 13798 GCGACGATGGTGTATCCCTTGGCCAGTGCACGCTGCTGTGTGATGATAAAGTCTCCCGTGA 13739
QY 2999 ACATTAACCGCTCTCTCTTTTATAGGTGTAACCTTAAACTGATTTTAC- -----AGT 3052
Db 13738 ACTTTACCGGTTGGTCATATCGGGATGAAGAGCTGGCGCATGATGACCAACCGATATGGC 13679
QY 3053 CCCTGTTCTCGTCAGCAAAAGACCGCTTTCATTTCAATAAACCGGCGGACCTCAGCCATCC 3112

Db	13678	CAGTGTGCGGCTCTCCGTTATTCGGGGAAGAGTGGCTGATCTAGCCACCGCGAAATGA	13619
Qy	3113	CTTCTGATTTTCGGCTTTCCAGCGTTCC--GGCAGCGAGACGAGCGGCTTCATTTCTGCA	3169
Db	13618	CATCAAAACGGCATTAACCTGATGTTCTGGGAATATAAATGTCAGGCTCCCTTATACA	13559
Qy	3170	TGG---TTGTGCTTACCCAGACGGGAGATATTGACATCATATATGCTTGAGCAACTGATA	3226
Db	13558	CAGCCAGCTGCGAGTCCGATACAGTAGAAATATACAGAACTTTATCACGTTTAGTAAGTA	13499
Qy	3227	GCTGTGCGCTGCAACTGTCTGATGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA	3286
Db	13498	TAGAGGCTGAATAATCCAGATGAAGCCGACGACTTGTGAAGAAAGTATGAAGTTGTG	13439
Qy	3287	CTTCTGTTCTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAG	3346
Db	13438	AAATTTGTTCTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAG	13379
Qy	3347	ATGTTTATTTTGTGCACAAAAAGAGGCTGCGACCTCTTTTCTTATTTCTTTTAT	3406
Db	13378	ATGTTTATTTTGTGCACAAAAAGAGGCTGCGACCTCTTTTCTTATTTCTTTTAT	13319
Qy	3407	GATTTAATACGCAATGAGGACAAATAGCGAGTAGGCTGGATACGAGATTCGGTTTGAGA	3466
Db	13318	GATTTAATACGCAATGAGGACAAATAGCGAGTAGGCTGGATACGAGATTCGGTTTGAGA	13259
Qy	3467	AGAACTTTGGAGGCTGTCGTCGACTAAGTTGGCAGCATCACCCGAAAGACATTTGGA	3526
Db	13258	AGAACTTTGGAGGCTGTCGTCGACTAAGTTGGCAGCATCACCCGAAAGACATTTGGA	13199
Qy	3527	AGGCTGCGTGCAGTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGG	3586
Db	13198	AGGCTGCGTGCAGTACAGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGG	13139
Qy	3587	ATATGTTGTTTACAGTATATGATGCTGTTTTTATGCAAAATCTAAATTAATATA	3646
Db	13138	ATATGTTGTTTACAGTATATGATGCTGTTTTTATGCAAAATCTAAATTAATATA	13079
Qy	3647	TTGATATTATATCATTTTACGTTTCTCGTTAGCTTTTGTACAAACTGTCTAGAG	3705
Db	13078	TTGATATTATATCATTTTACGTTTCTCGTTAGCTTTTGTACAAACTGTCTAGAG	13020

RESULT 8

US-10-055-001A-24/c

Sequence 24, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Waterhouse, Peter

APPLICANT: Hellmuth, Christopher A. for producing efficient silencing constructs

TITLE OF INVENTION: Method and means for recombinational cloning

FILE REFERENCE: HELIGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 24

LENGTH: 17476

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: acceptor vector pHELLSGATE8

US-10-055-001A-24

Query Match 28.4%; Score 1273; DB 15; Length 17476;

Best Local Similarity 62.1%; Pred. No. 5.5e-183;

Matches 2316; Conservative 0; Mismatches 1325; Indels 88; Gaps 16;

Qy 21 CTCGAGACAAAGTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAAT 80

1148 ACCTCTCAATTTTCGCCAAAAGTTGGCCACGGCTTCCCGGTATCAACAGGACACACAGGA 1207
15585 ACCTCTCAATTTTCGCCAAAAGTTGGCCACGGCTTCCCGGTATCAACAGGACACACAGGA 15526
1208 TTATTTATTTCTCGGAAGTGAATCTTCGGTCAAGGTATTTATTTTCGGCGCAAGTGGGTGG 1267
15525 TTATTTATTTCTCGGAAGTGAATCTTCGGTCAAGGTATTTATTTTCGGCGCAAGTGGGTGG 15466
1268 GGTGATGTCGCCAACTTAGTCGACTACAGGTCACTTAATACCATCTAAGTAGTTGATTCAT 1327
15465 GGTGATGTCGCCAACTTAGTCGACTACAGGTCACTTAATACCATCTAAGTAGTTGATTCAT 15406
1328 AGTGACTGGATATGTTGTGTTTACAGTATTTATGTAGTCTGTGTTTATGCAAAATCTAA 1387
15405 AGTGACTGGATATGTTGTGTTTACAGTATTTATGTAGTCTGTGTTTATGCAAAATCTAA 15346
1388 TTATAATATATGATATTTATATCATTTTACGTTTCTCGTTACGTTTCTTGTTGTAACAAGTG 1447
15345 TTATAATATATGATATTTATATCATTTTACGTTTCTCGTTACGTTTCTTGTTGTAACAAGTG 15286
1448 GTCTCGAGGAATTCGGTACCCAGCTTGGTAAGAAA-----TAATTTATTTCTT 1497
15285 GTCTAGAGATCCAGCTTATCGATTTTCGAACCCAGCTTCCCAACTGTAATCAATCCAAA 15226
1498 TTTTCCCTTTAGTATAAAATAGTTAAGTGAAGTGAATTTAGTATGATTAATTAATATAGT 1557
15225 TGTAAAGATCAATGATACACAATGACATGATCTATCATGTTACCTGTTTATTCATGTTTC 15166
1558 TGTATAATTTGTGAAAAAATATTTATTAATATATTTGTTTACATAAACAATAGTAATG 1617
15165 GACTAATTCATTAATTAATAGTCAATCCATTTAGAAAGTTTAATAAACTACAAGTATAT 15106
1618 TAAAAAATATGACAAGTATGTTGAAGACGAAGATAAAGTTGAGAGTAAGTATAT 1677
15105 TTAGAATTAATAGAATGTTGATTTGAATATATCTATTAATAAAGATAGATCTTGGCG 15046
1678 TATTTTAAAGATTTGATCGAACATGTAAGATGATATATAGCAATTAATTAATTTGTTTTA 1737
15045 TTTGTTATATAGCAATTAGATATGTTTGTACATATAGATTTACTGTTCTATAGTTTG 14986
1738 ATCATATATGATTTCTAGCTGTTTGAATCAATTAATTAATCAATGATTAATTAATAGT 1797
14985 ATATTTTCTGTTACTTTAGCTTGTATTTTAATATTTTGTGTTATTTGAATAATCAAGCAG 14926
1798 AAAAATAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1857
14925 ATTGGAATTTCTAACAAAATATTTAATACTTTTAACTAATAATTTAGTATGTTAT 14866
1858 TTAATAATCTATACCAATTAATAATTTTAAAGTTTAAAGTTTAAATAATTTTGTGTA 1917
14865 GATAATTTAATATATAAATACTTAATCAATAAATAAATAAATAAATAAATAAATAAATA 14806
1918 AATTCCAACTCGCTGTGTAATTTATCAATAAACAATAAATAAATAAATAAATAAATAAATA 1977
14805 CTATTTTACTATAGTATTTTATCATGATATTTAATCATCAACACAGCTAGATTTAC 14746
1978 AAATAATATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACATAAATCTAATGCTAA 2037
14745 TATTATGATTAAACAATAATTAATGCTAGTATATCATCTTACATGTTCCGATCAAAATCA 14686
2038 TATAACAAGCGCAGATCTATCATTTTATATAGTATATTTTCAATCAACATTTCTTAT 2097
14685 TTAATAAATAATATACCTTACTCTCAACTTTTATCTTCTCTCTCTCTCTCTCTCTCTCTCT 14626
2098 AATTTCTAAATAATATCTAGTTTATTAACITCTTAATGATTTGACTATTAATTAAT 2157
14625 ATTTTTTACATTAATGATGTTTATGTAACAAATATATTTAATAATTTTTTTCACA 14566
2158 GAATTTAGTCGAACATGAATAAACAAGGTAACATGATAGATCATGTCATTTGTTATCAT 2217
14565 ATTATACAACTATATTTATATATATCATCTAATTAACATCACTTAACATTTTATACTA 14506

2218 GATCTTACATTTTGGATTGATTACAGTTTGGGAAGCTGGTTTGGAAATCGATAAGCTTGGAT 2277
14505 AAGGGAATAAAGAAATAATTAATTT-----TCTTACCAGCTGGGTACCGAAT 14456
2278 CTTCTAGACCACTTTGTACAGAAAAGCTGAAACGAGAAAAGCTAAATATATATAATCA 2337
14455 CTTCTAGACCACTTTGTACAGAAAAGCTGAAACGAGAAAAGCTAAATATATATAATCA 14396
2338 TATATTAATTAATAGATTTTGCATAAATAAACAAGTACATATATCTGTAAACAACATAT 2397
14395 TATATTAATTAATAGATTTTGCATAAATAAACAAGTACATATATCTGTAAACAACATAT 14336
2398 CCAGTCACTATGAATCAACTACTTATAGTGTATTTAGTACCTGTAGTCCAGTAAAGTTGGC 2457
14335 CCAGTCACTATGAATCAACTACTTATAGTGTATTTAGTACCTGTAGTCCAGTAAAGTTGGC 14276
2458 AGCATCACCCGAGCACTTTTGGCCGAATAAATACCTGTGACGGAAGATCATCTTCGAGA 2517
14275 AGCATCACCCGAGCACTTTTGGCCGAATAAATACCTGTGACGGAAGATCATCTTCGAGA 14216
2518 ATAAATAAATCCTGTGTCTCTGTTGATACCGGAAGCCCTGGCCAACTTTTGGGAAA 2577
14215 ATAAATAAATCCTGTGTCTCTGTTGATACCGGAAGCCCTGGCCAACTTTTGGGAAA 14156
2578 ATGAGACGTTGATCGGATTTCAAACTTTATATCTTTCTTTACAAGCTGTTTCGGCTTC 2637
14155 ATGAGACGTTGATCGG-----CACTACCCGAAGTATGTCAAAAAGAGGTGTGCTATGAAGC 14100
2638 ATCTGGAATTTTCACTCTATATCTTAAACGTAATAAGTTTCTGTAAATTTCTACTGT 2697
14099 AGCGTATTAACAGTACAGTGTGACGACAGCTATCAGTTGCTCAAGGCATATATGATGT 14040
2698 ATCGACCTCGACAGCTGG-----CTGTGATTAAGGAGCCTGACATTTATATTCCTCC 2748
14039 CAATATCTCGGTCTGTGTAAGCAACCAATGCAAGATGAAGCCGCTGCTGCGTGC-- 13982
2749 AGAACATCAGGTTAATGCGGTTTTTGTATCTATTTTTCGCGTGGCTGAGATCAGCCACT 2808
13981 -GAACGCTGGAAGCGGAAATCAGGAAGGATGGCTGAGTCCGCGGTTTATTGAAAT 13923
2809 CTTCCCGGATACGGAGACGGCAGCACTGGCCATATCGGTGCTCATCATCGCCAGCTTT 2868
13922 GAACGCTCTTTTGTGTAAGCAACAGG-----ACTGGTGAATGCAAGTTTAAGGTTT 13869
2869 CATCCCGGATATGCAACACCGGTAAGTTTACGGGAGACTTTATCTGACAGCAGACGTG 2928
13868 ACACCTATAAAGAGAGAGCGGTTATCGTCTGTTGTGATGTACAGAGTATATTTG 13809
2929 CACTGGCCAGGGGATCACCATCCGTCGCCCGCGGTGTCAATAATATCATCTGTACAT 2988
13808 ACACGCCGGGCGACGGATGGTGTATCCCGCTGGCCAGTGCAGTCTGTGTGATATAAG 13749
2989 CCACAACAGAGCATTAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAITTCAC 3048
13748 TCTCCCGTGAACCTTTACCCGGTGTGATATCGGGATGAAGAGCTGGCCATGATGACCA 13689
3049 C-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTTCAITTCATAATAACCGGCGACC 3102
13688 CCGATATGCCAGTGTGCCGGTCTCGTTATCGGGGAAGAGTGGCTGATCTCAGCCACC 13629
3103 TCAGCCATCCCTTCTGATTTTTCGGCTTTCCAGCGTTC---GGCAGCAGACGAGCGGT 3159
13628 GCGAAAATGACATCAAAAACGCGCATTAACCTGATGTTCTGGGGAATATAAATGTGAGGT 13569
3160 TCATTTCTGATG---TTGTGCTTACCAGCCGAGATATTGACATCATATATGCTTCA 3216
13568 CCGTTATACAGCCCGAGCTGCGAGTGCAGTAGAATAATACAGAAATTTATCACT 13509
3217 GCAACTGATAGCTGTGCTGTCAACTGTCACTGTATACGCTGTCTATAGCACACCTCT 3276
13508 TTAGTAAGTATAGAGGCTGAAAATCCAGATGAAGCCGACGACTTGTAGAGAAAGTAT 13449
3277 TTTTGACATACTTCTGTTCTGATGAGATGATTTTTCAGGACTATGACACTAGCGTATAT 3336

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Db 13448 AAGAGTGTGAAATGTTCTTTGATGCGAGATGATTTTCAGGACTATGACACTAGCGGTATAT 13389
Qy 3337 GAATAGGTAGATGTTTATTTATTTTGTACACAAAAAGAGGCTCGCACCCTCTTTTCTTTAT 3396
Db 13388 GAATAGGTAGATGTTTATTTTGTACACAAAAAGAGGCTCGCACCCTCTTTTCTTTAT 13329
Qy 3397 TTTCTTTTATGATTTAATPACGGCATTTAGGACAATAGCGAGTAGGCTGGATACGACGATT 3456
Db 13328 TTTCTTTTATGATTTAATPACGGCATTTAGGACAATAGCGAGTAGGCTGGATACGACGATT 13269
Qy 3457 CGTTTGTAGAGACAACTTGGAGGCTCGGTGACCTAAAGTTGGCAGCATCACCCGAAG 3516
Db 13268 CGTTTGTAGAGACAACTTGGAGGCTCGGTGACCTAAAGTTGGCAGCATCACCCGAAG 13209
Qy 3517 AACATTTGGAAGGCTGTCGGTGCAGTACAGGTCACCTAAATCAATCAATCAATCAATCAATCA 3576
Db 13208 AACATTTGGAAGGCTGTCGGTGCAGTACAGGTCACCTAAATCAATCAATCAATCAATCAAT 13149
Qy 3577 TAGTGACTGGATATGTTGTTTGTATGATTTTACAGTATATGATGATGATGATGATGATGATGAT 3636
Db 13148 TAGTGACTGGATATGTTGTTTGTATGATTTTACAGTATATGATGATGATGATGATGATGATGAT 13089
Qy 3637 ATTTAATATATGATATTTATATATATATATATATATATATATATATATATATATATATATAT 3696
Db 13088 ATTTAATATATGATATTTATATATATATATATATATATATATATATATATATATATATATAT 13029
Qy 3697 TGTCTAGAG 3705
Db 13028 TGTCTAGAG 13020

RESULT 9
US-10-385-546-7/c
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Helliwell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7

Query Match 28.4%; Score 1273; DB 15; Length 17476;
Best Local Similarity 62.1%; Pred. No. 5.5e-183;
Matches 2316; Conservative 0; Mismatches 1325; Indels 88; Gaps 16;

Qy 21 CTCGAGACAAAGTTGTACAAAAAGCTGAACGAGAAACGTPAAATGATATATAATCAAT 80
Db 16704 CTCTAGACAGTTTGTACAAAAAGCTGAACGAGAAACGTPAAATGATATATAATCAAT 16645
Qy 81 ATATTAATTAGATTTTGCATATAAAAAACAGACTACATAATCTGTATAAACACAACTATC 140
Db 16644 ATATTAATTAGATTTTGCATATAAAAAACAGACTACATAATCTGTATAAACACAACTATC 16585
Qy 141 CAGTCATATGAATCACTACTTAGATGGTATTTAGTACCTGTAGTACCGGACGCGCTT 200
Db 16584 CAGTCATATGAATCACTACTTAGATGGTATTTAGTACCTGTAGTACCGGACGCGCTT 16525
Qy 201 CCAATGTCTCTCGGGTGTGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTCTT 260
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Db 16524 CCAATGTCTCTCGGGTGTGCTGCCAACTTAGTCGACCGACAGCCCTTCCAAATGTCTT 16465
Qy 261 CTCAAACGGGAATCGTGTATCCAGCCCTATCTCGCTATTTGTCTCAATGCCCTTATAATCA 320
Db 16464 CTCAAACGGGAATCGTGTATCCAGCCCTATCTCGCTATTTGTCTCAATGCCCTTATAATCA 16405
Qy 321 TAAAAAGAAATAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAATAAAAAATC 380
Db 16404 TAAAAAGAAATAGAAAAAGAGGTGGAGGCTCTTTTGTGTGACAAAAATAAAAAATC 16345
Qy 381 TACCTATTCATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAATATTC 440
Db 16344 TACCTATTCATATACGCTAGTGTCTGATAGTCTGAAAAATCATCTGCATCAAGAAATATTC 16285
Qy 441 ACAACTCTTATATCTTTTCTCTTCAAGTGTGTGGCTTCATCTGGATTTTCAGCCCTCAT 500
Db 16284 ATGTCAAAAAAGAGGTGTCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCA 16228
Qy 501 ACTTACTAAACGCTGATATAAGTTTCTGTAAATTTCTACTGTATCGACCTGCAGACTGGCTGT 560
Db 16227 GCTATCAGTTGCTCAAGGCAATATGATGATCAATATCTCCGGTCTGGTACAGCAACCAT 16168
Qy 561 GTATAAGGAGGCTGACATTTATATCCCGAAGACATCAGGTTAATGGCGTTTGTGATGT 620
Db 16167 GCAGATGAAGCCCGTCTGTCTGCGTGC---GAACGCTGGAAGCGGAAATCAGGAAG 16111
Qy 621 CATTTTCGGGTGGCTGAGATCAGCCACTTCTCCCGGATTAACCGAGACCGGACACTGG 680
Db 16110 GATGGCTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCTTTTGTACGAGAAACAGGG- 16052
Qy 681 CCATATCGGTGTCATCATGCGCCAGCTTTCATCCCGATATGCACACCCGGTAAAGTT 740
Db 16051 -----ACTGGTGAATGCAGTTTAAAGTTTACACCTATAAAGAGAGAGCGCTTATCGTC 15997
Qy 741 CACGGGAGACTTTATCTGACAGACAGTGTGACCTGCGCCAGGGGATCACCATCCGTCGCC 800
Db 15996 TGTTTGTGGATGTACAGAGTGATATTATGACAGCCCGCGGACGGATGGTGTATCCGCC 15937
Qy 801 CGGGGTGTCAATAATATCATCTGTATATCCAAACAGACAGATACGGGTCTCTCTTT 860
Db 15936 TGGCCAGTGCACGCTGCTGTGACATAAAGTCTCCCGTGAACCTTTACCCGGTGTGCA 15877
Qy 861 TATAGTGTAAACCTTAAACTGCAATTCACCC-----AGTCCCTGTTCTCGTCAGCAAAA 914
Db 15876 TCGGGGATGAAGCTGCGCGCATGATGACCAACGATATGCCAGTGTGCGGTCTCCGTTA 15817
Qy 915 GAGCCGTTTCAATTAATAAACCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTC 974
Db 15816 TCGGGGAAGAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAAACGCCATTAACC 15757
Qy 975 CAGCCGTTTC---GGCAGCAGACGAGCGGCTTCATCTGATGTTGTGCTTACCAGACCG 1031
Db 15756 TGATGTTCTGGGGAATATAAATGTGAGGCTCCCTTATACAG-----CCAGTCTG 15706
Qy 1032 GAGATATTGACATCATATATGCTTGTGACCACTGATAGTGTGCTGTCAACTGTCAGT 1091
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Qy 1092 TAAATAGCTGTCTTATAGCAGACCTCTTTTGTACATCTCTGGGTAGTG---CCGATCA 1147
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Db 15585 AGTCTCTATTTTCGCCAAAAAGTTGGCCAGGCTTCCCGGTATCAACAGGACACAGGA 15526
Qy 1208 TTTATTTATTCGGAAGTGTCTTCCGTCAAGGTATTTATTCGCGCAAAAGTCCGTG 1267
Db 15525 TTTATTTATTCGGAAGTGTCTTCCGTCAAGGTATTTATTCGCGCAAAAGTCCGTG 15466
Qy 1268 GGTGATGTGCCAACTTAGTGTGACCTATAGTGTCACTTAATCACTTAAAGTAGTGTATCAT 1327
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Db 15465 GGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATTCAAGTAGTTGATTCAT 15406
Qy 1328 AGTGACTGATGATGTTGTTTACAGTATATATAGTCTGTTTATATGCGAAATCTTAA 1387
Db 15405 AGTGACTGATGATGTTGTTTACAGTATATATAGTCTGTTTATATGCGAAATCTTAA 15346
Qy 1388 TTTAATATATGATATTTATATACATTTTACGTTTCTCGTTTACGTTTCTTGTGACAAAGTG 1447
Db 15345 TTTAATATATGATATTTATATACATTTTACGTTTCTCGTTTACGTTTCTTGTGACAAAGTG 15286
Qy 1448 GTCTCGAGGAATTCGGTACCCGAGCTTGGTAAGGAAA-----TAATATTTTCTT 1497
Db 15285 GTCTAGAGGATCCAAAGCTTATCGATTTGAAACCCAGCTTCCCAACTGTAATCAATCCAAA 15226
Qy 1498 TTTTCTCTTTTGTATATATATATAGTATAGTATGATGTTTAAATAGTATGATATATATATAGT 1557
Db 15225 TGTAGATCAATGATATACCAATGATGATGATCTATCATGTTTACCTTGTGTTTATTCATGTTTC 15166
Qy 1558 TGTATATATGTAAGAAATATTTTATATATATATTTTATATATATATTTTATATATATATATAT 1617
Db 15165 GACTAATTCATTTAT 15106
Qy 1618 TAAAAAATATATGAAAGTATGATGTTAAGAGCAAGAAAGATAAAGTTGAGAGTAAGTATAT 1677
Db 15105 TTAGAAATTAATAGAAATGTTGATTCGAAATAATATCTATATATAATATGATAGATCTTGGCG 15046
Qy 1678 TATTTTATGATTTGATCGACATGTAAGATGATATATAGTATATATATATATATATATATATATAT 1737
Db 15045 TTTGTTATATATAGCATATAGATATATGTTTGTTCATTTAGATATATCTGTTTCTATATAGTTTG 14986
Qy 1738 ATCATATATAGTAATTTCTAGCTGTTTGTATGAAATTAATATATCAATGATATATATATATATAT 1797
Db 14985 ATATATTTGTTACTTTAGCTTGTATTTATATATATTTGTTTATGATATATATATATATATAT 14926
Qy 1798 AAAAAATAGAAATTAAT 1857
Db 14925 ATGGAATTTCTAAACAAATATTTATATATATTTTAAACTAAAAATATTTAGTATATATATAT 14866
Qy 1858 TTTAAATATCTATACCATATATATATATATATTTTATGTTTAAAGTTATATATATATATATATAT 1917
Db 14865 GATATTTAAT 14806
Qy 1918 AATTCCAATCTGCTGTGTAATTTATCAATAAACAATAATTTATTAATAACAAGCTAAAGTAAC 1977
Db 14805 CTATTTTATCTAT 14746
Qy 1978 AATAATATCAAACTAATAGAAACAGTAATCTAATGTAAACAATAATCTAATGTAA 2037
Db 14745 TATATGATTTAAACAATAATATATATGCTAGTATATATATCTTATCATGTTTGGATCAAAATTC 14686
Qy 2038 TATAACAAGCGCAAGATCTATCATTTTATATATATATATATATATATATATATATATATATAT 2097
Db 14685 TTTAAATAAT 14626
Qy 2098 AATTTCTAAATAAT 2157
Db 14625 ATTTTTTATCAT 14566
Qy 2158 GAATTAGTGAACATGAAATTAACAAGGTAAATGATGATGATGATGATGATGATGATGATGAT 2217
Db 14565 ATTATAACAAT 14506
Qy 2218 GATCTTACATTTGGATTTGATTTACAGTTGGGAGCTGGGTTTCAAAATCGAATGCTTGGAT 2277
Db 14505 AAAGGAAAAAAGAAATATATATTT-----TCCTTACCAAGCTGGGGTACCGAAT 14456
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Db 14455 CCTCGAGACCACTTTGTACAGAAAGCTGTAACGAGAAACGTAAAAATGATATATATATATATAT 14396
Qy 2338 TATATTAATATAGATTTTGTAT 2397
Db 14395 TATATTAATATAGATTTTGTAT 14336

Qy 2398 CCAGTCACTATGAAATCAACTACTTAGATGTTATAGTACCTGTAGTACGACTTAAGTTGGC 2457
Db 14335 CCAGTCACTATGAAATCAACTACTTAGATGTTATAGTACCTGTAGTACGACTTAAGTTGGC 14276
Qy 2458 AGCATCACCCGACGCACTTTGGCGCGAATAAATACCTGTGACGGAAGATCATCTTCGAGA 2517
Db 14275 AGCATCACCCGACGCACTTTGGCGCGAATAAATACCTGTGACGGAAGATCATCTTCGAGA 14216
Qy 2518 ATAAATAATCTGTGTGTCCTGTGTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAA 2577
Db 14215 ATAAATAATCTGTGTGTCCTGTGTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAA 14156
Qy 2578 ATGAGACGTTGATCCGATTTTCAAACTCTTATATCTTTTCTTTTCTTACAAGTCGTTCCGCTTC 2637
Db 14155 ATGAGACGTTGATCGG-----CACTACCCGAAATGATGTCAAAAAGAGGTGTCTATGAAGC 14100
Qy 2638 ATCTGGATTTTCAGCTCTATATCTTACTAAACGATGATAAGTTTCTGTAAATTTCTACTGT 2697
Db 14099 AGCGTATTACAGTGCAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATATGATGT 14040
Qy 2698 ATCGACCTGCAGACTGG-----CTGTGTATAGGAGCTGACATTTATATTCCTCC 2748
Db 14039 CAATATCTCCGTCTGGTTAAGCACACCAACATGAGAAATGAAAGCCGCTGCTGGTGCC-- 13982
Qy 2749 AGAAATCATAGGTTAATGGCGTTTGTGATGTCTATTTTCGCGTGGTGTGAGATCAGCCACTT 2808
Db 13981 -GAAAGCTGAAAGCGGAAATCAGGAAGGATGGCTGAGGTCCGCGGTTTATTGAAAT 13923
Qy 2809 CTTTCCCGATTAAGAGAGACCGGACACTGGCCATATCGTGTGTGATCATGATCGCCAGCTTT 2868
Db 13922 GAAGCGCTTTTGTGCTGACGAGAACAGG-----ACTGGTGAATGCGAGTTTAAAGTTT 13869
Qy 2869 CATCCCGATATGCAACCCGCTAAAGTTTACGGGAGACTTTTATCTGACAGCAGACGTTG 2928
Db 13868 ACACCTATTAAGAGAGACCGGTTATCTGTTTGTGATGTACAGATGATATATTG 13809
Qy 2929 CACTGCCAGGGGATCACCTCCGTCGCCCGGCTGTCAATAATATCATCTGTATCAT 2988
Db 13808 ACAGCCCGGGCGACGATGTTGATCCCGCTGGCCAGTGCACGCTGCTGTCTCAGATAAAG 13749
Qy 2989 CACAAACAGACGATACCGCTCTCTTTTATAGGTGTAAACCTTAAATGCAATTCAC 3048
Db 13748 TCTCCCGTGAACCTTTACCGGTTGTCATATCGGGATGAAAGCTGGCGATGATGACCA 13689
Qy 3049 C-----AGTCCCTGTTCTCGTCAGCAAAAGAGCCCTTCATTTTCAATAAACCAGGCGACC 3102
Db 13688 CCGATATGCCAGTGTGCGGCTCTCGTTTATCGGGAAAGAGTGGCTGATCTCAGCCACC 13629
Qy 3103 TCAGCCATCCCTTCTGTATTTTCCGCTTTCCAGCGTTC---GGCAGCAGACGCGGCT 3159
Db 13628 GCGAAATGACATCAAAACCGCATTAACCTGATGTTCTGGGGAATATAAATGTCAGGCT 13569
Qy 3160 TCAATCTGATGG---TTGTGCTTACAGACCGGAGATATGATCATATATATGCTTGA 3216
Db 13568 CCCTTATACACAGCCAGTCTGAGGTGATACAGTAGAATACAGAACTTTATCAGT 13509
Qy 3217 GCACTGATAGTGTGCTGCTCAACTGTCTACTTAATACGCTGCTTCATAGCACACCTCT 3276
Db 13508 TTATGATATAGAGGCTGAAATCCAGATGAAGCCGACGACTTGTGAAGAGAAAGTAT 13449
Qy 3277 TTTTGACATATCTCTGTTGTGATGATGATTTTTCAGGATATGACACTACGCTATAT 3336
Db 13448 AAGAGTTGTGAATTTGTTTGTATGACGATGATTTTTCAGGACTATGACACTACGCTATAT 13389
Qy 3337 GATAGTAGATGTTTTTATTTTGTCTACACAAABAGGCTCGACCTCTTTTCTTAT 3396
Db 13388 GAATAGTAGATGTTTTTATTTTGTACACAAAAAGAGCTCGACCTCTTTTCTTAT 13329
Qy 3397 TTTCTTTTATGATTTAATACGCAATGAGGACAAATAGCAGTAGGCTGTGATACGAGAT 3456
Db 13328 TTTCTTTTATGATTTAATACGCAATGAGGACAAATAGCAGTAGGCTGTGATACGAGAT 13269

QY 3457 CCCTTTGAGAGAACATTTTGAAGGCTGTGGTGGCTAGTGTGGCAGCATCCCGAAG 3516
Db |||||||
QY 13268 CCCTTTGAGAGAACATTTTGAAGGCTGTGGTGGCTAGTGTGGCAGCATCCCGAAG 13209
Db |||||||
QY 3517 AACATTTGGAAGGCTGTGGTGGCTAGTGTGGCAGCATCCCGAAG 3576
Db |||||||
QY 13208 AACATTTGGAAGGCTGTGGTGGCTAGTGTGGCAGCATCCCGAAG 13149
Db |||||||
QY 3577 TAGTGACTGATATGTTGTTTACAGTATTAATGAGTCTGTTTATGCAAAATCTA 3636
Db |||||||
QY 13148 TAGTGACTGATATGTTGTTTACAGTATTAATGAGTCTGTTTATGCAAAATCTA 13089
Db |||||||
QY 3637 ATTAAATATATGATATTTATATCAATTTTACAGTATTAATGAGTCTGTTTATGCAAAATCTA 3696
Db |||||||
QY 13088 ATTAAATATATGATATTTATATCAATTTTACAGTATTAATGAGTCTGTTTATGCAAAATCTA 13029
Db |||||||
QY 3697 TGCTAGAG 3705
Db |||||||
QY 13028 TGCTAGAG 13020

RESULT 10

US-10-151-690-21
; Sequence 21, Application US/10151690
; Publication No. US2003012455A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR201
; NAME/KEY: gene
; LOCATION: (29)..(260)
; OTHER INFORMATION: attpl
; FEATURE:
; NAME/KEY: gene
; LOCATION: (656)..(961)
; OTHER INFORMATION: ccdb
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1099)..(1184)
; OTHER INFORMATION: ccda
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1303)..(1962)
; OTHER INFORMATION: cmr
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2210)..(2442)
; OTHER INFORMATION: attp2
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2565)..(3374)
; OTHER INFORMATION: kmr
; FEATURE:
; NAME/KEY: gene

; LOCATION: (3495)..(4134)
; OTHER INFORMATION: ori
US-10-151-690-21

Query Match 24.8%; Score 1108.8; DB 15; Length 4470;
Best Local Similarity 99.8%; Pred. No. 2.5e-158;
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 GACAAAGTTTGTCAAAAAGCTGAACGAGAAAGCTAAAGTATATAATATCAATATATT 85
Db |||||||
QY 102 GCCAACTTTTGTCAAAAAGCTGAACGAGAAAGCTAAAGTATATAATATCAATATATT 161
Db |||||||
QY 86 AATATAGATTTTGTCAAAAAGCTGAACGAGAAAGCTAAAGTATATAATATCAATATATT 145
Db |||||||
QY 162 AATATAGATTTTGTCAAAAAGCTGAACGAGAAAGCTAAAGTATATAATATCAATATATT 221
Db |||||||
QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTGCACGAGCGCTTCCAAA 205
Db |||||||
QY 222 ACTATGAATCAACTACTTAGATGGTATTAGTACCTGTAGTGCACGAGCGCTTCCAAA 281
Db |||||||
QY 206 TGTTCCTCGGGTGTGCTGCCAACTTAGTGCACGAGCGCTTCCAAATGTTCTTCTCAA 265
Db |||||||
QY 282 TGTTCCTCGGGTGTGCTGCCAACTTAGTGCACGAGCGCTTCCAAATGTTCTTCTCAA 341
Db |||||||
QY 266 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 325
Db |||||||
QY 342 ACGGAATCGTGTATCCAGCTACTCGCTATTGTCTCAATGCCGTATTAAATCATAAAA 401
Db |||||||
QY 326 AGAATAAGAAAAAGAGTGCAGAGCTCTTTTGTGTGACAAATPAAAAATCATCTACCT 385
Db |||||||
QY 402 AGAATAAGAAAAAGAGTGCAGAGCTCTTTTGTGTGACAAATPAAAAATCATCTACCT 461
Db |||||||
QY 386 ATTATATACGTAGTGTCTGAAATCATCTGAAATCATCTGAAATCATCTGAAATCATCT 445
Db |||||||
QY 462 ATTATATACGTAGTGTCTGAAATCATCTGAAATCATCTGAAATCATCTGAAATCATCT 521
Db |||||||
QY 446 TCTTATACCTTTCTCTTACAAGTCTGCTCGGCTTCACTGGAATTTTCAGGCTCTATATCTTA 505
Db |||||||
QY 522 TCTTATACCTTTCTCTTACAAGTCTGCTCGGCTTCACTGGAATTTTCAGGCTCTATATCTTA 581
Db |||||||
QY 506 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTATTA 565
Db |||||||
QY 582 CTAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTATTA 641
Db |||||||
QY 566 AGGAGGCTTGACATTTTATATCCCGAAGATCATGCTGAAATTTTCAGGCTCTATATCTTA 625
Db |||||||
QY 642 AGGAGGCTTGACATTTTATATCCCGAAGATCATGCTGAAATTTTCAGGCTCTATATCTTA 701
Db |||||||
QY 626 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGAATACCGAGACCGGCTCACTGGCCATA 685
Db |||||||
QY 702 TCGCGTGGCTGAGATCAGCCACTTCTTCCCGAATACCGAGACCGGCTCACTGGCCATA 761
Db |||||||
QY 686 TCGGTTGCTCATATGCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTACGG 745
Db |||||||
QY 762 TCGGTTGCTCATATGCGCCAGCTTTTCATCCCGATATGACACCGGGTAAAGTTACGG 821
Db |||||||
QY 746 GAGACTTTTATCTGACAGCAGAGTGCACCTGGCCAGGGGATCACCATCGTCGCGCGGC 805
Db |||||||
QY 822 GAGACTTTTATCTGACAGCAGAGTGCACCTGGCCAGGGGATCACCATCGTCGCGCGGC 881
Db |||||||
QY 806 GTGTCATATATATCTCTGTATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG 865
Db |||||||
QY 882 GTGTCATATATATCTCTGTATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG 941
Db |||||||
QY 866 GTGTCATATATATCTCTGTATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG 925
Db |||||||
QY 942 GTGTCATATATATCTCTGTATCCCAAAACAGACGATAACGGCTCTCTCTTTTATAG 1001
Db |||||||
QY 926 TTCAATATAACCGGGGAGCTCCCTTCCCTGATTTTCCGCTTTTCCAGGTTTCGGC 985
Db |||||||
QY 1002 TTCAATATAACCGGGGAGCTCCCTTCCCTGATTTTCCGCTTTTCCAGGTTTCGGC 1061
Db |||||||
QY 986 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTCTTACACACCGGAGATATGACATC 1045
Db |||||||

QY	1106	ATAGCACACCTCTTTTGGACATCTTCGGGTA	1137	QY	566	AGGGAGCCTGACATTTATATATCCCGAAGACATCAGGTTAATGGCGTTTTTGATGTCAATTT	625
Db	1182	ATAGCACACCTCTTTTGGACATCTTCGGGTA	1213	Db	4943	AGGGAGCCTGACATTTATATATCCCGAAGACATCAGGTTAATGGCGTTTTTGATGTCAATTT	4884
RESULT 12							
US-10-151-690-61/c							
; Sequence 61, Application US/10151690							
; Publication No. US20030124555A1							
; GENERAL INFORMATION:							
; APPLICANT: BRASCH, MICHAEL A.							
; APPLICANT: CHEO, DAVID							
; APPLICANT: LI, XIAO							
; APPLICANT: ESPOSITO, DOMINIC							
; APPLICANT: BYRD, DEVON R.N.							
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI							
; FILE REFERENCE: 0942.5120001							
; CURRENT APPLICATION NUMBER: US/10/151,690							
; CURRENT FILING DATE: 2002-05-21							
; PRIOR APPLICATION NUMBER: US 10/151,690							
; PRIOR FILING DATE: 2002-05-21							
; PRIOR APPLICATION NUMBER: US 60/291,973							
; PRIOR FILING DATE: 2001-05-21							
; NUMBER OF SEQ ID NOS: 64							
; SOFTWARE: PatentIn version 3.1							
; SEQ ID NO 61							
; LENGTH: 5584							
; TYPE: DNA							
; ORGANISM: Artificial sequence							
; FEATURE:							
; OTHER INFORMATION: plasmid pDONR207							
US-10-151-690-61							
Query Match 24.8%; Score 1108.8; DB 15; Length 5584;							
Best Local Similarity 99.8%; Pred. No. 2.7e-158;							
Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;							
QY	26	GACAAAGTTTGTACAAAAAGCTGAACGAGAAAGCTAAATGATATAATCAATATATT	85	QY	1106	ATAGCACACCTCTTTTGGACATCTTCGGGTA	1137
Db	5483	GCCAACTTGTACAAAAAGCTGAACGAGAAAGCTAAATGATATAATCAATATATT	5424	Db	4403	ATAGCACACCTCTTTTGGACATCTTCGGGTA	4372
QY	86	AAATAGATTTGCATAAAAAAGAGCTACATATCTGTAAACACAAACATATCCAGTC	145	QY	986	ACGCAGACAGCGGGCTTCATTCTGCATGGTTGTGCTTACACAGCCGAGATATTTGACATC	1045
Db	5423	AAATAGATTTGCATAAAAAAGAGCTACATATCTGTAAACACAAACATATCCAGTC	5364	Db	4523	ACGCAGACAGCGGGCTTCATTCTGCATGGTTGTGCTTACACAGCCGAGATATTTGACATC	4464
QY	146	ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCAGCAGACAGCCTTCCAAA	205	QY	1045	ATATATGCTTGGAGCAACTGATAGCTGCGCTGTCACACTGTCTGTAATTCAGCGTTTCGGC	1105
Db	5363	ACTATGAATCAACTACTTAGATGGTATTAGTAGCCTGTAGTCAGCAGACAGCCTTCCAAA	5304	Db	4463	ATATATGCTTGGAGCAACTGATAGCTGCGCTGTCACACTGTCTGTAATTCAGCGTTTCGGC	4404
QY	206	TGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAATGTTTCTCAA	265	QY	1106	ATAGCACACCTCTTTTGGACATCTTCGGGTA	1137
Db	5303	TGTTCTTCGGGTGATGTCGCAACTTAGTCGACCGACAGCCTTCCAAATGTTTCTCAA	5244	Db	4403	ATAGCACACCTCTTTTGGACATCTTCGGGTA	4372
QY	266	ACGGAATCGTCGATATCAGCCTACTCGCTATTGCTCAATGCGGTATTAATCAATAAA	325	QY	986	ACGCAGACAGCGGGCTTCATTCTGCATGGTTGTGCTTACACAGCCGAGATATTTGACATC	1045
Db	5243	ACGGAATCGTCGATATCAGCCTACTCGCTATTGCTCAATGCGGTATTAATCAATAAA	5184	Db	4523	ACGCAGACAGCGGGCTTCATTCTGCATGGTTGTGCTTACACAGCCGAGATATTTGACATC	4464
QY	326	AGAAATAAGAAAAAGAGGTGGAGCCTCTTTTTGTGTGACAAAATAAAACATCTACCT	385	QY	1045	ATATATGCTTGGAGCAACTGATAGCTGCGCTGTCACACTGTCTGTAATTCAGCGTTTCGGC	1105
Db	5183	AGAAATAAGAAAAAGAGGTGGAGCCTCTTTTTGTGTGACAAAATAAAACATCTACCT	5124	Db	4463	ATATATGCTTGGAGCAACTGATAGCTGCGCTGTCACACTGTCTGTAATTCAGCGTTTCGGC	4404
QY	386	ATTCAATACGCTAGTGTGATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCACAAC	445	QY	1106	ATAGCACACCTCTTTTGGACATCTTCGGGTA	1137
Db	5123	ATTCAATACGCTAGTGTGATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCACAAC	5064	Db	4403	ATAGCACACCTCTTTTGGACATCTTCGGGTA	4372
QY	446	TCATTATCTTTCTCTTACAGTGGTTGGGCTTCATCTGATTTTCAGCCTCTATCTTA	505	QY	986	ACGCAGACAGCGGGCTTCATTCTGCATGGTTGTGCTTACACAGCCGAGATATTTGACATC	1045
Db	5063	TCATTATCTTTCTCTTACAGTGGTTGGGCTTCATCTGATTTTCAGCCTCTATCTTA	5004	Db	4523	ACGCAGACAGCGGGCTTCATTCTGCATGGTTGTGCTTACACAGCCGAGATATTTGACATC	4464
QY	506	CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTCGAGACTGGCTGTGATA	565	QY	1045	ATATATGCTTGGAGCAACTGATAGCTGCGCTGTCACACTGTCTGTAATTCAGCGTTTCGGC	1105
Db	5003	CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTCGAGACTGGCTGTGATA	4944	Db	4463	ATATATGCTTGGAGCAACTGATAGCTGCGCTGTCACACTGTCTGTAATTCAGCGTTTCGGC	4404

Query Match 24.6%; Score 1102.4; DB 15; Length 4428;
Best Local Similarity 99.5%; Pred. No. 2.3e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

RESULT 13
US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

1106 ATAGCACACCTCTTTTGGACATCTTCGGGTA 1137
4403 ATAGCACACCTCTTTTGGACATCTTCGGGTA 4372

QY 566 AGGGAGCCTGACATTTATATATCCCGAAGACATCAGGTTAATGGCGTTTTTGATGTCAATT 625
Db 4943 AGGGAGCCTGACATTTATATATCCCGAAGACATCAGGTTAATGGCGTTTTTGATGTCAATT 4884
QY 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAAAGAGACCGGACACACTGGCCATA 685
Db 4883 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAAAGAGACCGGACACACTGGCCATA 4824
QY 686 TCGGTGGTCATCATGCGCGAGCTTTTCATCCCGATATGACACCGGGTAAAGTTCAAG 745
Db 4823 TCGGTGGTCATCATGCGCGAGCTTTTCATCCCGATATGACACCGGGTAAAGTTCAAG 4764
QY 746 GAGACTTTATCTGACAGACAGCTGCTGCGCAGGGGATCAACCATCGTCGCCCGGCG 805
Db 4763 GAGACTTTATCTGACAGACAGCTGCTGCGCAGGGGATCAACCATCGTCGCCCGGCG 4704
QY 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTTATAG 865
Db 4703 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATACGGCTCTCTCTTTTATAG 4644
QY 866 GTGTAAACCTTAACTGCAATTTTCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTCA 925
Db 4643 GTGTAAACCTTAACTGCAATTTTCAGTCCCTGTTCTGTCAGCAAAAGAGCGGTTCA 4584
QY 926 TTCAATAAACCGGCGAGCCTCAGCCATCCCTTCCTGATTTTCGGTTTCCAGCGTTCGGC 985
Db 4583 TTCAATAAACCGGCGAGCCTCAGCCATCCCTTCCTGATTTTCGGTTTCCAGCGTTCGGC 4524
QY 986 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTGTTTACAGACCGGAGATTTGACATC 1045
Db 4523 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTGTTTACAGACCGGAGATTTGACATC 4464
QY 1045 ATATATGCTTTCAGCAACTGATGCTGCGTGTCACTGTCACTGTATACGCTGCTTC 1105
Db 4463 ATATATGCTTTCAGCAACTGATGCTGCGTGTCACTGTCACTGTATACGCTGCTTC 4404
QY 1106 ATAGCACACCTCTTTTGGACATCTTCGGGTA 1137
Db 4403 ATAGCACACCTCTTTTGGACATCTTCGGGTA 4372

QY 26 GACAAGTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATAATCAATATATT 85
Db |||||
QY 939 GCGAAGTTTGTACAAAAAAGCTGATATCGAAACGTAATAATGATATAATAATCAATATATT 998
Db |||||
QY 86 AAATTAGATTTCATAAAAAAGCTACATAATCTGTAAACACACATATCCAGTC 145
Db |||||
QY 999 AAATTAGATTTCATAAAAAAGCTACATAATCTGTAAACACACATATCCAGTC 1058
Db |||||
QY 146 ACTATGAATCAACTACTTAGATGATATAGTACCTGTAGTCGACCGAGCCCTCCAAA 205
Db |||||
QY 1059 ACTATGAATCAACTACTTAGATGATATAGTACCTGTAGTCGACCGAGCCCTCCAAA 1118
QY |||||
QY 206 TGTCTTCGCGGTGATGTCGCACTTAGTTCGACGAGCGCTTCCAAATGCTTCTCAA 265
Db |||||
QY 1119 TGTCTTCGCGGTGATGTCGCACTTAGTTCGACGAGCGCTTCCAAATGCTTCTCAA 1178
QY |||||
QY 266 ACGGAATCGTCGATATCCAGCCTACTCGCTTATGTCCTCAATGCGGTATTAATCAATAAA 325
Db |||||
QY 1179 ACGGAATCGTCGATATCCAGCCTACTCGCTTATGTCCTCAATGCGGTATTAATCAATAAA 1238
QY |||||
QY 326 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 385
Db |||||
QY 1239 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 1298
QY |||||
QY 386 ATTCAATAGCTAGTGTCTAGTCCTGAAATCATCTGCATCAAGAACAAATTCACAAC 445
Db |||||
QY 1299 ATTCAATAGCTAGTGTCTAGTCCTGAAATCATCTGCATCAAGAACAAATTCACAAC 1358
QY |||||
QY 446 TCTTATATCTTTCTTACAGTCTGTCGCTTCAATCTGATCTGAGCTTCTATATCTTA 505
Db |||||
QY 1359 TCTTATATCTTTCTTACAGTCTGTCGCTTCAATCTGATCTGAGCTTCTATATCTTA 1418
QY |||||
QY 506 CTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGACTGCGAGCTGGCTGTGATA 565
Db |||||
QY 1419 CTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGACTGCGAGCTGGCTGTGATA 1478
QY |||||
QY 566 AGGAGGCTGACATTTATATTCCCGAGAACATCAGGTTAATGGGTTTTTGTATGTCATTT 625
Db |||||
QY 1479 AGGAGGCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGGTTTTTGTATGTCATTT 1538
QY |||||
QY 626 TCGCGGTGGTGAGATCAGCCACTTTTCCCGGATAACGGAGACCGGCACACTGGCCATA 685
Db |||||
QY 1539 TCGCGGTGGTGAGATCAGCCACTTTTCCCGGATAACGGAGACCGGCACACTGGCCATA 1598
QY |||||
QY 686 TCGGTGTGTATCATGCGCGAGCTTTATCCCGGATGACCCAGCGGTAAAGTTCACGG 745
Db |||||
QY 1599 TCGGTGTGTATCATGCGCGAGCTTTATCCCGGATGACCCAGCGGTAAAGTTCACGG 1658
QY |||||
QY 746 GAGACTTTTATCTGACAGCAGACGTGSCACTGGCCAGGGGGATCAGCATCCGTCGCCCGGGC 805
Db |||||
QY 1659 GAGACTTTTATCTGACAGCAGACGTGSCACTGGCCAGGGGGATCAGCATCCGTCGCCCGGGC 1718
QY |||||
QY 806 GTGTCAATAATATCACTCTGTATCATCCAAACAGACGATAACGGCTCTCTCTTTTATAG 865
Db |||||
QY 1719 GTGTCAATAATATCACTCTGTATCATCCAAACAGACGATAACGGCTCTCTCTTTTATAG 1778
QY |||||
QY 866 GTGTAAACCTTAAACTGCATTTTCAACAGTCCCTGCTCTGTCGACAAAGAGCGGTTTCAT 925
Db |||||
QY 1779 GTGTAAACCTTAAACTGCATTTTCAACAGTCCCTGCTCTGTCGACAAAGAGCGGTTTCAT 1838
QY |||||
QY 926 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCCAGCGTTCCGGC 985
Db |||||
QY 1839 TTCAATAAACCGGCGACCTCAGCCATCCCTTCTGATTTTTCGCTTTCCAGCGTTCCGGC 1898
QY |||||
QY 986 ACGCAGACGAGCGGCTTCATTTCTGCATGGTTGTGCTTACAGACCGGAGATATTCGATC 1045
Db |||||
QY 1899 ACGCAGACGAGCGGCTTCATTTCTGCATGGTTGTGCTTACAGACCGGAGATATTCGATC 1958
QY |||||
QY 1046 ATATATCCCTTGACCACTGATGCTGTCGTGTCACCTGCTCACTGTAAACGCTGCTTC 1105
Db |||||
QY 1959 ATATATCCCTTGACCACTGATGCTGTCGTGTCACCTGCTCACTGTAAACGCTGCTTC 2018
QY |||||
QY 1106 ATAGCACACCTCTTTTGGACATATCTCGGGTA 1137

Db 2019 ATAGCACACCTCTTTTGGACATATCTCGGGTA 2050

RESULT 14

US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
; FILE REFERENCE: 0942.5120001
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63

Query Match 24.8%; Score 1102.4; DB 15; Length 4627;

Best Local Similarity 99.5%; Pred. No. 2.4e-157;

Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 26 GACAAGTTTGTACAAAAAAGCTGAAACGAGAAACGTAATAATGATATAATAATCAATATATT 85
Db |||||
QY 90 GCGAAGTTTGTACAAAAAAGCTGATATCGAAACGTAATAATGATATAATAATCAATATATT 149
Db |||||
QY 86 AAATTAGATTTCATAAAAAAGCTACATAATCTGTAAACACACATATCCAGTC 145
Db |||||
QY 150 AAATTAGATTTCATAAAAAAGCTACATAATCTGTAAACACACATATCCAGTC 209
QY 146 ACTATGAATCAACTACTTAGATGATATAGTACCTGTAGTCACCGAGCCCTTCCAAA 205
Db |||||
QY 210 ACTATGAATCAACTACTTAGATGATATAGTACCTGTAGTCACCGAGCCCTTCCAAA 269
QY 206 TGTCTTCGCGGTGATGTCGCACTTAGTTCGACGAGCGCTTCCAAATGCTTCTCTCAA 265
Db |||||
QY 270 TGTCTTCGCGGTGATGTCGCACTTAGTTCGACGAGCGCTTCCAAATGCTTCTCTCAA 329
QY 266 ACGGAATCGTCGATATCCAGCCTACTCGCTTATGTCCTCAATGCGGTATTAATCAATAAA 325
Db |||||
QY 330 ACGGAATCGTCGATATCCAGCCTACTCGCTTATGTCCTCAATGCGGTATTAATCAATAAA 389
QY 326 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 385
Db |||||
QY 390 AGAATAAGAAAAAGAGGTGGAGCCCTCTTTTGTGTGACAAATAAAAAACATCTACCT 449
QY 386 ATTCAATAGCTAGTGTCTAGTTCCTGAAATCATCTGCATCAAGAACAAATTCACAAC 445
Db |||||
QY 450 ATTCAATAGCTAGTGTCTAGTTCCTGAAATCATCTGCATCAAGAACAAATTCACAAC 509
QY 446 TCTTATATCTTTCTTCAAGTCGTTCCGGTTCATCTCGAATTTTCAGCTCTATATCTTA 505
Db |||||
QY 510 TCTTATATCTTTCTTCAAGTCGTTCCGGTTCATCTCGAATTTTCAGCTCTATATCTTA 569
QY 506 CTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGACTGCGAGCTGGCTGTGATA 565
Db |||||
QY 570 CTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGACTGCGAGCTGGCTGTGATA 629
QY 566 AGGAGGCTGACATTTATATTCCCGAGAACATCAGGTTAATGGGTTTTTGTATGTCATTT 625

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Db 630 AGGAGCTGACATTTATATTTCCCGAGAACATCAGTTAATGGGTTTGTGATGTCATTT 689
Qy 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATTAACGAGACCGGCACACTCGCCATA 685
Db 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATTAACGAGACCGGCACACTCGCCATA 749
Qy 686 TCGGTGGTCATCAGCGCCAGCTTTCATCCCGGATATGACACCGGGTAAAGTTACGG 745
Db 750 TCGGTGGTCATCAGCGCCAGCTTTCATCCCGGATATGACACCGGGTAAAGTTACGG 809
Qy 746 GAGACTTTATCTGACAGCAGCGTGCATCGCCAGGGGATCACCATCCGTCGCCCGGGC 805
Db 810 GAGACTTTATCTGACAGCAGCGTGCATCGCCAGGGGATCACCATCCGTCGCCCGGGC 869
Qy 806 GTGTCAATAATATCTCTGTATACATCCACAAACAGACGATTAAGCGCTCTCTTTATAG 865
Db 870 GTGTCAATAATATCTCTGTATACATCCACAAACAGACGATTAAGCGCTCTCTTTATAG 929
Qy 866 GTGTAAACCTTAAACTGCTATTCACAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTAT 925
Db 930 GTGTAAACCTTAAACTGCTATTCACAGTCCCTGTTCTCGTCAGCAAAAGACCGTTTAT 989
Qy 926 TTCAATAAACCGGGGACCTCAGCCATCCCTTCCGTTTCCAGCGTTCCGC 985
Db 990 TTCAATAAACCGGGGACCTCAGCCATCCCTTCCGTTTCCAGCGTTCCGC 1049
Qy 986 ACGCAGACGCGGCTTCAATCTGATGTTGCTGTTACCGACGCGGAGATTTGACATC 1045
Db 1050 ACGCAGACGCGGCTTCAATCTGATGTTGCTGTTACCGACGCGGAGATTTGACATC 1109
Qy 1046 ATATATGCTTTGAGCAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Db 1110 ATATATGCTTTGAGCAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1169
Qy 1106 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1137
Db 1170 ATAGCACACCTCTTTTGGACATATCTTCGGGTA 1201

RESULT 15
US-10-151-690-64
; Sequence 64, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942-5120001
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-64

Query Match 24.6%; Score 1102.4; DB 15; Length 4627;
Best Local Similarity 99.5%; Pred. No. 2.4e-157;
Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 90 GCCAACTTTGTACAAAAAGCTGATATCGAAACGTAATAATGATATAATATCAATATATT 149
Qy 86 AAATTAGATTTTGCATAAAAAAGCAGACTACATAATATCTGTAAACCAACATATCCAGTC 145
Db 150 AAATTAGATTTTGCATAAAAAAGCAGACTACATAATATCTGTAAACCAACATATCCAGTC 209
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Db 210 ACTATGAAATCAACTACTTAGATGGTATTAGTACCTGTAGTGCACCGACAGCCTTCCAAA 269
Qy 206 TGTTCCTTCGGGTGATGCTGCCAACTTAGTGCAGCGACGCTTCCAAATGTTCTTCTCAA 265
Db 270 TGTTCCTTCGGGTGATGCTGCCAACTTAGTGCAGCGACGCTTCCAAATGTTCTTCTCAA 329
Qy 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATGTTCTCAATGCGTATTAATAATCAAAAA 325
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Db 630 AGGAGCGCTGACATTTATATTTCCCGAGAACATCAGGTTAATGGCGTTTTCGATGTCATTT 689
Qy 626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATTAACGAGACCGGCACACTGGCCATA 685
Db 690 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATTAACGAGACCGGCACACTGGCCATA 749
Qy 686 TCGGTGCTCATCATGCGCCAGCTTTCATCCCGGATATGACACCGGGTAAAGTTACGG 745
Db 750 TCGGTGCTCATCATGCGCCAGCTTTCATCCCGGATATGACACCGGGTAAAGTTACGG 809
Qy 746 GAGACTTTATCTGACAGCAGACGTCGACTGGCCAGGGGATCAACATCCGTCGCCCGGGC 805
Db 810 GAGACTTTATCTGACAGCAGACGTCGACTGGCCAGGGGATCAACATCCGTCGCCCGGGC 869
Qy 806 GTGTCAATAATATCCTCTGTATCCACAAACAGACGATAAGCGCTCTCTTTTATAG 865
Db 870 GTGTCAATAATATCCTCTGTATCCACAAACAGACGATAAGCGCTCTCTTTTATAG 929
Qy 866 GTGTAAACCTTAAACTGCAATTTCCAGTCCCTGTTCTCTGACAGAAAAGACGGTTTAT 925
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Qy 1046 ATATATGCTTTGAGCAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
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Db 1170 ATAGCACCTCTTTTTCACATACCTTCGGTA 1201

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Run on: May 8, 2004, 10:39:35 ; Search time 193.335 Seconds
(without alignments)

12850.857 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	728.8	16.3	7639	1	US-08-232-016-22
3	709.8	15.9	5399	1	US-08-084-121-1
4	709.8	15.9	5399	1	US-08-478-015-1
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7	709.8	15.9	6555	1	US-08-351-413-2
8	709.8	15.9	6555	1	US-08-025-583-2
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21	182.8	4.1	13188	4	US-08-961-527-70
22	152.8	3.4	4909	3	US-08-556-978B-78
23	152.8	3.4	4909	3	US-08-556-978B-78
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30	148.4	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
31	148.4	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
32	148.4	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
33	148.4	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
34	148.4	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
35	148.4	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
36	148.4	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli
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39	146.2	3.3	4411	2	US-08-929-967-5	Sequence 5, Appli
40	146.2	3.3	5838	2	US-08-850-880-3	Sequence 3, Appli
41	146.2	3.3	5838	2	US-08-944-916-3	Sequence 3, Appli
42	146.2	3.3	5838	2	US-08-814-877-3	Sequence 3, Appli
43	146.2	3.3	5838	4	US-09-272-432A-3	Sequence 3, Appli
44	146.2	3.3	6363	2	US-08-929-967-6	Sequence 6, Appli
45	146.2	3.3	8906	4	US-09-027-169-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-232-016-23
; Sequence 23, Application US/08232016
; Patent No. 5952547
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; APPLICANT: VAN AARSSSEN, Roel
; TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
; TITLE OF INVENTION: PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,016
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: FR 91402920.2
; FILING DATE: 30-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92400820.4
; FILING DATE: 25-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K
; REGISTRATION NUMBER: P39,300
; REFERENCE/DOCKET NUMBER: 010830-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

ORGANISM: plasmid DNA designated as pps0212
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OTHER INFORMATION: truncated modified bt2 (cryIab) gene, also designated as the
OTHER INFORMATION: cryIab6 gene."
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NAME/KEY: misc feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA gene 7."
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NAME/KEY: misc feature
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OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
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NAME/KEY: misc feature
LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
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NAME/KEY: misc feature
LOCATION: 3582..4407
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
OTHER INFORMATION: Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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NAME/KEY: misc feature
LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
US-08-232-016-23
Query Match 16.3%; Score 728.8; DB 2; Length 7566;
Best Local Similarity 99.7%; Pred. No. 3.2e-143;
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 3692 GTCTAGAGTCTGCTTTAAATGAGATATCGGAGACGCGCTATGATCGCATGATATTGCTTT 3751
QY 3758 CAATCTGTTGTGACGTTGTAATAAAGCTGAGCATGTGTAGCTCAGATCTTACCGCG 3817
DB 3752 CAATCTGTTGTGACGTTGTAATAAAGCTGAGCATGTGTAGCTCAGATCTTACCGCG 3811
QY 3818 GTTTCGGTTCATTCTAATGAATATATCACCGTTACTATCTGATTTTATGAAATAATT 3877
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QY 3878 CTCGGTTCAATTTACTGATTTACCTACTACTTATATGTACATATTAATAATGAAACA 3937
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QY 4298 AGCATTTTTTGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACTTGCACAGTACG 4357
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QY 4358 ACAAATCGTTGGCGGTCCAGGGGCGAATTTTGGCACAACATGTGAGGCTCAGCAGGAC 4417
DB 4352 ACAAATCGTTGGCGGTCCAGGGGCGAATTTTGGCACAACATGTGAGGCTCAGCAGGAC 4411
QY 4418 CTGACGAGCATGC 4429
DB 4412 CTGACGAGCATTC 4423
RESULT 2
US-08-232-016-22
Sequence 22, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
APPLICANT: CORNELIJSSEN, Marc
APPLICANT: SOETABERT, Piet
APPLICANT: STAM, Maïke
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ER 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: F39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: plasmid DNA designated as pJD884
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1869
;   OTHER INFORMATION: /note= "Coding region of a
;   OTHER INFORMATION: truncated bt2 (cryIab) gene, also designated as the bt884 gen
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 1877..2110
;   OTHER INFORMATION: /note= "3' regulatory sequence
;   OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
;   OTHER INFORMATION: T-DNA gene 7."
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 2480..3005
;   OTHER INFORMATION: /note= "35S promoter sequence
;   OTHER INFORMATION: derived from Cauliflower mosaic virus."
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 3006..3665
;   OTHER INFORMATION: /note= "Coding sequence of
;   OTHER INFORMATION: chloramphenicol acetyl transferase gene."
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 3666..4491
;   OTHER INFORMATION: /note= "3' regulatory sequence
;   OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
;   OTHER INFORMATION: T-DNA octopine synthase gene."
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 5684..6541
;   OTHER INFORMATION: /note= "Sequence complementary to
;   OTHER INFORMATION: Patent No. 5952547
;   OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 7155..7639
;   OTHER INFORMATION: /note= "TR1' and TR2' promoter
;   OTHER INFORMATION: derived from Agrobacterium T-DNA."
; US-08-232-016-22
;
; Query Match 16.3%; Score 728.8; DB 2; Length 7639;
; Best Local Similarity 99.7%; Pred. No. 3.2e-143;
; Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; Qy 3698 GTCTAGAGTCCTGCTTTTAATGAGATATGCGAGAGCGCTATGATGCGCATGATATTGCTTT 3757
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; Qy 3758 CAATTCTGTTGTGACACGTTGTAATAAACCTTGAGCACTGTAGCTCAGATCCTTACCGCG 3817
; Db 3836 CAATTCTGTTGTGACACGTTGTAATAAACCTTGAGCACTGTAGCTCAGATCCTTACCGCG 3895
; Qy 3818 GTTTCGGTTCAATTCATTAATGAATATATCACCGTTTACTATGCTATTTTATGAATAATTT 3877
; Db 3896 GTTTCGGTTCAATTCATTAATGAATATATCACCGTTTACTATGCTATTTTATGAATAATTT 3955
; Qy 3878 CTCGGTTCAATTTACTGATTGTACCCCTACTATATATGATATGACAAATATTAATAAGAAACA 3937
; Db 3956 CTCGGTTCAATTTACTGATTGTACCCCTACTATATATGATATGACAAATATTAATAAGAAACA 4015
; Qy 3938 ATATAITGCTGAATAGTTTATAGGACATCTATGATAGAGCGCACAAATACAAACA 3997
; Db 4016 ATATAITGCTGAATAGTTTATAGGACATCTATGATAGAGCGCACAAATACAAACA 4075
; Qy 3998 ATTGCGTTTTATTAATCAAAATCAATTTTAAAAAGCGCAGAACCGGTCAAACTAA 4057
; Db 4076 ATTGCGTTTTATTAATCAAAATCAATTTTAAAAAGCGCAGAACCGGTCAAACTAA 4135

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; Qy 4058 AGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGCTAGTATCTACGA 4117
; Db 4136 AGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGCTAGTATCTACGA 4195
; Qy 4118 CACACCGAGCGCGAACTAATAACGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCG 4177
; Db 4196 CACACCGAGCGCGAACTAATAACGTTTCACTGAAGGGAATCTCCGGTTCCCGCGCGCGCG 4255
; Qy 4178 CATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCGCTCCGCTTACCGAAAGTTACGGGCA 4237
; Db 4256 CATGGGTGAGATTCCTTGAAGTTGAGTATTTGGCGCTCCGCTTACCGAAAGTTACGGGCA 4315
; Qy 4238 CCATTCAACCCCGTCCAGACGCGCGCGGTAACCGACTTGTCTGCCCGGAGAAATTATGC 4297
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; Qy 4298 AGCAATTTTGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAACTTTGACAGTGACG 4357
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; Qy 4358 ACAAATCGTTGGCGCGGTCCAGGCGGAATTTTCGCAACATGTCAGGCTCAGCAGGAC 4417
; Db 4436 ACAAATCGTTGGCGCGGTCCAGGCGGAATTTTCGCAACATGTCAGGCTCAGCAGGAC 4495
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; Db 4496 CTGCAGGAATTC 4507

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RESULT 3

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; US-08-064-121-1
; Sequence 1, Application US/08064121
; Patent No 5641664
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,121
; FILING DATE: 24-MAY-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
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; OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"
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; NAME/KEY: -
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; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from the
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; US-08-064-121-1
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; Best Local Similarity 99.7%; Pred. No. 2.7e-139; Indels 0; Gaps 0;
; Matches 711; Conservative 0; Mismatches 32;
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; QY 3707 CTTGCTTTTAAATGAGATATCGAGACGCTATGATCGCATGATATTTGCTTTCAATTCTGT 3766
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; Db 2333 TGTGACGTTGTAAAAAAGCTGAGCATGTGTAGCTCAGATCCTTACGGCGGTTTCGGTT 2392
; QY 3827 CATCTAATGAATATATCACCCTTACTATCGTATTTTATGAATAATATTTCTCCGTTC 3886
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; QY 3887 ATTTACTGATGTACCTACTATATATGTAACAATATTTAAATGAAACAATATATTTGT 3946
; Db 2453 ATTTACTGATGTACCTACTATATGTAACAATATTTAAATGAAACAATATATTTGT 2512
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; Db 2633 TACATAATCTTATCAAAATTTCAAAAGCCCGGAGGCTAGTATCTACGACACACCGAG 2692
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; Db 2873 TTGGTGTATGTGGGCCCCCAAAATGAAGTGAAGTCAAGTCAAACTTGACAGCAAAATCGT 2932
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; RESULT 4
; US-08-478-015-1
; Sequence 1, Application US/08478015
; Patent No. 5712135
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/478,015
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDE108
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451

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; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
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; LOCATION: 452..1284
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosaic virus isolate CabbB-JI"
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; NAME/KEY: -
; LOCATION: 2101..3160
; OTHER INFORMATION: /label= 3'ocs
; OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation site derived from the Agrobacterium T-DNA octopine synthase"
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; LOCATION: 3161..5399
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; US-08-478-015-1
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Best Local Similarity 99.7%; Pred. No. 2.7e-139;
Matches 711; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 3707 CTGCTTTTATGAGATATCGAGACCGCTATGATCGCATGATTTTGCATTTCAATTCGT 3766
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DB 2333 TGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCTTACCGCGGGTTTCGGTT 2392
QY 3827 CATCTTAATGAATATATCACCGGTTACTATCGTATTTTATGATTAATATTCCTCGTTCA 3886
DB 2393 CATCTTAATGAATATATCACCGGTTACTATCGTATTTTATGATTAATATTCCTCGTTCA 2452
QY 3887 ATTTACTGATTTGACCTTACTTATATGATCAATTAATTAATGAATTAATATTCCTCGTTCA 3946
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RESULT 5
US-08-475-975-1
; Sequence 1, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; APPLICANT: GOBEL, Elke
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING MONOCOTYLEDONOUS PLANTS
; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,975
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,121
; FILING DATE: 24-MAY-1993
; APPLICATION NUMBER: EP 90403332.1
; FILING DATE: 23-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: plasmid pDE108
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; Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; US-08-489-1
; Sequence 1, Application US/09084889
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; Patent No. 6074877
; GENERAL INFORMATION:
; APPLICANT: D'HALLUIN, Kathleen
; TITLE OF INVENTION: PROCESS FOR TRANSFORMING MONOCOTYLEDONOUS PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,121
; FILING DATE:
; PRIOR APPLICATION NUMBER: EP 91401888.2
; FILING DATE: 08-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pDEL08
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..451
; OTHER INFORMATION: /label= pUC18
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; OTHER INFORMATION: /label= NPTII
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; LOCATION: 3161..5399
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
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US-09-084-889-1
Query Match 15.9%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3707 CCTGCTTTAATGAGATATCGAGACGCTTATGATCGCATGATATTTGCTTTCAATTCTGT 3766
Db 2273 CCTGCTTTAATGAGATATCGAGACGCTTATGATCGCATGATATTTGCTTTCAATTCTGT 2332
QY 3767 TGTGCACTGTTGAAAAAAGCTGAGCATGCTAGCTCAGATCTTACCGCGGTTTCGGTT 3826
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Db 2393 CATTTCAATGAATATATCAACCGCTTACTATCGTATTTTATGAATATATTTCTCCGTTCA 2452
QY 3887 ATTACTGATTTGACCTACTACTATATATGTAACAATTAATAATGAATAATATATTTGT 3946
Db 2453 ATTACTGATTTGACCTACTACTATATGTAACAATTAATAATGAATAATATATTTGT 2512
QY 3947 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGCCCAATTAACAACAATTTGCGTTT 4006
Db 2513 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGCCCAATTAACAACAATTTGCGTTT 2572
QY 4007 TATTATTACAAATCCAAATTTTAAAAAAGCGGAGAACCGGTCAAACTAAAGACTGAT 4066
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QY 4127 CGGGAATTAATACGTTTACTGAAGGAACTCCGGTTCCCGCGCGGCGCATGGGTGA 4186
Db 2693 CGGGAATTAATACGTTTACTGAAGGAACTCCGGTTCCCGCGCGGCGCATGGGTGA 2752
QY 4187 GATTCCTTTGAGTTGAGTATTTGGCGTCCGCTTACCGAAAGTTACGGGACCAATCAAC 4246
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QY 4247 CCGGTCACGACGGCGCGGCTAACCGACTTCTGCCCCGAGAAATATGAGCATTTT 4306
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RESULT 7
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; Sequence 2, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
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; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
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; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pVE144 (replicable in E.coli)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..396
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; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
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; OTHER INFORMATION: Nicotiana tabacum"
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; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA octopine synthase gene"
; FEATURE:
; NAME/KEY:
; LOCATION: 4316..6555
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; US-08-351-413-2
Query Match 15.9%; Score 709.8; DB 1; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3707 CTTGCTTTAATGAGATATGCGACGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3766
Db 3429 CTTGCTTTAATGAGATATGCGACGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3488
QY 3767 TGTGACGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 3826
Db 3489 TGTGACGTTGTAATAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 3548
QY 3827 CATTCCTAATGAATATATCACCGGTTACTATCGTATTTTATGATATATATTCCTCGTTCA 3886
Db 3549 CATTCCTAATGAATATATCACCGGTTACTATCGTATTTTATGATATATATTCCTCGTTCA 3608
QY 3887 ATTACTGATGTPACCTACTACTATATGTACAAATATTAATAAATGAAAAACAATATTTGT 3946
Db 3609 ATTACTGATGTPACCTACTACTATATGTACAAATATTAATAAATGAAAAACAATATTTGT 3668
QY 3947 GCTGATAGTTTATAGCGACATCTATGATAGCGGCCCAATTAACAACAAATGCGTTT 4006
Db 3669 GCTGATAGTTTATAGCGACATCTATGATAGCGGCCCAATTAACAACAAATGCGTTT 3728
QY 4007 TATTATTACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 4066
Db 3729 TATTATTACAAATCCAAATTTTAAAAAGCGGAGAACCGGTCAAACTTAAAGACTGAT 3788
QY 4067 TACATAAATCTTATTTCAAAATTTCAAAAGGCCCGGAGGCTAGTATCTACGACACCGGAG 4126
Db 3789 TACATAAATCTTATTTCAAAATTTCAAAAGGCCCGGAGGCTAGTATCTACGACACCGGAG 3848
QY 4127 CGCGGACTAATAACCTTCACTGAAGGACTCGGTTCGCCCGCGCGCATGGTGA 4186
Db 3849 CGCGGACTAATAACCTTCACTGAAGGAACTCCGGTTCGCCCGCGCGCATGGTGA 3908
QY 4187 GATTCCTTGAAGTTGAGTATTTGCCCTCCGCTCTACCGAAAGTTACGGGACCAATTCAC 4246
Db 3909 GATTCCTTGAAGTTGAGTATTTGCCCTCCGCTCTACCGAAAGTTACGGGACCAATTCAC 3968
QY 4247 CCGGTCAGACGCGCGCGGTAACCGACTTGTGCGCCGAGAAATATGACGATTTT 4306
Db 3969 CCGGTCAGACGCGCGCGGTAACCGACTTGTGCGCCGAGAAATATGACGATTTT 4028
QY 4307 TTGCTGATGTCGGCCCAATGAAGTGAAGTCAAACTTTGACAGTGACGACAAATCGT 4366
Db 4029 TTGCTGATGTCGGCCCAATGAAGTGAAGTCAAACTTTGACAGTGACGACAAATCGT 4088
QY 4367 TGGCGGGTCCAGGGCGAATTTTTCGACAAATGTTCGAGGCTCAGCAGGACCT 4419
Db 4089 TGGCGGGTCCAGGGCGAATTTTTCGACAAATGTTCGAGGCTCAGCAGGACCT 4141
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RESULT 8

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US-09-025-583-2
; Sequence 2, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
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; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,583
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: plasmid pVE144 (replicable in E.coli)
; FEATURE:
; NAME/KEY:
; LOCATION: 1..396
; OTHER INFORMATION: /label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (397..751)
; OTHER INFORMATION: /label= 3'nos
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (752..1024)
; OTHER INFORMATION: /label= barstar
; OTHER INFORMATION: /note= "coding region of the barstar gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY:
; LOCATION: complement (1025..1607)
; OTHER INFORMATION: /label= TA29
; OTHER INFORMATION: /note= "promoter derived from the TA29 gene of
; OTHER INFORMATION: Nicotiana tabacum"
; FEATURE:
; NAME/KEY:
; LOCATION: 1508..2440
; OTHER INFORMATION: /label= 35S3
; OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"

FEATURE:
NAME/KEY: 2441..3256
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OTHER INFORMATION: /note= "coding region of the neomycine
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NAME/KEY: 3257..4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: 4316..6555
LOCATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
US-09-025-583-2

Query Match 15.9%; Score 709.8; DB 2; Length 6555;
Best Local Similarity 99.7%; Pred. No. 2.9e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3707 CTGCTTTAATGAGATATCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3766
Db 3429 CTGCTTTAATGAGATATCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3488
QY 3767 TGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3826
Db 3489 TGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3548
QY 3827 CATCTCAATGAATATATCACCCTTACTATCGTATTTTATGATTAATATTTCTCCGTTCA 3886
Db 3549 CATCTCAATGAATATATCACCCTTACTATCGTATTTTATGATTAATATTTCTCCGTTCA 3608
QY 3887 ATTTACTGATTGTACCTTACTTATGATGATGATTAATTAATGAAACCAATATATGT 3946
Db 3609 ATTTACTGATTGTACCTTACTTATGATGATGATTAATTAATGAAACCAATATATGT 3668
QY 3947 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGGCCAATTAACAAATTCGGTTT 4006
Db 3669 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGGCCAATTAACAAATTCGGTTT 3728
QY 4007 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAACTTAAAGACTGAT 4066
Db 3729 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAACTTAAAGACTGAT 3788
QY 4067 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGAGGCTAGTATCTACGACACCCGAG 4126
Db 3789 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGAGGCTAGTATCTACGACACCCGAG 3848
QY 4127 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGGCGATGGGTGA 4186
Db 3849 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGGCGATGGGTGA 3908
QY 4187 GATTCTTGAAGTTGAGTATTTGCGCTCTACCGAAGTTACGGGACCATTCAC 4246
Db 3909 GATTCTTGAAGTTGAGTATTTGCGCTCTACCGAAGTTACGGGACCATTCAC 3968
QY 4247 CCGGTCCAGCAGCGCGGCTAAACGACTTGTGCTCCCGAGAAATTTATGACGATTTTT 4306
Db 3969 CCGGTCCAGCAGCGCGGCTAAACGACTTGTGCTCCCGAGAAATTTATGACGATTTTT 4028
QY 4307 TTGTTGATGTGGGCCCAATGAAGTGAGGTCAAACTTGTGACGAGTACGACCAATCGT 4366
Db 4029 TTGTTGATGTGGGCCCAATGAAGTGAGGTCAAACTTGTGACGAGTACGACCAATCGT 4088
QY 4367 TGGCGGGTCCAGGGCGAAATTTTGGACAAACATGTGAGGCTCAGCAGGACCT 4419
Db 4089 TGGCGGGTCCAGGGCGAAATTTTGGACAAACATGTGAGGCTCAGCAGGAGGCT 4141

RESULT 9

US-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 15.9%; Score 709.8; DB 4; Length 14194;
Best Local Similarity 99.7%; Pred. No. 3.7e-139;
Matches 711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3707 CTGCTTTAATGAGATATCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 3766
Db 9830 CTGCTTTAATGAGATATCGAGAGCGCTATGATCGCATGATATTTGCTTTCAATTCGT 9889
QY 3767 TGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 3826
Db 9890 TGTGACGTTGTAAAAAACCCTGAGCATGTGTAGCTCAGATCCCTTACCGCGGTTTCGGTT 9949
QY 3827 CATCTCAATGAATATATCACCCTTACTATCGTATTTTATGATTAATATTTCTCCGTTCA 3886
Db 9950 CATCTCAATGAATATATCACCCTTACTATCGTATTTTATGATTAATATTTCTCCGTTCA 10009
QY 3887 ATTTACTGATTGTACCTTACTTATGATGATGATTAATTAATGAAACCAATATATGT 3946
Db 10010 ATTTACTGATTGTACCTTACTTATGATGATGATTAATTAATGAAACCAATATATGT 10069
QY 3947 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGGCCAATTAACAAATTCGGTTT 4006
Db 10070 GCTGAATAGTTTATAGCGCATCTATGATAGAGCGGCCAATTAACAAATTCGGTTT 10129
QY 4007 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAACTTAAAGACTGAT 4066
Db 10130 TATTATTACAAATCCAAATTTTAAAAAGCGGAGACCGGTCAAACTTAAAGACTGAT 10189
QY 4067 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGAGGCTAGTATCTACGACACCCGAG 4126
Db 10190 TACATAAATCTTATTCAAATTTTCAAAGGCCCGGAGGCTAGTATCTACGACACCCGAG 10249
QY 4127 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGGCGATGGGTGA 4186
Db 10250 CGCGCAACTAATAAGTTCTAGAGGGAATCTCGGTTTCCCGCGCGCGGCGATGGGTGA 10309
QY 4187 GATTCTTGAAGTTGAGTATTTGCGCTCTACCGAAGTTACGGGACCATTCAC 4246
Db 10310 GATTCTTGAAGTTGAGTATTTGCGCTCTACCGAAGTTACGGGACCATTCAC 10369
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Db 10370 CCGGTCCAGCAGCGCGGCTAAACGACTTGTGCTCCCGAGAAATTTATGACGATTTTT 10429
QY 4307 TTGTTGATGTGGGCCCAATGAAGTGAGGTCAAACTTGTGACGAGTACGACCAATCGT 4366
Db 10430 TTGTTGATGTGGGCCCAATGAAGTGAGGTCAAACTTGTGACGAGTACGACCAATCGT 10489
QY 4367 TGGCGGGTCCAGGGCGAAATTTTGGACAAACATGTGAGGCTCAGCAGGACCT 4419
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RESULT 10
5428147-1/c
; PATENT NO. 5428147
; APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO: 1:
; LENGTH: 24595
5428147-1

Query Match      15.8%; Score 707; DB 6; Length 24595;
Best Local Similarity 100.0%; Pred. No. 1.7e-138;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3708 CTGCTTTAATGAGATATGCGAGACGCTTATGATCGCATGATATTTGCTTTCAATTCGTG 3767
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QY 3828 ATTCTAATGAATATATACACCGGTTACTATGATGATTTTATGAATAATATCTCGGTTCAA 3887
DB 12421 ATTCTAATGAATATATACACCGGTTACTATGATGATTTTATGAATAATATCTCGGTTCAA 12362
QY 3888 TTCTACTGATTTGACCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATG 3947
DB 12361 TTCTACTGATTTGACCTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATG 12302
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QY 4008 ATTATTACAAATCCAAATTTTAAACAAAGCGGCGAGAACCGGTCAAACTTAAAGACTGATT 4067
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QY 4128 GCGCAACTAATAACGTTCACTGAAGGAACTCCGGTTTCCCGCGCGCGCATGGGTGAG 4187
DB 12121 GCGCAACTAATAACGTTCACTGAAGGAACTCCGGTTTCCCGCGCGCGCATGGGTGAG 12062
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DB 11941 TCGTGTATGTGGGCCCCCAAAATGAAGTGCAGGTCAAAACCTTGACGTGACGACAAATCGTT 11882
QY 4368 GGGCGGTCCTCAGGCGGAATTTTGGCACAACATGTGAGGCTCAGCAG 4414
DB 11881 GGGCGGTCCTCAGGCGGAATTTTGGCACAACATGTGAGGCTCAGCAG 11835

RESULT 11
US-08-673-768-1
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match      12.7%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 3.8e-109;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3707 CTTGCTTTAATGAGATATGCGAGAGCCCTATGATCGCATGATTTGCTTTCAATTCGT 3766
DB 7110 CTTGCTTTAATGAGATATGCGAGAGCCCTATGATCGCATGATTTGCTTTCAATTCGT 7169
QY 3767 TGTGACGCTGTGTAACCAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 3825
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Db 7170 TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCTTACCGCGGTTTCGGTT 7229
QY 3827 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATTTCTCGTTCA 3886
Db 7230 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATTTCTCGTTCA 7289
QY 3887 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATAATGAACAATATATTTCT 3946
Db 7290 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATAATGAACAATATATTTCT 7349
QY 3947 GCTGAATAGTTTATAGCAGCATCTATGATAGAGCGCCCAATAAACAACAATTTGGTTT 4006
Db 7350 GCTGAATAGTTTATAGCAGCATCTATGATAGAGCGCCCAATAAACAACAATTTGGTTT 7409
QY 4007 TATTATACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT 4066
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Db 7530 CGCGCAACTAATAACGTTCACTGAAGGGAACCTCGGTTCCCGCGCGCGCATATGGTGA 7589
QY 4187 GATTCCTTGAAGTTGAGTATGTCCTCGCTACCGAAGTTACGGGACCAATTCAC 4246
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RESULT 12

US-08-673-768-1/c
; Sequence 1, Application US/08673768
; Patent No. 5952546
; GENERAL INFORMATION:
; APPLICANT: Bedbrook, John R.
; APPLICANT: Dunsuir, Pamela
; APPLICANT: Howie, William J.
; APPLICANT: Joe, Lawrence K.
; APPLICANT: Lee, Kathleen Y.
; TITLE OF INVENTION: Delayed Ripening Tomato Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,768
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,721
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 012176-005010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-673-768-1

Query Match 12.7%; Score 566.4; DB 2; Length 15397;
Best Local Similarity 99.8%; Pred. No. 3.8e-109;
Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3707 CTGCTTTAATCAGATATGCGAGACGCTATGATCGCATGATATTTGCTTCAATCTGT 3766
Db 14394 CTGCTTTAATCAGATATGCGAGACGCTATGATCGCATGATATTTGCTTCAATCTGT 14335
QY 3767 TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCTTACCGCGGTTTCGGTT 3826
Db 14334 TGTGACGTTGTAAACAACTGAGCATGTAGCTCAGATCTTACCGCGGTTTCGGTT 14275
QY 3827 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATTTCTCGTTCA 3886
Db 14274 CATTCTAATGAATATATACCCGGTTACTATCGTATTTTATGAATAATATTTCTCGTTCA 14215
QY 3887 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATAATGAACAATATATTTCT 3946
Db 14214 ATTACTGATGTACCCCTACTCTATATGTACAAATATTAATAATGAACAATATATTTCT 14155
QY 3947 GCTGAATAGTTTATAGGAGCATCTATGATAGAGCGCCCAATAAACAACAATTTGGTTT 4006
Db 14154 GCTGAATAGTTTATAGGAGCATCTATGATAGAGCGCCCAATAAACAACAATTTGGTTT 14095
QY 4007 TATTATACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT 4066
Db 14094 TATTATACAAATCCAAATTTTAAACAAAGCGGAGAACCGGTCAACCTTAAAGACTGAT 14035
QY 4067 TACATAAATCTTATTCAAATTTTCAAAAGGCCCCAGGGGTAGTATCTACGACACACCGAG 4126
Db 14034 TACATAAATCTTATTCAAATTTTCAAAAGGCCCCAGGGGTAGTATCTACGACACACCGAG 13975
QY 4127 CGCGCAACTAATAACGTTCACTGAAGGGAACCTCGGTTCCCGCGCGCGCATATGGTGA 4186
Db 13974 CGCGCAACTAATAACGTTCACTGAAGGGAACCTCGGTTCCCGCGCGCGCATATGGTGA 13915
QY 4187 GATTCCTTGAAGTTGAGTATGTCCTCGCTACCGAAGTTACGGGACCAATTCAC 4246
Db 13914 GATTCCTTGAAGTTGAGTATGTCCTCGCTACCGAAGTTACGGGACCAATTCAC 13855
QY 4247 CGGTCACGACGCGCGGTAACCG 4274
Db 13854 CGGTCACGACGCGCGGTAACAG 13827

RESULT 13

US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION NUMBER: 08/379614
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; FILING DATE: 02-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA10.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
;
US-08-379-614-2

Query Match 7.3%; Score 325.4; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 3.3e-59;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 617
Db 403 TGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 344
QY 618 TGTCAATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 677
Db 343 TGTCAATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 284
QY 678 TGGCCATATCGGTGTCATATGCGCGACGCTTTCATCCCGATATGCCACCGGTAAA 737
Db 283 TGGCCATATCGGTGTCATATGCGCGACGCTTTCATCCCGATATGCCACCGGTAAA 224
QY 738 GTTCACGGAGACTTTATCTGACAGCAGTGCCTGCGCCAGGGGGATCACCATCCGTC 797
Db 223 GTTCACGGAGACTTTATCTGACAGCAGTGCCTGCGCCAGGGGGATCACCATCCGTC 164
QY 798 GCCCGGGCGTCAATAATATCACTGTGTACATCCAAACAGACGATAACGGCTCTCTC 857
Db 163 GCCCGGGCGTCAATAATATCACTGTGTACATCCAAACAGACGATAACGGCTCTCTC 104
QY 858 TTTTATAGGTAAACCTTAAACTGCA 884
Db 103 TTTTATAGGTAAACCTTAAACTGCA 77

RESULT 14
US-09-225-152A-2/c
; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANMA10.001CPI
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; CURRENT APPLICATION NUMBER: US/09/225,152A
; CURRENT FILING DATE: 1998-01-04
; PRIOR APPLICATION NUMBER: 08/379614
; PRIOR FILING DATE: 1995-07-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(378)
; OTHER INFORMATION: ccdB gene of pKIL 18.
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US-09-225-152A-2

Query Match 7.3%; Score 325.4; DB 3; Length 420;
Best Local Similarity 99.7%; Pred. No. 3.3e-59;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 617
Db 403 TGTGTATAAGGAGCCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGA 344
QY 618 TGTCAATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 677
Db 343 TGTCAATTTTCGGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACAC 284
QY 678 TGGCCATATCGGTGTCATATGCGCGACGCTTTCATCCCGATATGCCACCGGTAAA 737
Db 283 TGGCCATATCGGTGTCATATGCGCGACGCTTTCATCCCGATATGCCACCGGTAAA 224
QY 738 GTTCACGGAGACTTTATCTGACAGCAGTGCCTGCGCCAGGGGGATCACCATCCGTC 797
Db 223 GTTCACGGAGACTTTATCTGACAGCAGTGCCTGCGCCAGGGGGATCACCATCCGTC 164
QY 798 GCCCGGGCGTCAATAATATCACTGTGTACATCCAAACAGACGATAACGGCTCTCTC 857
Db 163 GCCCGGGCGTCAATAATATCACTGTGTACATCCAAACAGACGATAACGGCTCTCTC 104
QY 858 TTTTATAGGTAAACCTTAAACTGCA 884
Db 103 TTTTATAGGTAAACCTTAAACTGCA 77

RESULT 15
US-08-379-614-3/c
; Sequence 3, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; APPLICANT: Gabant, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/379,614
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/BE93/00051
; APPLICATION NUMBER: 02-AUG-1993
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ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: VANMA10.001APC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 714-760-0404
 TELEFAX: 714-760-9502
 TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 416 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: Genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: ccdB gene of plasmid pKIL 19

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...378

OTHER INFORMATION:

US-08-379-614-3

Query Match 7.2%; Score 323.2; DB 2; Length 416;
 Best Local Similarity 99.1%; Pred. No. 9.5e-59;
 Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	559	GTGATATAGGAGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGTGAT	618
Db	402	GTGATATACGGAGCTGACATTTATATCCCGAGAACATCAGGTTAATGGCGTTTGTGAT	343
QY	619	GTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATACCGGAGACCGGCACACT	678
Db	342	GTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATACCGGAGACCGGCACACT	283
QY	679	GGCCATATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATATGCACCCCGGTAAG	738
Db	282	GGCCATATCGGTGTCATCATGCGCCAGCTTTTCATCCCGGATATGCACCCCGGTAAG	223
QY	739	TTACGGGAGACTTTTATCTGACGAGACGTGCACTGGCCAGGGGGATCACCATCCGTCG	798
Db	222	TTACGGGAGACTTTTATCTGACGAGACGTGCACTGGCCAGGGGGATCACCATCCGTCG	163
QY	799	CCCGGCGGTGCAATAATATACCTCTGTACATCCCAAAACAGACGATACCGCTCTCTCT	858
Db	162	CCCGGCGGTGCAATAATATACCTCTGTACATCCCAAAACAGACGATACCGCTCTCTCT	103
QY	859	TTTATAGGTGTAACCTTAACTGCATT	886
Db	102	TTTATAGGTGTAACCTTAACTGCATT	75

Search completed: May 9, 2004, 22:13:01
 Job time : 195.335 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 6944.51 Seconds
(without alignments)
19251.609 Million cell updates/sec

Title: US-10-055-001B-24_COPY_13000_17476

Perfect score: 4477

Sequence: 1 ttctattggagagacacg.....atagtgcaacataatctgc 4477

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518.4	11.6	698	29	AG012840 Homo sapi
2	496.6	11.1	713	29	AG000762 Homo sapi
3	437.2	9.8	542	14	CD109790 AGENCOURT
4	411.8	9.2	723	29	AG000761 Homo sapi

C	5	408.4	9.1	725	29	AG013450
C	6	404	9.0	522	14	CB997937
C	7	398.4	8.9	722	29	AG000763
C	8	357	8.0	487	14	CB395230
C	9	347.4	7.8	487	14	CB395230
C	10	340.2	7.6	384	12	B1174407
C	11	325.4	7.3	384	12	B1174407
C	12	301.4	6.7	337	12	BJ555980
C	13	273.2	6.1	1068	14	CF469981
C	14	271.8	6.1	1037	14	CF469981
C	15	264.4	5.9	724	29	AG000791
C	16	262.4	5.9	816	14	CF469496
C	17	257.4	5.7	557	12	BG220129
C	18	255.8	5.7	656	14	CK291800
C	19	254	5.7	656	14	CF469084
C	20	252.4	5.6	819	14	CF469247
C	21	247.4	5.5	320	29	GG206516
C	22	246	5.5	329	28	BH739300
C	23	245.4	5.5	1041	14	CF468941
C	24	243.6	5.4	1035	14	CF470036
C	25	242.8	5.4	1017	14	CF470004
C	26	239.2	5.3	659	14	CK287298
C	27	235.6	5.3	859	14	CF468865
C	28	234.8	5.2	506	14	CF468964
C	29	234.8	5.2	657	14	CF468948
C	30	229	5.1	628	14	CF469215
C	31	227.2	5.1	968	14	CF469474
C	32	220	4.9	583	14	CB403882
C	33	220	4.9	583	14	CB403882
C	34	215.2	4.8	393	14	CB403984
C	35	215.2	4.8	1020	14	CB403984
C	36	215.2	4.8	1020	14	CF469337
C	37	214.6	4.8	1017	14	CF468787
C	38	214.2	4.8	1042	14	CF468958
C	39	213.8	4.8	945	14	CF468807
C	40	213.2	4.8	509	14	CF468864
C	41	213.2	4.8	716	29	AG000792
C	42	204.6	4.6	398	14	CF974207
C	43	203.4	4.5	1013	14	CF469353
C	44	203.2	4.5	973	14	CF469399
C	45	200.4	4.5	586	14	CF470068

ALIGNMENTS

RESULT 1
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LOCUS AG012840
DEFINITION Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic survey sequence.
ACCESSION AG012840
VERSION AG012840.1 GI:3435047
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 698)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Published Only in Database (1998)
JOURNAL
REFERENCE 2 (bases 1 to 698)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES
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1..698
/organism="Homo sapiens"
/mol_type="genomic DNA"


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/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="f65H12X16"

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Best Local Similarity 98.9%; Pred. No. 7.5e-82;
Matches 553; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

579 TTTATATCCCGAAGACATCAGGTTAATGCGTTTTGATGTCAATTTTCGCGTGGCTGA 638
Db      |||||
34 TTTATATCCCGAAGACATCAGGTTAATGCGTTTTGATGTCAATTTTCGCGTGGCTGA 93
QY      |||||
639 GATCAGCACTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCA 698
Db      |||||
94 GATCAGCACTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCA 153
QY      |||||
699 TGGCCAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTCAACGGAGACTTTATCTG 758
Db      |||||
154 TGGCCCA-NTTTCATCCCGATATGACACCGGGTAAAGTTTCAACGGAGACTTTATCTG 212
QY      |||||
759 ACAGCAGAGTGCACCTGGCCAGGGGATCACCATCGTCGCCCGGCGTGTCAATAATAT 818
Db      |||||
213 ACAGCAGAGTGCACCTGGCCAGGGGATCACCATCGTCGCCCGGCGTGTCAATAATAT 272
QY      |||||
819 CACTGTGTACATCCAAACAGACGATACGGCTCTCTTTTATAGGTGTAAACCTTAA 878
Db      |||||
273 CACTGTGTACATCCAAACAGACGATACGGCTCTCTTTTATAGGTGTAAACCTTAA 332
QY      |||||
879 ACTGCAATTTACCAGTCCCTCTCTCGTCAGCAAAAGAGCCGTTCAATTAACACCGG 938
Db      |||||
333 ACTGCAATTTACCAGTCCCTCTCTCGTCAGCAAAAGAGCCGTTCAATTAACACCGG 392
QY      |||||
939 GGCACCTAGCAACCTCTCTCGTTTCGCTTTCCAGGTTTCGCGACGACGACGCG 998
Db      |||||
393 GGCACCTAGCAACCTCTCTCGTTTCGCTTTCCAGGTTTCGCGACGACGACGCG 452
QY      |||||
999 GCTTCAATTCGATGTTGCTTACAGACCGGATATGACATCATATATGCTTCA 1058
Db      |||||
453 GCTTCAATTCGATGTTGCTTACAGACCGGATATGACATCATATATGCTTCA 510
QY      |||||
1059 GCAACTGATAGCTGCTGCTCACTGCTCACTGCTGCTTCACTAGCACACTCT 1118
Db      |||||
511 GCAACTGATAGC-GTGCCTGCTCACTGCTCACTGCTGCTTCACTAGCACACTCT 569
QY      |||||
1119 TTTTGACATCTTCGGGTA 1137
Db      |||||
570 TTTTGACATCTTCGGGTA 588

RESULT 2
AG000762/c 713 bp DNA linear GSS 06-FEB-1999
LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
DEFINITION survey sequence.
ACCESSION AG000762
VERSION AG000762.1 GI:2579570
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 713)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1997)
REFERENCE 2 (bases 1 to 713)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp)
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Tel:0427-78-9732, Fax:0427-78-9561)
Location/Qualifiers
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/mol_type="genomic DNA"
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Query Match      11.1%; Score 496.6; DB 29; Length 713;
Best Local Similarity 94.2%; Pred. No. 5.4e-78;
Matches 523; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

583 TATTCGCCAGAACATCAGGTTAATGCGTTTTGATGTCAATTTTCGCGTGGCTGAGATC 642
Db      |||||
599 TATATCCCGGANCATCNGTTAATGCCGTTTTTGAAGGNAATTTTCGCGTGGCTGAGAAT 540
QY      |||||
643 AGCAGCTTCTTCCCGATTAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCGG 702
Db      |||||
539 CACCAACTTTTTCGCGATTAACGGAGACCGGCACACTGNCATATCGGTGGTCATCGG 480
QY      |||||
703 CCAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTCAACGGAGACTTTTATCTGACAG 762
Db      |||||
479 CCAGCTTTTCATCCCGGATATGACACCGGGTAAAGTTTCAACGGAGACTTTTATCTGACAG 420
QY      |||||
763 CAGAGTGCTGCTGGCCAGGGGATCACCATCGTCGCCCGGCGTGTCAATAATATCACT 822
Db      |||||
419 CAGAGTGCTGCTGGCCAGGGGATCACCATCGTCGCCCGGCGTGTCAATAATATCACT 360
QY      |||||
823 CTGTACATCCAAACAGACGATACGGCTCTCTTTTATAGGTGTAAACCTTAAACCTG 882
Db      |||||
359 CTGTACATCCAAACAGACGATACGGCTCTCTTTTATAGGTGTAAACCTTAAACCTG 300
QY      |||||
883 CATTTCCAGGTCCTCTCTCGTCAGCAAAAGAGCCGTTCAATTAACACCGGCGCA 942
Db      |||||
299 CATTTCCAGGTCCTCTCTCGTCAGCAAAAGAGCCGTTCAATTAACACCGGCGCA 240
QY      |||||
943 CTTAGCCATCCCTCTCTGATTTTCGCTTTCAGGTTTCGCGACGACGACGCGGCTT 1002
Db      |||||
239 CTTAGCCATCCCTCTCTGATTTTCGCTTTCAGGTTTCGCGACGACGACGCGGCTT 180
QY      |||||
1003 CATTTCTGATGTTGCTGCTTACAGACCGGAGATATGACATCATATATGCTTTCAGCAA 1062
Db      |||||
179 CATTTCTGATGTTGCTGCTTACAGACCGGAGATATGACATCATATATGCTTTCAGCAA 122
QY      |||||
1063 CTGATAGCTGCTGCTGCTCACTGCTCACTGCTCACTGCTTTCAGCACTCTCTTTT 1122
Db      |||||
121 CTGATANTGCTGCTCACTGCTCACTGCTCACTGCTTTCAGCACTCTCTTTT 62
QY      |||||
1123 GACATCTTCGGGTA 1137
Db      |||||
61 GACATCTTCGGGTA 47

RESULT 3
LOCUS CD109790
DEFINITION IMAGE:30346919 5', mRNA sequence.
ACCESSION CD109790
VERSION CD109790.1 GI:30753999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: cgabbs-re@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Cloning Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM387 row: c column: 24
 High quality sequence start: 144
 High quality sequence stop: 251.

FEATURES

Location/Qualifiers
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 /db_xref="taxon:9606"
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 /lab host="DH10B Tona"
 /clone lib="NIH MGC 147"
 /note="Organ: Placenta; Vector: pBluescriptR; Site_1:
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 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH MGC library."

ORIGIN

Query Match 9.8%; Score 437.2; DB 14; Length 542;
 Best Local Similarity 95.5%; Pred. No. 2e-67; Mismatches 18; Indels 5; Gaps 4;
 Matches 493; Conservative 0;

546 CTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCCTCCAGAACATCAGGTAA 605
 23 CTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCCTCCAGAACATCAGGTAA 82
 606 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATACCG 665
 83 TGGCGTTTGTGATGTCATTTTCGGTGGCTGAGATCAGCCACTTCTTCCCGATACCG 142
 666 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGACAGCTTTCATCCCGATATGCA 725
 143 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGTACGCTTTCATCCCGATATGCA 202
 726 CACCGGGTAAAGTTCA CGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 785
 203 CACCGGGTAAAGTTCA CGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 262
 786 TCACCATCGTCGCGGGGCTGTCATATATCATCTGTACATCCACAAACAGACGAT 845
 263 TCACCATCGTCGCGGGGCTGTCATATATCATCTGTACATCCACAAACAGACGAT 322
 846 AACGGCTCTCTCTTTATAGGTGTAACCTTAAACTGCACTTTCACAGTCCCTGTTCTCG 905
 323 AACGGCTCTCTCTTTATAGGTGTAACCTTAAACTGCACTTTCACAGTCCCTGTTCTCG 382
 906 TCAGCAAAAGAGCGGTTTCATTAATAAACCGGGGACCTTCAGCCATCCCTTCTGATTT 965
 383 TCAGCAAAAGAGCGGTTTCATTAATAAACCGGGGACCTTCAGCCATCCCTTCTGATTT 442
 966 TCCGCTTTTCA-CGGTTCGCGACGACAGC-ACGGGTTTCATTC--TGCATGTTGTGCT 1021
 443 TCCCTTTCCACGTTTTCGGCAGCAGACGAAAGGGGCTTCATTCCTGATGTTGTGCT 502
 1022 TACCAGACCGG-AGATATTGACATCATATATGCTTT 1056
 503 TACCAGACCGGAGATATTGACATCATATATGCTTT 538

RESULT 4

AG000761/c 723 bp DNA linear GSS 06-FEB-1999
 LOCUS Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
 DEFINITION survey sequence.
 ACCESSION AG000761
 VERSION AG000761.1 GI:2579569
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Homo sapiens genomic DNA, chromosome 21q
 JOURNAL Published Only in DataBase (1997)
 REFERENCE 2 (bases 1 to 723)
 AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
 Tel:0427-78-9732, Fax:0427-78-9561)
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ORIGIN

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 Matches 416; Conservative 0;

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 666 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGACAGCTTTCATCCCGATATGCA 725
 330 AGACCGGCACACTGGCCATATCGTGTGTCATATGCGGACAGCTTTCATCCCGATATGCA 271
 726 CACCGGGTAAAGTTCA CGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 785
 270 CACCGGGTAAAGTTCA CGGAGACTTTATCTGACAGACAGCTGCACTGGCCAGGGGA 211
 786 TCACCATCGTCGCGGGGCTGTCATATATCATCTGTACATCCACAAACAGACGAT 845
 210 TCACCATCGTCGCGGGGCTGTCATATATCATCTGTACATCCACAAACAGACGAT 151
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 150 AACGGCTCTCTCTTTATAGGTGTAACCTTAAACTGCACTTTCACAGTCCCTGTTCTCG 91
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RESULT 5
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 LOCUS

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DEFINITION Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
survey sequence.
ACCESSION AG013450 AG005773
VERSION AG013450.1 GI:3549208
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in DataBase (1998)
REFERENCE 2 (bases 1 to 725)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
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DB 366 GGGACCTCAGCCATCCCTTCCTGATTTTCGGTTTCCAGGTTTCGGCAGCGACGACG 307
QY 998 GGCTTCATTCGATGTTGTGCTTACAGACCGGAGATATTGACATCATATATGCGTTG 1057
DB 306 GGCTTCATTCGATGTTGTGCTTACAGACCGGAGATATTGACATC--ATATGCGTTG 249
QY 1058 AGCAACTGATAGCTGTGCTGTCAACTGTCACTGTAATAGCTGTCTTCATAGCACACCTC 1117
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AGENCOURT_13894516 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
CB997937
EST.
CB997937.1 GI:30292457
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
cdna Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM391 row: e column: 05
High quality sequence start: 68
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        /note="Organ: placenta; Vector: pBluescriptR; Site 1:
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        directionally cloned using primer
        5'-TTTCTTTTCTTTTCTTTT-3', size-selected for average insert
        size 2.3 kb and normalized to ROT 5. This is a primary
        library enriched for full-length clones and constructed
        using the Cap-trapper method (Carninci, in preparation).
        Library constructed by M. Brownstein (NHGRI,
        National Institutes of Health). Note: this is a NIH_MGC
        Library."
ORIGIN
    Query Match          9.0%; Score 404; DB 14; Length 522;
    Best Local Similarity 96.2%; Pred. No. 1.5e-61;
    Matches 435; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
QY 546 CTGCACATCGCTGTGTATTAAGGAGCCCTGACATTTATATTCGCCAGAACATCAGTTAA 605
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QY 606 TGGCGTTTGTGATGTCTATTTTCGGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGG 665
DB 83 TGGCGTTTGTGATGTCTATTTTCGGTGTGCTGAGATCAGCCACTTCTTCCCGATAACGG 142
QY 666 AGACCGGCACACTGGCCATATCGGTGTGCTCATATGCGCCAGCTTTTCATCCCGATATGCA 725
DB 143 AGACCGGCACACTGGCCATATCGGTGTGCTCATATGCGCCAGCTTTTCATCCCGATATGCA 202
QY 726 CCACCGGGTAAAGTTACCGGAGACTTTTATCTGACAGCAGAGCTGCGACGGCGGGA 785
DB 203 CCACCGGGTAAAGTTACCGGAGACTTTTATCTGACAGCAGAGCTGCGACGGCGGGA 262
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QY	1021	TTACCAAGACCGGAGATATTGACATCAATATATGCTTCAGCAACTGATGCTGCGTGC	1080		
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DEFINITION	OSTR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.				
ACCESSION	CB395230				
VERSION	CB395230.1	GI:30736941			
KEYWORDS	EST.				
SOURCE	Caenorhabditis elegans				
ORGANISM	Caenorhabditis elegans				
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.				
AUTHORS	1 (bases 1 to 487)				
TITLE	Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.				
JOURNAL	C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression				
COMMENT	Nat. Genet. (2003) In press Contact: Vidal M Marc Vidal Laboratory Dana Farber Cancer Institute 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 632 5180 Fax: 617 632 5739 Email: Marc.Vidal@dfci.harvard.edu Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david.hill@dfci.harvard.edu or marc.vidal@dfci.harvard.edu POLYA=No.				
FEATURES					
source					
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ORIGIN					
Query Match 8.0%; Score 357; DB 14; Length 487;					
Best Local Similarity 93.6%; Pred. No. 3.3e-53;					
Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;					

philippe_vaglio@dfci.harvard.edu

POLYA=No_ Location/Qualifiers

FEATURES

source

1..384

/organism="Caenorhabditis elegans"

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ORIGIN

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Best Local Similarity 97.7%; Pred. No. 3.4e-50;
Matches 345; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 161 CTTAGATGGTATTAGTCACTGTAGTCGCGACGCGCTTCCAAATGTTCTTCGGGTGAT 220
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QY 401 TGTCATAGTCCTGAAATCATCTGCATCAAGAACAAATTTCACTCTTATAC 453
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RESULT 11

BI174407/c

LOCUS

DEFINITION OSTF043E11.1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to

BI174407

ACCESSION BI174407.1 GI:14640210

VERSION

KEYWORDS

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.

1 (bases 1 to 384)

Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,

Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,

Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J. L., Temple, G. F.,

Brasch, M. A., Vandenhaute, J., Lamesch, P. E., Hill, D. E. and Vidal, M.

Open-reading-frame sequence tags (OSTs) support the existence of at

least 17,300 genes in C. elegans

Nat. Genet. 27 (3), 332-336 (2001)

21135099

11242119

COMMENT

Contact: Reboul J, Vaglio P

Marc Vidal Laboratory

Dana Farber Cancer Institute

44 Binney Street, Boston, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 2425

Email: Jerome.Reboul@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome.Reboul@dfci.harvard.edu or philippe_vaglio@dfci.harvard.edu

POLYA=No_ Location/Qualifiers

source

1..384

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

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QY 3351 TTTTATTTGTCAACAAAAGAGCTCGACCTCTTTCTTTCTTTCTTTTATGATT 3410
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QY 3411 TAATACGGCATTTGAGGACAAATAGCGATAGGCTGGGATAGACGATTCGGTTTGAGAAGAA 3470
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QY 3471 CATTGGAGGCTGTGCGTGAAGTGGGAGCATCACCAGAGACATTTGGGAGGC 3530
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QY 3531 TGTGCGTGCAGTACAGTCACTTAATACCATCTAAGTAGTTGATTCATAGTGTGATAT 3590
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QY 3591 GTTGTGTTTACAGTATTATGATGCTGTTTTTTA 3625
DB 66 GTTGTGTTTACAGTATTATGATGCTGTTTTTTA 32

RESULT 12

BJ555980

LOCUS

DEFINITION

BJ555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil

cDNA clone jml8n08 5', mRNA sequence.

ACCESSION BJ555980

VERSION BJ555980.1 GI:27237800

KEYWORDS

SOURCE

ORGANISM

Ipomoea nil (Japanese morning glory)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiales; Solanales; Convolvulaceae; Ipomoea.

1 (bases 1 to 337)

Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T.,

Nitase, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.

ESTs of Japanese morning glory

Unpublished (2002)

[illegible]

New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop01@med.nyu.edu
No Blast Hits ()

FEATURES source
1. .1037
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/notes="Vector: pCR4.OTOPO; 10 million Plasmodium yoelii 17X sporozoites were isolated from salivary glands of infected Anopheles stephensi mosquitoes and purified over a DE52 cellulose column. The sporozoites were cultured for 24h at 37C in the presence of 5% CO2 and 10% FBS as described in 'Transformation of sporozoites into early exoerythrocytic malaria parasites does not require host cells' (J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BDBiosciences SMART cDNA synthesis kit. Double stranded cDNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."

ORIGIN
Query Match 6.1%; Score 271.8; DB 14; Length 1037;
Best Local Similarity 91.9%; Pred. No. 3.1e-38;
Matches 294; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
QY 571 GCCTGACATTATATCCCGACACATCAGGTAAATGGCGTTTTCATGTCATTTTCGCG 630
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Db 376 GGTATCATCGCCAGCTTTCATCCCGATATGACACCGGGTAAAGTTTCACGGGAGAC 317
QY 751 TTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCGTCGCCCGGCGGTGC 810
Db 316 TTATCTGACAGCAGAGCTGCACTGGCCAGGGGATCACCATCGTCGCCCGGCGGTGC 257
QY 811 AATAATATCATCTGTATCATCCCAACAG--AGATAACGGCTCTCTTTTATAGTG 868
Db 256 AATAAGATCACTGTATCATCCCAACAG--AGATAACGGCTCTCTTTTATAGTG 197
QY 869 TAAACCTTAACTGATTC 888
Db 196 AAACCTTNNACNCCGNTC 177

RESULT 15
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ACCESSION AG000791
VERSION AG000791.1 GI:2579599
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)

AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 724)
AUTHORS Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgcl.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES source
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/organism="Homo sapiens"
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Db 27 ACGGCTCTCTCTTTTATAGGTGTAACCTTTAACTGCAATTCACAGTCCCTGTTCTCG 86
QY 906 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTT 965
Db 87 TCAGCAAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATTT 146
QY 966 TCGCTTTTCCAGGTTTCGGCAGCAGACGCGGCTTCATTTCTGCAATGGTTGTGTTACC 1025
Db 147 TCGCTTTTCCAGGTTTCGGCAGCAGACGCGGCTTCATTTCTGCAATGGTTGTGTTACC 206
QY 1026 AGACCGGAGATATGACATCATATATATGCTTGAAGCACTGATAGCTGCGCTGCACTG 1085
Db 207 AGACCGGAGATATGACATC--ATATGCTTGAAGCACTGATAGCTGCGCTGCACTG 264
QY 1086 TCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGGACATCTTCGGGTA 1137
Db 265 TCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGGACATCTTCGGGTA 316

Search completed: May 9, 2004, 21:55:51
Job time : 6945.71 secs

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model									
Run on:	May 8, 2004, 10:39:34	Search time 12095.6 Seconds (without alignments) 17418.703 Million cell updates/sec							
Title:	US-10-055-001B-13_COPY_13040_17900								
Perfect score:	4861								
Sequence:	1 cggggcccaataatgattt.....atcattatttggggcccgag 4861								
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0								
Searched:	3470272 seqs, 21671516995 residues								
Total number of hits satisfying chosen parameters:	6940544								
Minimum DB seq length:	0								
Maximum DB seq length:	2000000000								
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries								
Database :	GenEmbl.* 1: gb_ba.* 2: gb_htg.* 3: gb_in.* 4: gb_om.* 5: gb_ov.* 6: gb_pat.* 7: gb_ph.* 8: gb_pl.* 9: gb_pr.* 10: gb_ro.* 11: gb_sts.* 12: gb_sy.* 13: gb_un.* 14: gb_vi.* 15: em_ba.* 16: em_fun.* 17: em_hum.* 18: em_in.* 19: em_mu.* 20: em_om.* 21: em_or.* 22: em_ov.* 23: em_pat.*								
	Result No.	Score	Match	Length	DB	ID	Description		
	1	4861	100.0	18691	12	CVE311874	AJ311874 Cloning v		
	C 2	1462.6	30.1	18691	12	CVE311874	AJ311874 Cloning v		
	3	1193	24.5	4470	6	BD263377	BD263377 Compositi		
	4	1193	24.5	4939	6	BD263381	BD263381 Compositi		
	C 5	1193	24.5	5584	6	BD263402	BD263402 Compositi		
	C 6	1152.2	23.7	9019	12	AF408413	AF408413 Binary ve		
	7	1136	23.4	9019	12	AF408413	AF408413 Binary ve		
	8	1119	23.0	12677	12	AY196825	AY196825 PiggyBac		
	C 9	1111.2	22.9	12677	12	AY196825	AY196825 PiggyBac		
	10	1068.2	22.0	4165	6	BD263380	BD263380 Compositi		
	11	1032	21.2	4208	6	BD263379	BD263379 Compositi		
	C 12	876.4	18.0	4782	12	AY048740	AY048740 CRIM plas		
	C 13	876.4	18.0	6742	12	AY048739	AY048739 CRIM plas		
	14	846.2	17.4	4204	6	BD263378	BD263378 Compositi		
	C 15	846.2	17.4	4470	6	BD263377	BD263377 Compositi		
	16	846.2	17.4	5584	6	BD263402	BD263402 Compositi		
	17	844.6	17.4	1846	6	AX703501	AX703501 Sequence		
	C 18	844.6	17.4	4208	6	BD263379	BD263379 Compositi		
	19	844.6	17.4	5156	6	BD263382	BD263382 Compositi		
	20	844.6	17.4	5848	6	BD263361	BD263361 Compositi		
	21	844.6	17.4	5957	6	BD263353	BD263353 Compositi		
	22	844.6	17.4	5957	6	BD263354	BD263354 Compositi		
	23	844.6	17.4	6422	6	BD263362	BD263362 Compositi		
	24	844.6	17.4	6464	6	BD263349	BD263349 Compositi		
	25	844.6	17.4	6526	6	BD263356	BD263356 Compositi		
	26	844.6	17.4	6553	6	BD263350	BD263350 Compositi		
	27	844.6	17.4	6613	6	BD263366	BD263366 Compositi		
	28	844.6	17.4	6668	6	BD263367	BD263367 Compositi		
	29	844.6	17.4	6708	6	BD263358	BD263358 Compositi		
	30	844.6	17.4	6964	6	BD263352	BD263352 Compositi		
	31	844.6	17.4	13990	12	AF541939	AF541939 His-3 int		
	32	841.4	17.3	4554	6	BD263394	BD263394 Compositi		
	33	841.4	17.3	8815	6	BD263400	BD263400 Compositi		
	34	841.4	17.3	8923	6	BD263370	BD263370 Compositi		
	35	841.4	17.3	11713	6	BD263369	BD263369 Compositi		
	36	841.4	17.3	12288	6	BD263399	BD263399 Compositi		
	C 37	840	17.3	4165	6	BD263380	BD263380 Compositi		
	38	838.2	17.2	6823	6	BD263351	BD263351 Compositi		
	39	838.2	17.2	7026	6	BD263359	BD263359 Compositi		
	40	838.2	17.2	12464	6	BD263357	BD263357 Compositi		
	C 41	827	17.0	4204	6	BD263378	BD263378 Compositi		
	C 42	823.8	16.9	5156	6	BD263382	BD263382 Compositi		
	43	776.8	16.0	6025	6	BD263355	BD263355 Compositi		
	44	776.8	16.0	7278	6	BD263360	BD263360 Compositi		
	45	775.4	16.0	6264	6	BD263371	BD263371 Compositi		

ALIGNMENTS

RESULT 1	CVE311874	18691 bp	DNA	circular SYN 09-JUL-2002
LOCUS	CVE311874			
DEFINITION	Cloning vector pHELLSGATE.			
ACCESSION	AJ311874			
VERSION	AJ311874.1	GI:15982218		
KEYWORDS	kanomycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; spec gene; spectinomycin resistance protein; transposon Tn7.			
SOURCE	Cloning vector pHELLSGATE			
ORGANISM	Cloning vector pHELLSGATE			
REFERENCE	artificial sequences; vectors.			
AUTHORS	1			
	Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, P.S., Singh, S.R., Abbott, D., Stcutjesdijk, A., Robinson, S.P.,			

Pred. No. is the number of results predicted by chance to have a

GLEAVE, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)

JOURNAL MEDLINE
21451301
11576441
PUBMED
2 (bases 1 to 18691)

REFERENCE
Waterhouse, P.M.

TITLE
Direct Submission

JOURNAL
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

FEATURES

source
Location/Qualifiers
1. .18691
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DLFEALNETLTLWNSPPDWAGDERNVLTLSRIWYSAVTGKIAPKDVADWAMEKLPA
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Db 13520 CATCAAGAAACAATTTCAAACTCTTATACATTTCTCTTACAAGTCGTTGGCTCATCTG 13579
QY 541 GATTTTCAGGCTCTATACCTTAAACCGTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600
Db 13580 GATTTTCAGGCTCTATACCTTAAACCGTGATAAAGTTTCTGTAATTTCTACTGTATCGA 13639
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Db 13640 CCTGACACTGGCTGTGTATTAAGGGAGCTGTACATTTATATTCCTCCAGAACATCAGGTTA 13699
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Db 13700 ATGCGCTTTTGTATCTCATTTTCGCGTGGTGAGATCAGCACTCTCTCCCGATAACG 13759
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Db 14660 TGTAAAGGAAATAAATTAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 14719
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Db 14720 TTAGTATGATATTAATAATAATAGTCTGTATTAATTTGTAAGGAAATAATTTTATAATATATTT 14779
QY 1741 GTTTATACATAAAACAACATAGTAAATGTAAAAAATATGACAAGTGTATGTAAGAACAAGAA 1800
Db 14780 GTTTATACATAAAACAACATAGTAAATGTAAAAAATATGACAAGTGTATGTAAGAACAAGAA 14839
QY 1801 GATAAAAGTTGAGAGTAAGTATATTTTATGAATTTGATCGAACATGTAAAGTAT 1860
Db 14840 GATAAAAGTTGAGAGTAAGTATATTTTATGAATTTGATCGAACATGTAAAGTAT 14899
QY 1861 ATACGGCCGTAAGAGGTTCCAACTTTTCCACATAAATAAGATCACTTACCGGGCGTA 1920
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DEFINITION      AJ311874
ACCESSION      AJ311874
VERSION      AJ311874.1 GI:15982218
KEYWORDS      kanomycin resistance protein; neomycin phosphotransferase II; nptII
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SOURCE      Cloning vector pHELLSGATE
ORGANISM      Cloning vector pHELLSGATE
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REFERENCE      1
AUTHORS      Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
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              Construct design for efficient, effective and high-throughput gene
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              Plant J. 27 (6), 581-590 (2001)
JOURNAL      21461301
MEDLINE      11576441
PUBMED
REFERENCE      2 (bases 1 to 18691)
AUTHORS      Waterhouse,P.M.
TITLE      Direct Submission
JOURNAL      Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
              C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
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Matches 2920; Conservative 0; Mismatches 1889; Indels 104; Gaps 22;

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QY 2485 AAATATTATACGCAAGCGCAAGAGTCTGATGCGCTGGCGATTCAGGTTTCATCATGCC 2544
Db 15394 CAGTTTTACCGTTAAACAGCCCATCTTGGGAATATATGTAGAACTTGC CGGAATC 15335
QY 2545 GTCGTGATGGCTTCCATGTCGGGAGAAATGCTTTAATGAATATCAACAGTACTGCGATGAG 2604
Db 15334 GTCGTGATTTCACTCCAGACGATGAAACGTTTTTCAGTTTGTCTCATGSAAG--GTG 15277
QY 2605 TGGCAGGCGGGGATATCGCGTGGATCCGCTTACTTAAAGCCAGATAACAGTATGCG 2664
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QY 3021 AAAGCGAAGATCTATCATTTTATATAGTATATTTTCAATCAACATCTTTATTAATTC 3080
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QY 3141 GTCGAACATGATAAACAAGGTAAACATGATGATCATGTCTATGTTTATCATGATCTT 3200
Db 14746 ACAACTATATTTATATCACTAATTAATTAACATCACTTAATTTTATATACTAAAGGA 14687
QY 3201 ACATTTGGATTCATTTACAGTTGGGAAATTTGGTTCGAAATCGATTAAGCTTGATCTCTA 3260
Db 14686 AAAAAAGAAATAAT-----ATTCTCTACCAATTTGGGTACCGAATTCCTCGA 14638
QY 3261 GAGAGCTGAGCTGGATGCAATAATGATTTTTTTTACGTGATGAGTACCTGTTCTGT 3320
Db 14637 G-GAGCTGAGCTGGATGCAATAATGATTTTTTATTTTACGATGATGACCTGTTCTGT 14579
QY 3321 GCAACAAATTTGATAAGCAATGCTTTCTTATAATGCCAATTTGTACAAGAAAGCTGAAG 3380
Db 14578 GCAACAAATTTGATAAGCAATGCTTTCTTATAATGCCAATTTGTACAAGAAAGCTGAAG 14519
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QY 3561 ACCTGTGAGGGAAGATCACTTTCGAGAAATAATAATCTCTGTTGCTGCTGTTGATACCG 3620
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QY 3621 GAAGCCCTGGCCAACTTTTGGGAAATGAGACGTTGATCGGCACTTACCCATTTTCAAA 3680
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QY 3741 ACTAAAGGTGATAAAGTTTCTGTAAATTTTACTGTATCGACCTGCAGACTGGCTGTGAT 3800
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QY 3921 ATCGTGTCTCATATGCGCCAGCTTTTATCCCGATATGACACCGGTAAGTTTCAAG 3980
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QY 3981 GGAGACTTTTATCTGACAGCAGACGTCACCTGGCCAGGGGATCACCATCCCTCGCCCGG 4040
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Db 13570 CCGAACGACTTGTAAAGAGAAAGTATAAGAGTTGTGAAATTTGTTCTTGTATGATGATGAT 13511
QY 4389 TTCAGACTATGACACTAGCTGATATGATAGTAGTATGTTTTTATTTTGTACACAAAA 4448
Db 13510 TTCAGACTATGACACTAGCTGATATGATAGTAGTATGTTTTTATTTTGTACACAAAA 13451
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RESULT 3

BD263377

LOCUS

DEFINITION BD263377 4470 bp DNA linear PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of
nucleic acids.

ACCESSION

BD263377

VERSION

BD263377.1 GI:33073145

KEYWORDS

JP 2002537790-A/155.

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1 (bases 1 to 4470)

AUTHORS

Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.

TITLE

Compositions and methods for use in recombinational cloning of
nucleic acids

JOURNAL

Patent: JP 2002537790-A 155 12-NOV-2002;

INVITROGEN CORP

COMMENT

OS Artificial Sequence

PN JP 2002537790-A/155

PD 12-NOV-2002

PF 02-MAR-2000 JP 2000602252

PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/125049 PR

PI 28-MAY-1999 US 60/136744

PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC

00, C12N5/00

CC PDNR201

CC attP1

CC ccdB

CC ccdA

CC Cmr

CC attP2

CC Ker

CC ori

FH Key

FT gene

FT gene

FT gene

FT gene

FT gene

FT gene

FT gene

FT gene

FT gene

FEATURES

source

1..4470

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 24.5%; Score 1193; DB 6; Length 4470;
Best Local Similarity 100.0%; Pred. No. 4.5e-174; Indels 0; Gaps 0;
Matches 1193; Conservative 0; Mismatches 0

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QY 121 TGATATATATATCAATATATTAATTTAGATTTTGCATATAAAACAGACTACATAACTG 180
Db 141 TGATATATATATCAATATATTAATTTAGATTTTGCATATAAAACAGACTACATAACTG 200
QY 181 TAAACACAAACATATCCAGTCACATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 240
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QY 421 ACAAAATATAAAGCAATCTACCTATTATATAGCTAGTGTATAGTCTGAAATCATCTG 480
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QY 601 CCTCGACACTGGCTGTGTATAAGGAGCGCTGACATTTATATCCCGAGACATCAGGTGA 660
Db 621 CCTCGACACTGGCTGTGTATAAGGAGCGCTGACATTTATATTTCCCGAGACATCAGGTGA 680
QY 661 ATGCGGTTTTTGTATGTCTATTTTTCGGGTGGCTGAGATCAGCACTTCTTCCCGATAACG 720
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QY 1141 GTCACCTGTAATACGCTGCTCATAGCACACCTCTTTTGGACATCTTCCGGTA 1193
Db 1161 GTCACCTGTAATACGCTGCTCATAGCACACCTCTTTTGGACATCTTCCGGTA 1213

RESULT 4
BD263381
LOCUS BD263381 4939 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263381
VERSION BD263381.1 GI:33073149
KEYWORDS JP 2002537790-A/159.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 4939)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of nucleic acids
JOURNAL Patent: JP 2002537790-A 159 12-NOV-2002;
INVITROGEN CORP
COMMENT OS Artificial Sequence
PN JP 2002537790-A/159
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/136744
PI JAMES L. HARTLEY, MICHAEL A. BRASCH, GARY F. TEMPLE, DAVID CHEO PC C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC 00, C12N5/00
CC PDONR205
FH Key
FT source
FT Location/Qualifiers
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/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Query Match 24.5%; Score 1193; DB 6; Length 4939;
Best Local Similarity 100.0%; Pred. No. 4.4e-174;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAATGATTTTATTTTGTACTGATAGTACCTGTTGCTGTTGCAACAAATTGA 60
Db 3555 CGGGCCCCAAATAATGATTTTATTTTGTACTGATAGTACCTGTTGCTGTTGCAACAAATTGA 3614
QY 61 TGAGCAATGCTTTTATTAATGCCAACTTTGTACAAAAGCTGAACGAGAAACGTAAAA 120
Db 3615 TGAGCAATGCTTTTATTAATGCCAACTTTGTACAAAAGCTGAACGAGAAACGTAAAA 3674

QY 121 TGATAAATAATCAATATTAATAATAGATTTTGCATATAAAAAACAGACTACATAACTG 180
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QY 181 TAAACACAAACATATCCAGTCACTATGAAATCAACTTATAGTATGATAGTACCTGTA 240
Db 3735 TAAACACAAACATATCCAGTCACTATGAAATCAACTTATAGTATGATAGTACCTGTA 3794
QY 241 GTCGACCGACACCTTCCTCAAAATGTTCTTCGGGTGATGCTGCCAATAGTACGACGACAG 300
Db 3795 GTCGACCGACACCTTCCTCAAAATGTTCTTCGGGTGATGCTGCCAATAGTACGACGACAG 3854

QY 301 CTTTCCAAATGTTTCTTCTCAAAACGGAATCGTGGTATCCAGCTACTCGCTATTGTCCTCA 360
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QY 361 ATCCGCTATTAAATATATAAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTG 420
Db 3915 ATCCGCTATTAAATATATAAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTG 3974
QY 421 ACAAATATAAAACATCTACCTATTATATACGCTAGTGTCTGAAAATCATCTG 480
Db 3975 ACAAATATAAAACATCTACCTATTATATACGCTAGTGTCTGAAAATCATCTG 4034
QY 481 CATCAAGAACAAATTTCAAACTCTTATACATTTTCTTCTTAAAGTCGTTCCGCTTCACTG 540
Db 4035 CATCAAGAACAAATTTCAAACTCTTATACATTTTCTTCTTAAAGTCGTTCCGCTTCACTG 4094
QY 541 GATTTTCAGCCTCTATATCTTACTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGA 600
Db 4095 GATTTTCAGCCTCTATATCTTACTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGA 4154
QY 601 CTGACACTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAGAACATCAGTTA 660
Db 4155 CTGACACTGGCTGTGTATTAAGGAGCCCTGACATTTATATTTCCCGAGAACATCAGTTA 4214
QY 661 ATGCGGTTTTTGTATGTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 720
Db 4215 ATGCGGTTTTTGTATGTCATTTTTCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 4274
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Db 4275 GAGACCGGCACACTGGCCATATCGGNGGTATCATATGCGCCAGCTTTCATCCCGATATGC 4334
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Db 4335 ACCACCGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGAGCTGACCTGGCCAGGGG 4394
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Db 4695 GTCACCTGTAATACGCTCTTCATAGCACACCTCTTTTGGACATCTTCCGGTA 4747

RESULT 5
BD263402/C
LOCUS BD263402 5584 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for use in recombinational cloning of nucleic acids.
ACCESSION BD263402
VERSION BD263402.1 GI:33073170
KEYWORDS JP 2002537790-A/180.
SOURCE synthetic construct
ORGANISM artificial sequences.

1 (bases 1 to 5584)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
nucleic acids
Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/180
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252 60/126049 PR
PR 02-MAR-1999 US 60/136744
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/15, PC
00, C12N5/00
CC pDONR207
FH Key Location/Qualifiers
FT source 1..5584 /organism='Artificial Sequence'.
FT Location/Qualifiers
1..5584
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/db_xref='taxon:32630'

Query Match 24.5%; Score 1193; DB 6; Length 5584;
Best Local Similarity 100.0%; Pred. No. 4.4e-174;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATGATTTATTTGACTGATGACCTGCTGCTGTCACCAAAATGA 60
DB 5564 CGGGCCCCAAATGATTTATTTGACTGATGACCTGCTGCTGTCACCAAAATGA 5505
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DB 4724 ATCACCACCTCGTCCCGCGGGGTCTCAATATATCACTCTGTATCATCCAAACAGACGA 4665
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DB 4664 TAAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTTCCACAGTCCCTGTCTC 4605
QY 961 GTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT 1020
DB 4604 GTCAGCAAAAGAGCGGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT 4545
QY 1021 TTCCGCTTTCCAGCGTTTCGGCACGACGACGCGGCTTCATCTGCTGCTGCTGCTTAC 1080
DB 4544 TTCCGCTTTCCAGCGTTTCGGCACGACGACGCGGCTTCATCTGCTGCTGCTGCTTAC 4485
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGCTGCTGCTCACT 1140
DB 4484 CAGACCGGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTGCTGCTGCTCACT 4425
QY 1141 GTCAGTGAATACGCTGCTTCATAGCACACCTCTTTTGACATCTTGGGTA 1193
DB 4424 GTCAGTGAATACGCTGCTTCATAGCACACCTCTTTTGACATCTTGGGTA 4372

RESULT 5
AF408413/c 9019 bp DNA circular SYN 25-JUN-2002
LOCUS Binary vector pJawohl8-RNA1, complete sequence.
DEFINITION
ACCESSION AF408413
VERSION AF408413.1 GI:21552736
KEYWORDS
SOURCE Binary vector pJawohl8-RNA1
ORGANISM Binary vector pJawohl8-RNA1
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 9019)
AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somesich, I.E.
TITLE pJawohl8-RNA1 a binary vector for gene silencing in plants
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 9019)
AUTHORS Ulker, B., Lipka, V., Rademacher, T.R. and Somesich, I.E.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:188084'
/focus
/note='binary plant gene silencing vector for one-step
cloning of inverted sequences'
3803..9019
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/mol_type='genomic DNA'
/db_xref='taxon:176105'
26..1733
/note='sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, Cmr gene and ccdB'

source
repeat_region


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/protein_id="AAM62300.1"
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of DNA gyrase"
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/protein_id="AAM62301.1"
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/translation="MQFKVYTYKRESRYRLFVDVQSDIIDTPGRMVIPLASARLLSD
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1610..1736
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1762..2048
/notes="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"
complement(2073..3783)
/notes="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, Cmr gene and
ccdB gene"
complement(2073..2199)
/notes="attR2 of Gateway conversion cassette frame A"
complement(2241..2546)
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complement(2241..2546)
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of DNA gyrase"
/codon_start=1
/product="CcdB"
/protein_id="AAM62303.1"
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A"
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ORIGIN
Query Match 23.48; Score 1136; DB 12; Length 9019;
Best local similarity 68.44; Pred. No. 2.4e-165; Indels 126; Gaps 9;
Matches 1766; Conservative 0; Mismatches 690;

1263 TTTTGGCTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATGAGAAAAATCACTGG 281
262 TTAGGATCCCTCGAGATTTTCAGGAGCTAAGGAGCTAAATGAGAAAAATCACTGG 281
1983 ATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTTCAGGATTCAGTC 2042
282 ATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTTCAGGATTCAGTC 341
2043 AGTTGCTCAATGATACCTATTAACGAGCGGTTACGCTGATATACGCTTATTAAGAG 2102
342 AGTTGCTCAATGATACCTATTAACGAGCGGTTACGCTGATATACGCTTATTAAGAG 401
2103 CGTAAAGAAAAATAAGCACAAAGTTTTATCGGCGCTTTTATCACATTTCTTTCGCGCTGAT 2162
402 CGTAAAGAAAAATAAGCACAAAGTTTTATCGGCGCTTTTATCACATTTCTTTCGCGCTGAT 461
2163 GAATGCTCATCCGGAATTCGATATGGCAATGAAGAGCGGTGAGCTGATATGGGATAG 2222
462 GAATGCTCATCCGGAATTCGATATGGCAATGAAGAGCGGTGAGCTGATATGGGATAG 521
2223 TGTTCACCGCTGTTACACCGGTTTTCCCATGAGCAAACTGAAACGTTTTCATCGCTCTGAG 2282
522 TGTTCACCGCTGTTACACCGGTTTTCCCATGAGCAAACTGAAACGTTTTCATCGCTCTGAG 581
2283 TGAATACACACGAGATTTCCGCGCAGTTTCTACACATATATTCGCAAGATGTGGCTGTTA 2342
582 TGAATACACACGAGATTTCCGCGCAGTTTCTACACATATATTCGCAAGATGTGGCTGTTA 641
2343 CGGTGAAAAACCTGGCGCTATTTCCCATGAGCAAACTGAAACGTTTTCATCGCTCTGAG 2402
642 CGGTGAAAAACCTGGCGCTATTTCCCATGAGCAAACTGAAACGTTTTCATCGCTCTGAG 701
2403 CAATCCCTGGGTGAGTTTTCACGAGTTTGAATTTAAACGTCGCCCAATATGGAACAACCTCTT 2462
702 CAATCCCTGGGTGAGTTTTCACGAGTTTGAATTTAAACGTCGCCCAATATGGAACAACCTCTT 761
2463 CGCCCCCTTTTCCACATGGGCAAAATATATACGAGGCGACAAGGTGCTGATGCCGCT 2522
762 CGCCCCCTTTTCCACATGGGCAAAATATATACGAGGCGACAAGGTGCTGATGCCGCT 821
2523 GCGGATTCAGGTTTCATCGCTGAGTGGCTTCCATGTCGCGCAGAACTGCTTAATGA 2582
822 GCGGATTCAGGTTTCATCGCTGAGTGGCTTCCATGTCGCGCAGAACTGCTTAATGA 881
2583 ATTACAAACAGTACTCGGATGAGTGGCAGCGCGGCGGCTAAATCGCGCTGATCGGCTTACT 2642
882 ATTACAAACAGTACTCGGATGAGTGGCAGCGCGGCGGCTAAATCGCGCTTACT 941
2643 AAAAGCCAGATAACAGTATCGGCTATTTTCGCGCTGATATTAAGAAATATATAC 2702
942 AAAAGCCAGATAACAGTATCGGCTATTTTCGCGCTGATATTAAGAAATATATAC 1001
2703 TGATATGTCGCGCCCATTAATAGT---AATTCAGCTGCTGTTGATGAATTAATATCAATG 2759
1002 TGATATGTCGCGCCCATTAATAGT---AATTCAGCTGCTGTTGATGAATTAATATCAATG 1061
2760 ATAAAAATCTATAGTAAATAAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2819
1062 ACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGCTCAATATCTCCGGTTC 1121
2820 TAGTTTATATATTAATTAATATCTATACCATTAATTAATATTTTAGTTTAAAGTAAAT 2879
1122 TGGAAGCAACACCATGCGAAGATGAAGCCGCTGCTCGGTCGCCAACCGCTCGGAAGCGG 1181
2880 AAATATTTTGTAGAAATTTCCCAATCTGCTTGTGTAATTTATCAATAAACAATAATTAATA 2939
1182 AAATCGGAAGGATGGCTGAGGTGCGCGGTTTATTTGAAATGAACGCTCTTTTGCTG 1241
2940 ACAAGCTAAAGTAACAATAATATCAAACTAATAGAAACAGTAATCTAA-TGTAAACAAA 2998
1242 ACGAGAAACAGGACTGGTGAATGCAATTAAGGTTTACACCTATAAAGAGAGAGAGCGCT 1301
2999 CATATCTAATGCTAATATAAACAAGCGCAAGATCTATCTATTTATATAGTATTATTTTC 3058
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1302	DB	TATCGTCTGTTTGTGGATGTACAGATGTATATTATTGACACGCCCGGGCGACGATGGTG	1361
3059	QY	AATCAACATCTCTATTAAATTTCTAAATAATACTTTGTAGTTTATTAACTCTTAAATGGAT	3118
1362	DB	ATCCCCGTGCCAGTGCACGCTCTGCTGCATATAAAGTCTCCCGTGAACCTTTTACCCGGTG	1421
3119	QY	TGACTATTAAATTAATGAATTTAGTCCGACATGAATAAACAAGTAAACATGATAGATCATG	3178
1422	DB	GTGCATATCGGGGATGAAGACTGGCGCATGATGACCACCGATATGGCCAGTGTCCGGTCT	1481
3179	QY	TCATTT-----GTGTTATCATTTGATCTTTACATTTTGGATTGATTACAGTT	3221
1482	DB	TCCGTATCGGGGAAGAAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAACGCC	1541
3222	QY	GGGAAATGGGTTCT-----GAAATCGATAAGCTTTGGATCTCTCTAGAGA-----GCTGCA	3270
1542	DB	ATTAACCTGATGTTCTCGGGAATATAAATCTCAGGCTCCCTTATACACAGCCAGTCTGCA	1601
3271	QY	GCTGGATGGCAATAAATGATTTTATTTTGACTGATAGTGACCTGTTCTGTTGCAACAAAT	3330
1602	DB	GGTCGACCATAGTCAGTGGATATGTTCTGTTTACAGTATTATGTAGTCTGTTTTTTATG	1661
3331	QY	GATAAGCAA-----TGCTTTCTT	3348
1662	DB	CAAAATCTAAATTAATATTGATTTTATATCATTTTACGTTTCTCGTTTCAGCTTCTT	1721
3349	QY	ATATGCCAACTTTGTACAGAAAGCTGAACGAGAAACGTAAAAATGAT-----ATAAAT	3402
1722	DB	GTACAAAGTGGTGATCCCTCGTCCATGGGTAGAGCTTCTCGTCTCTGTCTAAACGTAA	1781
3403	QY	ATCAATATTTAAATTAGATTTTGCATATAAAAAACAGACTACATAATACTGTAAAAACAA	3462
1782	DB	GCCTCTGTGTTTTTTTCTCTGTCTCTTTTGAATGAATCAATTAGTGATGATAATCTG	1841
3463	QY	CATATCCAGTCACTATGAATCAACTACTTAGATGTTATTAGTGACCTGTAGTGCAGCTAAG	3522
1842	DB	TGTTTGATGTATCATTTGATTTAACTCTTGACAAATGATCGTATCGGAAGTGATAAAGT	1901
3523	QY	T-----TGGCAGCATCACCCGACGCACTTTGCG	3550
1902	DB	TATGGGTCAACGGTTTCAAAGAGAGAAAGACTTTTAGACTCAACTCTCGACTTTCT	1961
3551	QY	CCGAATAAATACCTGTGACGGAAGATCACTTCGCAGATAAATAAATTCCTGGTGTCCCTG	3610
1962	DB	TAATATGTATTATGCTATTTCTCTCTTTTCTGTGAAGTCTGAACAAATCTTTGGGATGTTT	2021
3611	QY	TTGATACCGGGAAGCCCTGGGCCCAACTTTTCGCAGAAATGAGAGCTTTGATCGGCACATCC	3670
2022	DB	TGCAGGTTCTAGCTTCTCCAAACACAGGAATTCTATCGCCCGGACTGGTTATCACCACT	2081
3671	QY	CATTTCAACACTCTATATCTTTTCTCTPACAAGTGGTTTCGGCTTCATCTGTGATTTTCAGC	3730
2082	DB	TTGTACAAGAAAGCTGAACGAGAAACGTAATAATGATATAAATATCAATATATTAAATTAG	2141
3731	QY	CTCTATATCTTAACCGTGATAAGTTTCTTGTAATTTCTACTGTA-----	3776
2142	DB	ATTTTGCATAAAAAACAGACTACTATACTGTGTAACACAACAATATCCAGTCACTATGG	2201
3777	QY	TCGACCTCGACACTGGCTGTGTATAAGGGAGCCCTGACATTTTATATTCGCCAGAACATCAG	3836
2202	DB	TCGACCTCGACACTGGCTGTGTATAAGGGAGCCCTGACATTTTATATTCGCCAGAACATCAG	2261
3837	QY	GTTAATGSGGTTTTGATGTCAATTTTCGGGTGGCTGAGATCAGGCACCTTCTCCCGCAT	3896
2262	DB	GTTAATGSGGTTTTGATGTCAATTTTCGGGTGGCTGAGATCAGGCACCTTCTCCCGCAT	2321
3897	QY	AACGAGACCGGCACACTGGCCATATCGTGTGTATCATGTCGCCAGCTTTTATCCCGCAT	3956
2322	DB	AACGAGACCGGCACACTGGCCATATCGTGTGTATCATGTCGCCAGCTTTTATCCCGCAT	2381
3957	QY	ATGCACCAACCGGGTAAAGTTTACCGGAGACTTTATCTCAACAGACAGCTGCACTGGCCAG	4016
2382	DB	ATGCACCAACCGGGTAAAGTTTACCGGAGACTTTATCTCAACAGACAGCTGCACTGGCCAG	2441

Qy	4017	GGGATACCATCGTCTCTCTTTTATAGGTGTAAACCTTTAAATGCACTCTGTACATCCACAAACAG	407
Db	2442	GGGATACCATCGTCTCTCTTTTATAGGTGTAAACCTTTAAATGCACTCTGTACATCCACAAACAG	2501
Qy	4077	ACGATACGGCTCTCTCTTTTATAGGTGTAAACCTTTAAATGCACTCTGTACATCCACAAACAG	4136
Db	2502	ACGATACGGCTCTCTCTTTTATAGGTGTAAACCTTTAAATGCACTCTGTACATCCACAAACAG	2561
Qy	4137	TCTCGTCAGCAAAAGAGCCGTTCAATTTCAATAAACCAGGCGAGCCTCAGCCATCCCTTCCT	4196
Db	2562	TCTCGTCAGCAAAAGAGCCGTTCAATTTCAATAAACCAGGCGAGCCTCAGCCATCCCTTCCT	2621
Qy	4197	GATTTTCGGCTTCCAGCGTTCCGACGAGACGAGCGGCTTCATCTGCATCGTTGTC	4256
Db	2622	GATTTTCGGCTTCCAGCGTTCCGACGAGACGAGCGGCTTCATCTGCATCGTTGTC	2681
Qy	4257	TTACGACGCGAGATATTGACATCATATATGCTTGAGCAACTGATAGCTGTGCTGTC	4316
Db	2682	TTACGACGCGAGATATTGACATCATATATGCTTGAGCAACTGATAGCTGTGCTGTC	2741
Qy	4317	AACGTCACTGTAATACGCTGCTTCATGACACACCTCTTTTGCATCTCTGTTCTTG	4376
Db	2742	AACGTCACTGTAATACGCTGCTTCATGACACACCTCTTTTGCATCTCTGTTCTTG	2801
Qy	4377	AT 4378	
Db	2802	AT 2803	
RESULT 8			
LOCUS	AY196825	12677 bp	DNA
DEFINITION	PiggyBac transformation vector pB-UGIR w+, complete sequence.		
ACCESSION	AY196825		
VERSION	AY196825.1	GI:28565731	
KEYWORDS			
SOURCE	PiggyBac transformation vector pB-UGIR w+		
ORGANISM	PiggyBac transformation vector pB-UGIR w+		
REFERENCE	1 (bases 1 to 12677)		
AUTHORS	Grissold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.		
TITLE	A toolkit for transformation and mutagenesis in Drosophila using		
JOURNAL	PiggyBac		
REFERENCE	2 (bases 1 to 12677)		
AUTHORS	Grissold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.		
TITLE	Direct Substitution		
JOURNAL	Submitted (13-DEC-2002) Invertebrate Targets, Syngenta		
FEATURES	Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC, 27709, USA		
source	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:221642"		
repeat_region	complement(11..>620)		
	/transposon="piggyBac transposable element"		
TATA_signal	632..998		
	/note="5x UAS hsp70 TATA signal"		
misc_feature	1003..2713		
	/note="Gateway recombination cassette A; attR1 CmR ccdB attR2"		
intron	2726..3040		
	/note="RpS5"		
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misc_feature	complement(3076..4788)		
	/note="Gateway recombination cassette B; attR1 CmR ccdB attR2"		
polyA_signal	4789..5246		
	/note="SV40"		
gene	5247..9369		
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		/notes="mini-white; derived from Drosophila" complement (<9370..9819) /transposon="piggyBac transposable element"					
repeat_region							
ORIGIN							
Query Match		23.0%; Score 1119; DB 12; Length 12677;					
Best Local Similarity		68.1%; Pred. No. 9.6e-163;					
Matches 1769; Conservative		0; Mismatches 675; Indels 155; Gaps 9;					
QY	1934	CGAGATTTTCAGGAGCTAAGGAAGCTAAATTTGGAGAAAAAATCACTGGATATACCACCG	1993	QY	2891	TAGAAATTCBAATCTGCTGTAAATTTATCAATAAACAAATATTAATAATAACAGCTAAAG	2950
DB	1210	CGAGATTTTCAGGAGCTAAGGAAGCTAAATTTGGAGAAAAAATCACTGGATATACCACCG	1269	DB	2170	GGGATGGCTGAGGTGCGCCGGTTTATTGAAATGAACGGCTCTTTTGTCTGACGAGAACAGG	2229
QY	1994	TTGATATATCCCAATGGCATGCTAAAGAACATTTTGGAGCAATTTTCAGTCAGTTGCTCAAT	2053	QY	2951	TAAACAAATAATATCAAACTAA-----	2971
DB	1270	TTGATATATCCCAATGGCATGCTAAAGAACATTTTGGAGCAATTTTCAGTCAGTTGCTCAAT	1329	DB	2230	GACTGGTGAATGCAGTTTAAAGTTTACCTATATAAGAGAGAGCGGTTATCGTCTGTT	2289
QY	2054	GTACCTATAACAGACCGTTTCAGCTGGATATTACGGCCCTTTTAAAGACCGTAAAGAAAA	2113	QY	2972	-----TAGAAACAGTAATCTAATGTAAACAAACATAATCTAATGCTAATATAACAAAGCGC	3027
DB	1330	GTACCTATAACAGACCGTTTCAGCTGGATATTACGGCCCTTTTAAAGACCGTAAAGAAAA	1389	DB	2290	TGTGGATGTACAGAGTGATATTATTGACACGCCCGGCGGAGCGGATGGTGTATCCCCCTGGC	2349
QY	2114	ATAAGCACAAGTTTATCCGGCCCTTTATTCACATTTCTTCCCGCCCTGATGAATGCTCATC	2173	QY	3028	AAGATCTATCATTTTATATAGTATTATTTCAAATCAACATTTCTTATTAAATTTCTAA-----	3083
DB	1390	ATAAGCACAAGTTTATCCGGCCCTTTATTCACATTTCTTCCCGCCCTGATGAATGCTCATC	1449	DB	2350	CAGTGCACGCTGCTGTCAGATAAAGTCTCCCGTGAATTTTACCCGGTGGTGCATATCGG	2409
QY	2174	CGGAATTCGGTATGGAATGAAGACGGTGAAGTATGGATATGGATAGTTTACACCCCTT	2233	QY	3084	--ATAATACTTGTAGTTTTTATTAACTTTCTAAATGG-----	ATTGA 3121
DB	1450	CGGAATTCGGTATGGAATGAAGACGGTGAAGTATGGATATGGATAGTTTACACCCCTT	1509	DB	2410	GGATGAAAGCTGGCGCATGATGACCACCGATATGGCAGTGTGCCGTCTCCGTTTATCGG	2469
QY	2234	GTTACACCGTTTCCATCAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAACG	2293	QY	3122	CTATTAAATTAATGAATAGTCTGAACATGAATAACAAAGGTAACATG-----	3168
DB	1510	GTTACACCGTTTCCATCAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAACG	1569	DB	2470	GGAAAGATGGCTGATCTCAGCCACCGGAAATGACATCAAAAACGCCATTAACCTGAT	2529
QY	2294	ACGATTTCCGGCAGTTTCTACATATATTCGCAAGATGTGGCGTGTACGGTGAAACACC	2353	QY	3169	-----ATAGATCATGTCTATTGTGTTATCATTTGATCTTACATTTTGGATTGAT	3214
DB	1570	ACGATTTCCGGCAGTTTCTACATATATTCGCAAGATGTGGCGTGTACGGTGAAACACC	1629	DB	2530	GTTCTGGGAATATAAAATGTCAGGCTCCCTTATACAGACCCAGTCTGCAGGTTCGACCATA	2589
QY	2354	TGGCCTATTTCCCTAAAGGTTTATGTGAATATGTTTTCTCTCAGCCAAATCCCTGGG	2413	QY	3215	TACAGTTGGGAAATTTGGGTTTTCGAAATCGATA---AGCTTGGATCCTCTAGAGAGCTGCG	3271
DB	1630	TGGCCTATTTCCCTAAAGGTTTATGTGAATATGTTTTCTCTCAGCCAAATCCCTGGG	1689	DB	2590	GTGACTGGATATGTTGTGTTTTTACAGATATATGATAGTCTGTTTTTATGCAAAATCTAAT	2649
QY	2414	TCAGTTTTCACCAAGTTTGAATTTAAAGCTGGCCAAATATGGAACACTTCTTCGCCCGCTTT	2473	QY	3272	CTGGATGGCAAAATATGATTTTATTTTGACTGATAGTGACCTGTGTTTGGTTTGCACAAATTTG	3331
DB	1690	TCAGTTTTCACCAAGTTTGAATTTAAAGCTGGCCAAATATGGAACACTTCTTCGCCCGCTTT	1749	DB	2650	TTAATATATTGATATTATATCATTTTACGTTTCTCGTTCAGCTTCTTGTAACAAAGTGG	2709
QY	2474	TCACCATGGGCAAAATATTATACGAAGCGCAAGGTGCTGATGCGCTGGCGATTCAGG	2533	QY	3332	ATAAG-----	3360
DB	1750	TCACCATGGGCAAAATATTATACGCAAGCGCAAGGTGCTGATGCGCTGGCGATTCAGG	1809	DB	2710	TGATGGCCGCTCTAGAACTAGTAGTGGGTTTCTTCTGAAGATTTTGCCCTCCAGATGCAT	2769
QY	2534	TTTCATCATGCGCTCTGTGATGCTTCCATGTGCGCAGAAATGCTTAAATGAATTTACAACTG	2593	QY	3361	TTGTACAAGAAAGCTCAACGAGAAACGTAATAATGATATAAATATCAATATATAAATTTAG	3420
DB	1810	TTTCATCATGCGCTCTGTGATGCTTCCATGTGCGCAGAAATGCTTAAATGAATTTACAACTG	1869	DB	2770	GTGCTCACGGTGGCGGTAGCAATGGCTTGTGGTTGCTGTTTAGAGACTGCTTGTCTTATAAC	2829
QY	2594	ACTGCGATGAGTGGCAGGCGGGCGGTAATCCGCTGGATCCGCTTACTAAAGCCAGAT	2653	QY	3421	ATTTTGTCAATAAAACAGACATACATACTGTAAACACACACATATCCAGTCACTATGA	3480
DB	1870	ACTGCGATGAGTGGCAGGCGGGCGGTAACCGCTGGATCCGCTTACTAAAGCCAGAT	1929	DB	2830	ACTTGGCCAGAACGAAATCTATCTAATATCCGTAGCGCTATAATGTGTAGTATAGCCGA	2889
QY	2654	AACAGATATGCGTATTTTGGCGCTGATTTTGGGATATAGAAATATATCTGATATGTCGG	2713	QY	3481	ATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGAC	3540
DB	1930	AACAGATATGCGTATTTTGGCGCTGATTTTGGGATATAGAAATATATCTGATATGTATA	1989	DB	2890	CATTTGGCGTATGAAACGAGAGACATTTCAATTTGCATATAACACTTTTCTTTTACTTAA	2949
QY	2714	GCCCAATAATAGT---AATTTCTAGCTGGTTTGTGATGAATTAATATCAATGATATAAATACTA	2770	QY	3541	GCATTTTGGCGCGAAATAAATACTGTGACGGAAGATCACTTGGCAGAAATAAATAATCCT	3600
DB	1990	CCCGAAGTATGTCAAAAGAGGTGCTGTATGAGCAGCGGTATTACAGTGACAGTTGACAG	2049	DB	2950	CGATAAGAACCCCAAAATTTCTTACGCTGCTGTGATTTGCTTCTATAAAGTTTACTTAAATTA	3009
QY	2771	TAGTAAAAATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	2830	QY	3601	GGTGTCCCTGTGTATACCGGGAAGCCCTGGGCCAACTTTTGGCGGAAAAATGAG-----	3652
DB	2050	CGACAGCTATCAGTTGCTCAAGGCATATATGATGCTCAATATCTCCGGTCTGGTAAGACA	2109	DB	3010	TTTTTTCCGATATATTTCTTTTAGGCACCTAGTGGATCCCGGGCTGCAGAAATTCGATAT	3069
QY	2831	ATAATTAATAATCTATACCAATTAATAATTTTGTATTTTAAAGTTTAAATAATTTTGT	2890	QY	3653	-----ACGTTGATCGGCACCTACCCANTTCAACTCTTTATACTTTTCTCTTA	3699
DB	2110	ACCATGAGAATGAAGCCCGTCTGCTGCTGCCGAAACGCTGGAAAGCGGAAATATCAGGAA	2169	DB	3070	CAAAGCTATCAACCACTTTGTACAAGAAAGCTGAACGAGAAACGTAATAATGATATAAATAT	3129

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Db 3249 ATTCCCGAAGACATCAGGTTAATGGCGTTTGTGATGTCATTTTCGGGTGGCTGAGATCA 3308
Qy 3880 GCCACTTCTCCCGATTAACGAGACCGGCACACCTGGCCATATCGGTGTCATCATGGC 3939
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DEFINITION PiggyBac transformation vector pB-UGIR w+, complete sequence.
ACCESSION AY196825
VERSION AY196825.1 GI:28565731
KEYWORDS
SOURCE piggyBac transformation vector pB-UGIR w+
ORGANISM piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE A toolkit for transformation and mutagenesis in Drosophila using piggyBac
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 12677)
AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2002) Invertebrate Targets, Syngenta Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC 27709, USA
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Best Local Similarity 68.6%; Pred. No. 1.5e-161;
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Qy 2054 GTACCTATPAACAGACCGGTTTCAGCTGGATATACGGCTTTTAAAGACCGTAAAGAAA 2113
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Qy 2294 ACGATTTCCGGCAGTTTCTACACATATATCGCAAGATGTGGCGTGTACCGTGAACACC 2353
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Db	3320	GGAAGAAGTGGCTGATCTCAGCCACCCGGAATGACATCAAAA	AGGCCATTAACTGAT	3261
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Db	2840	TCGTGCCAAGTGTATATAGCAAGCAGTCTCTAAACGAAC	CAAGCCATTTGCTACCGGCC	2781
Qy	3608	CTGTTGATACCGGAAGCCCTGGGCGCAACTTTTGGCGAAAT	GAGAGCT-----	3656
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QY	4301	GATAGCTGTCCGTGTCAACTGTCACTGTATAATACGCTGCTTCATAGCACACCTCTTTTGA	4360
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QY	4361	CATACTTCTGTTCTTGAT	4378
DB	2000	CATACTTCGGGTATACAT	1983

PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
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Db 2348 CTAAGTTGCGAGCATCACCGAGCACTTTGGCCGAATAAATACCTGTCAGCGGAGATC 2407
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JP 2002537790-A/157.
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ARTIFICIAL SEQUENCES
1 (bases 1 to 4208)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
nucleic acids
Patent: JP 2002537790-A 157 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
FN JP 2002537790-A/157
PD 12-NOV-2002
PR 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
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Best Local Similarity 100.0%; Pred. No. 2.8e-149;

Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	61	TGAGCAATGCTTTTATTAATGCTTGTATGCAAAAGAGTGAACGAGAAAGCTGAAAA	120
Db	3237	TGAGCAATGCTTTTATTAATGCTTGTATGCAAAAGAGTGAACGAGAAAGCTGAAAA	3296
QY	121	TGATTAATATCAATATTAATTAATTTGATTTTGCATTAATAAAGACAGTACATATATCTG	180
Db	3297	TGATTAATATCAATATTAATTAATTTGATTTTGCATTAATAAAGACAGTACATATATCTG	3356
QY	181	TAAACACAAATATCCAGTCACTATGATCAATCACTTATAGTGTATATAGTGCCTGTA	240
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QY	241	GTGACCGGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCACCGACAG	300
Db	3417	GTGACCGGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAATCTAGTCACCGACAG	3476
QY	301	CTTCCCAATGTTCTTCTCAAGCAATCGTCTGATCCAGCCTACTTCGGTATGTCCTCA	360
Db	3477	CTTCCCAATGTTCTTCTCAAGCAATCGTCTGATCCAGCCTACTTCGGTATGTCCTCA	3536
QY	361	ATGCCGTATTAATCATATAAAGAAATAGAAAAAGAGGTGGAGCTCTTTTGTGTG	420
Db	3537	ATGCCGTATTAATCATATAAAGAAATAGAAAAAGAGGTGGAGCTCTTTTGTGTG	3596
QY	421	ACAAATTAACATCTACTTATCATATACGTAGTGTATGCTCAAGTCTTCAAAATCATCTG	480
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QY	481	CATCAAGAACAAATTCACAACTCTTATCTTTCTTCAAGTCTGTCGGCTTCATCTG	540
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Db	3717	GATTTTCAGCTCTATACCTTATTAACGTTAAGTTCCTGTAATTTCTACGTATATCGA	3776
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QY	781	ACCACCGGTAAGTTTCAACGGGAGACTTTATCTGACAGCAGAGTGCACCTGGCCAGGGG	840
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Db	4017	ATCACCATCGCTCGCCGGCGGTGTCAATATATCATCTGTATCAATCAACACACACGA	4076
QY	901	TAAAGCTCTCTCTTTTATAGGTGTAACCTTAACCTTAACCTTAACCTTAACCTTAACCT	960
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QY	1021	TTCCGCTTTCCA 1032	
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DEFINITION CRIM plasmid pCAH63, 4782 bp DNA circular SYN 17-OCT-2001
ACCESSION AY048740
VERSION AY048740.1 GI:16209176
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VERSION AY048739.1 GI:16209172
KEYWORDS
SOURCE
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1 (bases 1 to 6742)
AUTHORS Haldemann, A. and Wanner, B.L.
TITLE Conditional-replication, integration, excision, and retrieval
plasmid-host systems for gene structure-function studies of
bacteria
J. Bacteriol. 183 (21), 6384-6393 (2001)
MEDLINE 21475783
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REFERENCE 2 (bases 1 to 6742)

AUTHORS	Haldemann, A. and Wanner, B.I.	
TITLE	Direct Submission	
JOURNAL	Submitted (29-JUL-2001) Biological Sciences, Purdue University, Lilly Hall, West Lafayette, IN 47907, USA	
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Query Match	18.0%; Score 876.4; DB 12; Length 6742;	
Best Local Similarity	71.6%; Pred. No. 2.3e-125;	
Matches 1259; Conservative	0; Mismatches 441; Indels 58; Gaps 6;	
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LOCUS
DEFINITION BD263378 4204 bp DNA linear PAT 17-JUL-2003
Compositions and methods for use in recombinational cloning of
nucleic acids.
ACCESSION BD263378
VERSION BD263378.1 GI:33073146
KEYWORDS JP 2002537790-A/156.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 4204)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 156 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/156
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
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Best Local Similarity 98.5%; Pred. No. 1.1e-120; Indels 0; Gaps 0;
Matches 854; Conservative 0; Mismatches 13;

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RESULT 15

BD263377/c

LOCUS

DEFINITION

BD263377

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD263377

Compositions and methods for use in recombination cloning of nucleic acids.

BD263377

JP 2002537790-A/155.

synthetic construct

artificial sequences.

1 (bases 1 to 4470)

Compositions and methods for use in recombination cloning of nucleic acids

Hartley J.L., Brasch M.A., Temple G.F. and Cheo D.

Compositions and methods for use in recombination cloning of nucleic acids

Patent: JP 2002537790-A 155 12-NOV-2002;

INVITROGEN CORP

PN JP 2002537790-A/155

PF 02-MAR-2000 JP 2000602252

PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR

PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

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 Db 1233 AGAATATATCTGATATGTCGGGCCCA 1207

Search completed: May 9, 2004, 11:27:37
 Job time : 12150.6 secs

FEATURES

source

1..4470

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 17.4%; Score 846.2; DB 6; Length 4470;
 Best Local Similarity 98.5%; Pred. No. 1.1e-120;
 Matches 854; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1852 TAAGATGATATACGCCGGTAAAGAGTTCCAACTTCCACCAATGAATAAGATCACTA 1911
 Db 2073 TGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTCCACCAATGAATAAGATCACTA 2014
 QY 1912 CCGGCGCTATTTTGGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAA 1971
 Db 2013 CCGGCGCTATTTTGGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAA 1954
 QY 1972 AAATCACTGGATATACCAAGCTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 2031
 Db 1953 AAATCACTGGATATACCAAGCTGATATATCCCAATGGCATCGTAAAGAACATTTTGAG 1894
 QY 2031 GCATTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGCTGGATATATACGCC 2091
 Db 1894 GCATTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGCTGGATATATACGCC 1834

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 23:36:51 ; Search time 1119.77 Seconds
(without alignments)
18441.778 Million cell updates/sec

Title: US-10-055-001B-13_COPY_13040_17900

Perfect score: 4861

Sequence: 1 cggggcccaataatgattt.....atcattattggggcccgag 4861

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq 25Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match		DB ID	Description
		Length	%		
1	4861	100.0	18691	6 ABQ82130	Abq82130 Acceptor
2	2563.2	52.7	17476	6 ABQ82141	Abq82141 Acceptor
3	2528	52.0	17681	6 ABQ82143	Abq82143 Acceptor
4	2510.6	51.6	17458	6 ABQ82142	Abq82142 Acceptor
c 5	1462.6	30.1	18691	6 ABQ82130	Abq82130 Acceptor
6	1193	24.5	4470	3 AAC55521	Aac55521 Donor pla
7	1193	24.5	4470	7 ABZ58767	Destinati
8	1193	24.5	4892	8 ADA50329	Plasmid v
9	1193	24.5	4939	3 AAC55525	Donor pla
c 10	1193	24.5	5584	3 AAC55632	Donor pla
c 11	1193	24.5	5584	7 ABZ58766	Donor pla
12	1186.6	24.4	4428	7 ABZ58768	Destinati
13	1186.6	24.4	4627	7 ABZ58769	Destinati
14	1186.6	24.4	4627	7 ABZ58770	Destinati
15	1068.2	22.0	4165	3 AAC55524	Donor pla
16	1032	21.2	4208	3 AAC55523	Donor pla
c 17	846.2	17.4	4204	3 AAC55522	Donor pla
c 18	846.2	17.4	4428	7 ABZ58768	Destinati
c 19	846.2	17.4	4470	3 AAC55521	Donor pla
c 20	846.2	17.4	4470	7 ABZ58767	Destinati
c 21	846.2	17.4	4627	7 ABZ58769	Destinati
c 22	846.2	17.4	4627	7 ABZ58770	Destinati
c 23	846.2	17.4	4892	8 ADA50329	Plasmid v

ALIGNMENTS

RESULT 1

ABQ82130

ID ABQ82130 standard; DNA; 18691 BP.

XX

AC ABQ82130;

XX

DT 11-DEC-2002 (first entry)

XX

DE Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.

XX

KW Chimeric nucleic acid construct; recombinational cloning; silencing;

XX

KW recombination site; double stranded RNA; plant; ds.

XX

OS Synthetic.

XX

PN WO200259294-A1.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-AU000073.

XX

PR 26-JAN-2001; 2001US-0264067P.

XX

PR 29-NOV-2001; 2001US-0333743P.

XX

(CSIR) COMMONWEALTH SCI & IND RES ORG.

XX

PA Wesley S, Waterhouse P, Helliwell C;

XX

PI WPI; 2002-682669/73.

XX

DR New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

XX

PT Claim 13; Page 62-72; 104pp; English.

XX

PS The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.

XX Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

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QY	1	CGGGCCCCAAATGATGATTTATTTGACTGATAGTGACCTGTCGTTGCCAACAATTGA	60		
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QY	61	TGAGCAATGCTTTTATATGCAACTTTGTACAAAAAGCTGAAACGAGAAACGTAAAA	120		
DB	13100	TGAGCAATGCTTTTATATGCAACTTTGTACAAAAAGCTGAAACGAGAAACGTAAAA	13159		
QY	121	TGATATAAATCAATATATTAATAGATTGCAATTTGCAATAAAAAACAGATACATATCTG	180		
DB	13160	TGATATAAATCAATATATTAATAGATTGCAATTTGCAATAAAAAACAGATACATATCTG	13219		
QY	181	TAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGTA	240		
DB	13220	TAAAAACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGTA	13279		
QY	241	GTGACCGCAGCCTTCCAAATGTTCTTCCGGTGATGCTGCCAATTTAGTGCACGACAG	300		
DB	13280	GTGACCGCAGCCTTCCAAATGTTCTTCCGGTGATGCTGCCAATTTAGTGCACGACAG	13339		
QY	301	CTTCCCAATGTTCTTCCAAACGGAAATCGTGTATCCAGCCTACTCGCTATTGCTCTCA	360		
DB	13340	CTTCCCAATGTTCTTCCAAACGGAAATCGTGTATCCAGCCTACTCGCTATTGCTCTCA	13399		
QY	361	ATGCCGTATTAAATCATATAAAGAAATAAGAAAAAGAGTGCAGGCTCTTTTGTGTG	420		
DB	13400	ATGCCGTATTAAATCATATAAAGAAATAAGAAAAAGAGTGCAGGCTCTTTTGTGTG	13459		
QY	421	ACAAATAAACAATCTACTATTCATATACGCTAGTGCATAGTCTCTGAAAATCATCTG	480		
DB	13460	ACAAATAAACAATCTACTATTCATATACGCTAGTGCATAGTCTCTGAAAATCATCTG	13519		
QY	481	CATCAAGAACAAATTCACAACTCTTATCTTCTCTCAAGTCTCGTTCGGCTCATCTG	540		
DB	13520	CATCAAGAACAAATTCACAACTCTTATCTTCTCTCAAGTCTCGTTCGGCTCATCTG	13579		
QY	541	GATTTTCAGCCTCTATCTACTATAACAGTGAATAAGTTTCTGTAATTTCTACTGTATCGA	600		
DB	13580	GATTTTCAGCCTCTATCTACTATAACAGTGAATAAGTTTCTGTAATTTCTACTGTATCGA	13639		
QY	601	CTGCGAGACTGGTGTATTAAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA	660		
DB	13640	CTGCGAGACTGGTGTATTAAGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA	13699		
QY	661	ATGGCGTTTTTGATGTCAATTTTCGGGTGGCTCAGATCAGCACTTCTTCCCGATAACG	720		
DB	13700	ATGGCGTTTTTGATGTCAATTTTCGGGTGGCTCAGATCAGCACTTCTTCCCGATAACG	13759		
QY	721	GAGACCGGCACTGCGCATATCCGGTGGTCAATCGCGCAGCTTTTATCCCGGATATGC	780		
DB	13760	GAGACCGGCACTGCGCATATCCGGTGGTCAATCGCGCAGCTTTTATCCCGGATATGC	13819		
QY	781	ACCACCGGGTAAGTTTCACGGGAGACTTTATCTGACAGCAGCTGCACCTGCCAGGGGG	840		

DB	13820	ACCACCGGGTAAGTTTCACGGGAGACTTTATCTGACAGCAGCTGCACCTGCCAGGGGG	13879		
QY	841	ATCACCATCCGTCGCCCCGGGGGTGTCAATAATATACATCTCTGTACATCCACAAACAGACGA	900		
DB	13880	ATCACCATCCGTCGCCCCGGGGGTGTCAATAATATACATCTCTGTACATCCACAAACAGACGA	13939		
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DB	14000	GTACAGCAAAAGAGCGGTTCAATTCATAAAGCGGCGACCTCAGCATCCCTTCTCTGATT	14059		
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QY	1081	CAGACCGGAGATTTGACATCATATATGCTTTGAGCACTGATAGTCTGCTGCTCAACT	1140		
DB	14120	CAGACCGGAGATTTGACATCATATATGCTTTGAGCACTGATAGTCTGCTGCTCAACT	14179		
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DB	14240	TCAAGCTCTCAATTTTCGGCAAAAGTTGGCCCGAGGCTTCCCGGTATCAACAGGACACCA	14299		
QY	1261	GGATTTATTTATTCGCGAAGTGATCTTCGCTCAGAGTATTTATTCGGCGCAAGTCGG	1320		
DB	14300	GGATTTATTTATTCGCGAAGTGATCTTCGCTCAGAGTATTTATTCGGCGCAAGTCGG	14359		
QY	1321	TGGGTGATGCTGCCAATCTAGTGCACCTACAGTCACTTAATACCATCTAAGTAGTTGAT	1380		
DB	14360	TGGGTGATGCTGCCAATCTAGTGCACCTACAGTCACTTAATACCATCTAAGTAGTTGAT	14419		
QY	1381	CATAGTGAAGTGCATATGTTGTTTACAGTATTTATAGTCTGTTTTTATGCAAAATC	1440		
DB	14420	CATAGTGAAGTGCATATGTTGTTTACAGTATTTATAGTCTGTTTTTATGCAAAATC	14479		
QY	1441	TAAATTAATATATGATATTTATATCAATTTTACGCTTCTTCGTTACAGCTTCTCTG	1500		
DB	14480	TAAATTAATATATGATATTTATATCAATTTTACGCTTCTTCGTTACAGCTTCTCTG	14539		
QY	1501	GTGCGCATTTAAGAAAGCATTTGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCAGT	1560		
DB	14540	GTGCGCATTTAAGAAAGCATTTGCTTATCAATTTGTTGCAACGAAACAGGTCACTATCAGT	14599		
QY	1561	CAAAATAAATCAATTTTGGCATCCAGCTCGAGTCTCGAGGAATTCGGTACCCCAAT	1620		
DB	14600	CAAAATAAATCAATTTTGGCATCCAGCTCGAGTCTCGAGGAATTCGGTACCCCAAT	14659		
QY	1621	TGTTAAGAAATAATTTATTTTCTTTTCTTTTATAGTATAAAATAGTTAAGTAGTTAA	1680		
DB	14660	TGTTAAGAAATAATTTATTTCTTTTCTTTTATAGTATAAAATAGTTAAGTAGTTAA	14719		
QY	1681	TTAGTATGATTAATAATATAGTTGTTTAAATTTGTGAAAAATAATTTTATAATATATT	1740		
DB	14720	TTAGTATGATTAATAATATAGTTGTTTAAATTTGTGAAAAATAATTTTATAATATATT	14779		
QY	1741	GTTTACATAAACAACATAGTAAATGTAAAAAATAATGACAAGTGTGTGTAAGACGAAGA	1800		
DB	14780	GTTTACATAAACAACATAGTAAATGTAAAAAATAATGACAAGTGTGTGTAAGACGAAGA	14839		
QY	1801	GATAAAGTTGAGAGTAAGTATATTTATTTTAAATGAAATTTTGTGAAACATGTAAGATGAT	1860		
DB	14840	GATAAAGTTGAGAGTAAGTATATTTATTTTAAATGAAATTTTGTGAAACATGTAAGATGAT	14899		
QY	1861	ATACCGCGGTAAAGGTTTCCAACTTCCCATTAATGAATAAGATCACTACCGGCGGTA	1920		

Db 14900 ATACGGCCGTAAGAGTTTCCAACTTTCCACATAATGAATAGATCACTACCGGGCGTA 14959
QY 1921 TTTTGTGAGTTATCGAGATTTTCAGAGCTAAGGAGCTAAATAGGAGAAAAAATCACT 1980
Db 14960 TTTTGTGAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATAGGAGAAAAAATCACT 15019
QY 1981 GGATATACACACGTTTGATATATCCCAATGGCATCGTAAAGACATTTTCAGGAGCACTTCAG 2040
Db 15020 GGATATACACACGTTTGATATATCCCAATGGCATCGTAAAGACATTTTCAGGAGCACTTCAG 15079
QY 2041 TCAGTTGCTCAATGTACCTATATAACAGACCGTTGAGCTGGATATACGGCTTTTAAAG 2100
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Db 15320 AGTGAATACACGACGATTTCCGGCAGTTTTCACACATATATTCGCAAGATGTGGCGTG 15379
QY 2341 TAGCGTGAACACCTGGCCCTATTCCCTAAAGGTTTATTGAGAATATGTTTTCGCTCA 2400
Db 15380 TAGCGTGAACACCTGGCCCTATTCCCTAAAGGTTTATTGAGAATATGTTTTCGCTCA 15439
QY 2401 GCCAATCCCTGGTGTAGTTTACCAGTTTGAATTAACGTCGGCACAATGAGCAACTTC 2460
Db 15440 GCCAATCCCTGGTGTAGTTTACCAGTTTGAATTAACGTCGGCACAATGAGCAACTTC 15499
QY 2461 TTCCGCCCCCGTTTTCACCATGGGCAATATATACGCAAGGGCACAAGGTGCTGATCGCG 2520
Db 15500 TTCCGCCCCCGTTTTCACCATGGGCAATATATACGCAAGGGCACAAGGTGCTGATCGCG 15559
QY 2521 CTGGCGATTCAGGTTTCATCGCGCTGTGTATGGCTTCCATGTCCGCAAGATGCTTAAT 2580
Db 15560 CTGGCGATTCAGGTTTCATCGCGCTGTGTATGGCTTCCATGTCCGCAAGATGCTTAAT 15619
QY 2581 GAATTACACAGTACTGCGATGAGTGGCAGGGGGGGCGGTAATCGCGTGGATCCGGCTTA 2640
Db 15620 GAATTACACAGTACTGCGATGAGTGGCAGGGGGGGCGGTAATCGCGTGGATCCGGCTTA 15679
QY 2641 CTAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTCGGGTATAAGAAATATAT 2700
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Db 15980 CAAGCTAAAGTAACAAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 16039

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QY 3061 TCAACATTTCTTATTAATTTCTAAATAATACTTGTAGTTTATTAATCTTCTAAATGGATTG 3120
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QY 3241 CGATAAGCTTGGATCCTCTAGAGAGCTGAGCTGGATGSCAAATAATGATTTTATTTGA 3300
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Db 16400 TTGTACAAAGAAAGCTGAACGAGAAAGCTAAATATATAATATCAATATATTAATAATTAG 16459
QY 3421 ATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAACATATCCAGTCACTATGA 3480
Db 16460 ATTTTGCATAAAAAACAGACTACATAATACTGTAAACACAAACATATCCAGTCACTATGA 16519
QY 3481 ATCAACTACTAGATGTTATTTAGTCACTGTTAGTCACTGTTAGTCACTGTTAGTCACTGTTAGT 3540
Db 16520 ATCAACTACTAGATGTTATTTAGTCACTGTTAGTCACTGTTAGTCACTGTTAGTCACTGTTAGT 16579
QY 3541 GCACCTTTCGCGCGAATAAATACCTGTGACGGAAGATCACTTCGCAAGATAAATAAATACTCT 3600
Db 16580 GCACCTTTCGCGCGAATAAATACCTGTGACGGAAGATCACTTCGCAAGATAAATAAATACTCT 16639
QY 3601 GGTGTCCTTGTGTATACCGGGAAGCCCTGGGCAACTTTTGGCGAAATAGAGACGTTGAT 3660
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Db 16700 CGGCACTACCACTTTCACAACTTTTACTTTTCTTACAGTCTGTTGCGCTTCTCATCTG 16759
QY 3721 GATTTTCAGCCTCTATACCTTAAACGTTGATAAAGTTTCTGTAAATTTCTACTGTATCGA 3780
Db 16760 GATTTTCAGCCTCTATACCTTAAACGTTGATAAAGTTTCTGTAAATTTCTACTGTATCGA 16819
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Db |||||||
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Db |||||||
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Db |||||||
QY 17180 GTCAGCAAAAGAGCCGTTTCATTTCAATAAACGGGGACCTCAGCCATCCCTTCCTGATT 17239
Db |||||||
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Db |||||||
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Db |||||||
QY 17300 CAGACCGAGATATTCACATCATATATGCTTCAGCACTGATAGCTGCTGCAACT 17359
Db |||||||
QY 4321 GTCACGTATATAGCTGCTTCATPAGCACACCTCTTTTTCACATPACTCTCTTTCATGAC 4380
Db |||||||
QY 17360 GTCACGTATATAGCTGCTTCATPAGCACACCTCTTTTTCACATPACTCTCTTTCATGAC 17419
Db |||||||
QY 4381 AGATGATTTTCAGGACTATCAGACTAGCTATATATAGTATGATGTTTATTTGTC 4440
Db |||||||
QY 17420 AGATGATTTTCAGGACTATCAGACTAGCTATATATAGTATGATGTTTATTTGTC 17479
Db |||||||
QY 4441 ACACAAAAAGAGGCTCGCACCTCTTTTCTTATTTCTTTTATGATTTTAAATACGGCAT 4500
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QY 4801 CAATTTGTTGCAAGACAGGTCATCTATCAGTCAAAATTAATATATATTTGGGGCCGA 4860
Db |||||||
QY 17840 CAATTTGTTGCAAGACAGGTCATCTATCAGTCAAAATTAATATATTTGGGGCCGA 17899
Db |||||||
QY 4861 G 4861
Db 17900 G 17900

RESULT 2

ABQ82141

ID ABQ82141 standard; DNA; 17476 BP.

XX AC

ABQ82141;

XX 11-DEC-2002 (first entry)

XX DE

XX AC

XX Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24.

XX DE

XX KW

XX Chimeric nucleic acid construct; recombinational cloning; silencing;

XX KW

XX recombination site; double stranded RNA; plant; ds.

XX OS

XX Synthetic.

XX PN

WO200259294-A1.

XX

PD

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PF

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01-AUG-2002.

24-JAN-2002; 2002WO-AU000073.

26-JAN-2001; 2001US-0264067P.

29-NOV-2001; 2001US-0333743P.

(CSTR) COMMONWEALTH SCI & IND RES ORG.

Wesley S, Waterhouse P, Helliwell C;

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 15; Page 74-83; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

Query Match 52.7%; Score 2563.2; DB 6; Length 17476;

Best Local Similarity 77.7%; Pred. No. 0;

Matches 3651; Conservative 0; Mismatches 23; Indels 1024; Gaps 5;

QY 82 GCCAATTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAAATATCAATATATT 141

Db 13025 GACAAATTTGTACAAAAAGCTGAACGAGAAACGTAAATGATATAAATATCAATATATT 13084

QY 142 AAATTAGATTTTGCATAAAAAACAGACTACATACTGTATAAAACACAAATATCCAGTC 201

Db 13085 AAATTAGATTTTGCATAAAAAACAGACTACATACTGTATAAAACACAAATATCCAGTC 13144

QY 202 ACTATGAATCAACTACTTAGTGGTATTAGTGCCTGTAGTCGACCGACGCTTCCAAA 261

Db 13145 ACTATGAATCAACTACTTAGTGGTATTAGTGCCTGTAGTCGACCGACGCTTCCAAA 13204

QY 262 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAA 321

Db 13205 TGTTCCTCGGTGATGCTGCCAACTTAGTCGACCGACGCTTCCAAATGTTCTTCTCAA 13264

QY 322 ACGGAATCGTGTATCCAGCCTACTCGCTATTGCTCAATGCGGTATTAAATCATATAAA 381

Db 13265 ACGGAATCGTGTATCCAGCCTACTCGCTATTGCTCAATGCGGTATTAAATCATATAAA 13324

QY 382 AGAATTAAGAAAGAGGTGCGACCTCTTTTGTGTGACAAATATAAAACATCTACCT 441

Db 13325 AGAATTAAGAAAGAGGTGCGACCTCTTTTGTGTGACAAATATAAAACATCTACCT 13384

QY	442	ATTCTATACGCTAGTGTCTAGTCTCTGAAATCACTGCAATCAAGAAACAATTTCAACAC	501	QY	1522	TGCTTATCAATTTGTTGCAACGAACAGGTCACTATCACTCAAAATAAAATCAATTTATTCG	1581
Db	13385	ATTCTATACGCTAGTGTCTAGTCTCTGAAATCACTGCAATCAAGAAACAATTTCAACAC	13444	Db	14448	-----	14447
QY	502	TCTTTATCTTTCTCTTCAAGTCTGCTCGCTCTCATCTGGATTTTTCAGCTCTATACCTTA	561	QY	1582	CATCCAGCTGAGTCTCTGAGGAATTCGGTACCCCA-ATTGGTAAAGGAATAATTTATTT	1640
Db	13445	TCTTTATCTTTCTCTTCAAGTCTGCTCGCTCTCATCTGGATTTTTCAGCTCTATACCTTA	13504	Db	14448	-----TCTCGAGGAATTCGGTACCCCAAGTTGGTAAAGGAATAATTTATTT	14492
QY	562	CTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTATATA	621	QY	1641	TCTTTTTCCTTTTCTGATATAAAATAGTTTAACTGATGTTAAATAGTATGATTAATAATA	1700
Db	13505	CTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGCTGGCTGTATATA	13564	Db	14493	TCTTTTTCCTTTTCTGATATAAAATAGTTTAACTGATGTTAAATAGTATGATTAATAATA	14552
QY	622	AGGAGCTCTGACATTTATATTTCCCGAAGACATCAGGTTAATGCGGTTTGTGATGCAATTT	681	QY	1701	TAGTTGTTTATTAATTTGTAAGAAAATAATTTTATAAATATATTTTGTACATAAACAATAGT	1760
Db	13565	AGGAGCTCTGACATTTATATTTCCCGAAGACATCAGGTTAATGCGGTTTGTGATGCAATTT	13624	Db	14553	TAGTTGTTTATTAATTTGTAAGAAAATAATTTTATAAATATATTTTGTACATAAACAATAGT	14612
QY	682	TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGAGACCGGCACACTGGCCATA	741	QY	1761	AATGTAAAAAATATGACAACTGATGTTGAACGAGAAAGATAAAAGTTGAGAGTAAGT	1820
Db	13625	TCGCGTGGCTGAGATCAGCCACTTCTTCCCGATAAACGAGACCGGCACACTGGCCATA	13684	Db	14613	AATGTAAAAAATATGACAACTGATGTTGAACGAGAAAGATAAAAGTTGAGAGTAAGT	14672
QY	742	TGCGTGGTCAATCGCGCAGCTTTTCATCCCGATATGCACCAACCGGTAAGTTTCAACGG	801	QY	1821	ATATTTATTTTAAATGCAATTTTGTATCGAACATGTTAAGATGATATACCGCGGTAAGAGTTTC	1880
Db	13685	TGCGTGGTCAATCGCGCAGCTTTTCATCCCGATATGCACCAACCGGTAAGTTTCAACGG	13744	Db	14673	ATATTTATTTTAAATGCAATTTTGTATCGAACATGTTAAGATGATATACCGCGGTAAGAGTTTC	14725
QY	802	GAGACTTTATCTGACAGCAGCTGCTGACCTGGCCAGGGGATCACCATCGTCCGCCGGC	861	QY	1881	CAACTTTTACCATAATGAATAAGATCACTACCGGCGTATTTTGTGAGTTATCGAGATT	1940
Db	13745	GAGACTTTATCTGACAGCAGCTGCTGACCTGGCCAGGGGATCACCATCGTCCGCCGGC	13804	Db	14726	-----	14725
QY	862	GTGTCAATATATCACTCTGTATCATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG	921	QY	1941	TTTCAGAGCTAAGGAAGCTTAAATGGAGNAAAAATCACTGGATATACACCGTTGATAT	2000
Db	13805	GTGTCAATATATCACTCTGTATCATCCACAAACAGACGATAACGGCTCTCTCTTTTATAG	13864	Db	14726	-----	14725
QY	922	GTGTAAACCTTAACTGCAATTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCA	981	QY	2001	ATCCCAATGGCATCGTAAAGAACATTTTGGAGCAATTTTCACTCAGTTGTCTCAATGTACCTA	2060
Db	13865	GTGTAAACCTTAACTGCAATTTCAACAGTCCCTGTTCTGTCAGCAAAAGAGCGTTTCA	13924	Db	14726	-----	14725
QY	982	TTCAATAAACGGGGACCTCAGCCATCCCTCTCTGATTTTCCGCTTCCAGCGTTCCGC	1041	QY	2061	TAAACAGACCGTTACGCTGGATATTAACGCCCTTTTAAAGACCGTAAAGAAAATAAGCA	2120
Db	13925	TTCAATAAACGGGGACCTCAGCCATCCCTCTCTGATTTTCCGCTTCCAGCGTTCCGC	13984	Db	14726	-----	14725
QY	1042	ACGACAGCAGCGGCTTCAITTCGATGTTGTTGCTTTACAGACCGGAGATATGACATC	1101	QY	2121	CAAGTTTATCCGGCTTTTATTTACATTTCTTGCCTGCTGATGAATGTCTCATCCGGAAT	2180
Db	13985	ACGACAGCAGCGGCTTCAITTCGATGTTGTTGCTTTACAGACCGGAGATATGACATC	14044	Db	14726	-----	14725
QY	1102	ATATATGCTTGAGCAATGATAGCTGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTG	1161	QY	2181	CCGTATGCAATGAAAGACGGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG	2240
Db	14045	ATATATGCTTGAGCAATGATAGCTGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTG	14104	Db	14726	-----	14725
QY	1162	ATAGCACACCTCTTTTGGACATCTTCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1221	QY	2241	CGTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCAACGAGATT	2300
Db	14105	ATAGCACACCTCTTTTGGACATCTTCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	14164	Db	14726	-----	14725
QY	1222	AAGTTGGCCAGGCTTCCCGGTATCAACAGGACACAGGATTTATTTCTGCGGAAG	1281	QY	2301	CCGCGAGTTTCTACACATATATTCCGCAAGATGTGGCGTGTACGGTGAACAACTGGCCTA	2360
Db	14165	AAGTTGGCCAGGCTTCCCGGTATCAACAGGACACAGGATTTATTTCTGCGGAAG	14224	Db	14726	-----	14725
QY	1282	TGATCTTCCGTCACAGGATTTATTTCCGCGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1341	QY	2361	TTTCCCTTAAAGGTTTATTGAGAATATGTTTTCGTCTCAGCCAACTCCCTGGGTGAGTTT	2420
Db	14225	TGATCTTCCGTCACAGGATTTATTTCCGCGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG	14284	Db	14726	-----	14725
QY	1342	GTCGACTACAGTCACTAATACCACTAAGTAGTGTGATTCATAGTGAAGTGAATGATGTTGT	1401	QY	2421	CACGAGTTTGAATTAACCGTGGCAATATGGAACAACTTCTTGGCCCCGTTTTCACCAT	2480
Db	14285	GTCGACTACAGTCACTAATACCACTAAGTAGTGTGATTCATAGTGAAGTGAATGATGTTGT	14344	Db	14726	-----	14725
QY	1402	GTTTTACAGTATATGATGCTGTTTATATGCAAAATCTAATTAATATATATGATATTT	1461	QY	2481	GGGCAATATATATACGCAAGCGCAGCAAGGTGCTGATGCCGCTGCGATTTCAGGTTTCATCA	2540
Db	14345	GTTTTACAGTATATGATGCTGTTTATATGCAAAATCTAATTAATATATATGATATTT	14404	Db	14726	-----	14725
QY	1462	ATATCATTTTACGTTTCTGTTTACAGTTTCTGTTTACAAAGTTGGCAATTTAAGAAAGCAT	1521	QY	2541	TGCGCTGTGATGGCTTCCATGTCCGAGAAATGCTTAAATGAATTAACAAGTACTCGGA	2600
Db	14405	ATATCATTTTACGTTTCTGTTTACAGTTTCTGTTTACAAAGTTGGCAATTTAAGAAAGCAT	14447	Db	14726	-----	14725
				QY	2601	TGAGTGGCAGGCGGGCGGTAAATCGCGTGGATCGGCTTACTTAAAGCCAGATAACAGTA	2660

Db	14165	AA	TTCCGGCCAGCGGCTTC	CCGGTATCAACAGGACACACAGAGTTATTATTTATCTCGGAAG	14222	
Qy	1282	TGA	TCTTCGGTCA	CAGGTATTTATTCCGGCGCAAGTGC	GTCCGGTATGCTGCCAACTTA	1341
Db	14225	TGATCTCCGT	CA	CAGGTATTTATTCCGGCGCAAGTGC	GTCCGGTATGCTGCCAACTTA	14284
Qy	1342	GT	CGACTACAGGTCAC	TATACCACTAAGTAGTGGTTCATAGTCAGTCAGGATATGTTGT	1401	
Db	14285	GT	CGACTACAGGTCAC	TATACCACTAAGTAGTGGTTCATAGTCAGTCAGGATATGTTGT	14344	
Qy	1402	GT	TTTACAGTATTA	GTAGTCGTTTTTTTATGCAGAAATCTAATTTAAATATATTCATATTT	1461	
Db	14345	GT	TTTACAGTATTA	GTAGTCGTTTTTTTATGCAGAAATCTAATTTAAATATATTCATATTT	14404	
Qy	1462	ATAT	CATTTTACGTTCTCG	TTCAGCTTCTTGTCAGAAAGTGGCATTTATTAAGAAAGCAT	1521	
Db	14405	ATAT	CATTTTACGTTCTCG	TTCAGCTTCTTGTCAGAAAGTGGCATTTATTAAGAAAGCAT	14447	
Qy	1522	TGCTTATCAATTTG	TGCAACGAA	CAGGTCATCATCAGTCAGTCAAAATAAAATCATTTATTG	1581	
Db	14448	-----	-----	-----	-----	14447
Qy	1582	CAT	CCAGCTCGAGCTCCT	CGAGAAATTCGGTACCCCA-ATTGGTAAAGAAATAATATT	1640	
Db	14448	-----	-----	-----	-----	14492
Qy	1641	TC	TTTTTTTCCTTTT	TAGTATATAAATAGTTAAGTCATGTTAAATAGTATGATTTATATATA	1700	
Db	14493	TC	TTTTTTTCCTTTT	TAGTATATAAATAGTTAAGTCATGTTAAATAGTATGATTTATATA	14552	
Qy	1701	TAG	TGTTTAAATTTGTG	AAAAATAATTTATAAATATATGTTTACATAAAACAAATAGT	1760	
Db	14553	TAG	TGTTTAAATTTGTG	AAAAATAATTTATAAATATATGTTTACATAAAACAAATAGT	14612	
Qy	1761	AAT	GTA	AAAAATATGAC	AGTGAATGTAAGACGAGAGATATAAAGTTGAGAGT	1820
Db	14613	AAT	GTA	AAAAATATGAC	AGTGAATGTAAGACGAGAGATATAAAGTTGAGAGT	14672
Qy	1821	AT	ATTTATTTTAAATG	AAATTTGATCGAACATGTAAGATGATATACGGCCGGTAAGAGTTC	1880	
Db	14673	AT	ATTTATTTTAAATG	AAATTTGATCGAACATGTAAGATGATATAC	TAGCATTA-14725	
Qy	1881	CA	ACTTTCACATTAATGA	ATAATAGTACATACGGCGGTATTTTTTGTAGTTATCGAGATT	1940	
Db	14726	-----	-----	-----	-----	14725
Qy	1941	TT	CAGGAGCTAAG	GAAGCTAAATGGAGAAAAAATCACTGGATATACCACGGTTGATAT	2000	
Db	14726	-----	-----	-----	-----	14725
Qy	2001	AT	CCCAATGCGATG	TAAAGAACATTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTA	2060	
Db	14726	-----	-----	-----	-----	14725
Qy	2061	TA	CCGACCGCTTCAG	CTGGNTATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCA	2120	
Db	14726	-----	-----	-----	-----	14725
Qy	2121	CA	AGTTTTTATCCG	GCCTTTATTCACATTCCTGGCCGCTGATGAATGCTCATCCGGAATT	2180	
Db	14726	-----	-----	-----	-----	14725
Qy	2181	CG	TATGCGAATGA	AAACGGTGAGCTGGTGATATGGATAGTGTTTACCCCTTGTTACAC	2240	
Db	14726	-----	-----	-----	-----	14725
Qy	2241	CG	TTTCCATGAGCA	AACTGAAACGTTTTTTCATCGCTCTGGAGTGAATACACGACGATTT	2300	
Db	14726	-----	-----	-----	-----	14725
Qy	2301	CG	CGAGTTTCTAC	ACATATATTCGCAAGATGTGGGTGTTACGGTGAAAAACCTGGCCTA	2360	
Db	14726	-----	-----	-----	-----	14725

Qy	2361	TTTCCCTAAAGGGTTATTGAGAAATATGTTTTTTCGTCTCAGCCAAATCCTCGGTGAGTTT	2420
Db	14726	-----	14725
Qy	2421	CACCAGTTTTTGATTTAAACGTGGCCAAATATGGACAACATCTTTCGCCCCCGTTTTTCACCAT	2480
Db	14726	-----	14725
Qy	2481	GGGCAAAATATATACGCAAGGCGACAAGTGCTGATGCGGTGGGATTCAGGTTCAATCA	2540
Db	14726	-----	14725
Qy	2541	TGCCGTCGTGTGGCTTCCATGTCGGCAGAAATGCTTAATGAATTACAAACAGTACTGCGA	2600
Db	14726	-----	14725
Qy	2601	TGAGTGGCAGGGCGGGCGTAATCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGTA	2660
Db	14726	-----	14725
Qy	2661	TGCGTATTTGCGCGCTGATTTTTCGGGTATAAGAATATATACTGATATGTCGGGCCCAT	2720
Db	14726	-----	14742
Qy	2721	ATAGTAATTCCTAGCTGGTTTGATGAATTAATAATCAATGATAAAAACTACTAGTAAAAAT	2780
Db	14743	ATAGTAATTCCTAGCTGGTTTGATGAATTAATAATCAATGATAAAAACTACTAGTAAAAAT	14802
Qy	2781	AAGAATAATAAATTAATAATAATTTTTTTTATGATTAATAGTTTATATATATAATTAAT	2840
Db	14803	AAGAATAATAAATTAATAATAATTTTTTTTATGATTAATAGTTTATATATAATTAAT	14862
Qy	2841	ATCTATACCAATTAATAATAATTTTTTAGTTTAAAAAGTTTAATAATAATTTTGTAGAAATCC	2900
Db	14863	ATCTATACCAATTAATAATAATTTTTTAGTTTAAAAAGTTTAATAATAATTTTGTAGAAATCC	14922
Qy	2901	AATCTGCTTGTAATTTTCAATAAACAATAATTAATAAACAGCTAAAGTAACAAATAAA	2960
Db	14923	AATCTGCTTGTAATTTTCAATAAACAATAATTAATAAACAGCTAAAGTAACAAATAAA	14982
Qy	2961	TATCAAACTAATAAGAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAATATAAC	3020
Db	14983	TATCAAACTAATAAGAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAATATAAC	15042
Qy	3021	AAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATCTTTAAATTC	3080
Db	15043	AAAGCGCAAGATCTATCATTTTATATAGTATTTATTTTCAATCAACATCTTTAAATTC	15102
Qy	3081	TAAATAATCTGTAGTTTTTAACTTCTAAATGGATTGACTATTAATTAATTAATGAATTA	3140
Db	15103	TAAATAATCTGTAGTTTTTAACTTCTAAATGGATTGACTATTAATTAATTAATGAATTA	15162
Qy	3141	GTCGAAATCAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTGTTATCATTTGATCTT	3200
Db	15163	GTCGAAATCAATAAACAAGGTAAACATGATAGATCATGTCAATGTGTGTTATCATTTGATCTT	15222
Qy	3201	ACATTTGGATTGATTACAGTTGGGAAATTTGGGTTCGAATCGATAAGCTTG-----GAT	3254
Db	15223	ACATTTGGATTGATTACAGTTGGGAAAGCTGGGTTCGAATCGATAAGCTTGCGCTGCAGT	15282
Qy	3255	CCTCTAGAGAGCTGCAGCTGGATGGCAATAATGATTTTTTTTTCACATGATAGTGACCTG	3314
Db	15283	TATCATCATCATATAGACACACGAAATTAAGTATTCAGATTATCAGTTAANGCTATGTA	15342
Qy	3315	TTCTGTTGCAACAAA-----	3328
Db	15343	ATATTTGGCCATPACCAATCAATTAATAAAATATAGATCAGTTTAAAGAAAGATCAAAAGCTC	15402
Qy	3329	-----	3328
Db	15403	AAAAAATAAAGAGAAAGGGTCTTAACCAAGAAATTAAGAGGAAAAAAGCTAGAAAT	15462

CC polyadenylation region functional in the eukaryotic cell. The first and
CC fourth recombination sites, or the second and third recombination sites
CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match 51.6%; Score 2510.6; DB 6; Length 17458;
Best Local Similarity 77.2%; Pred. No. 0;
Matches 3628; Conservative 0; Mismatches 29; Indels 1040; Gaps 6;
QY 82 GCGAATCTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 141
DB 13025 GACAAAGTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATATCAATATATT 13084
QY 142 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 201
DB 13085 AAATTAGATTTTGCATAAAAACAGACTACATAATCTGTAAACACACATATCCAGTC 13144
QY 202 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGCACGACGAGCTTCCCAA 261
DB 13145 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGCACGACGAGCTTCCCAA 13204
QY 262 TGTCTTCGGGTGATGCTGCAACTTAGTCGACCGACAGCTTCCGAAATGTTCTTCTCAA 321
DB 13205 TGTCTTCGGGTGATGCTGCAACTTAGTCGACCGACAGCTTCCGAAATGTTCTTCTCAA 13264
QY 322 ACGGAATCTGCTGATCAGCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAA 381
DB 13265 ACGGAATCTGCTGATCAGCTACTCGCTATTGTCTCAATGCGGTATTAAATCATATAAA 13324
QY 382 AGAAATTAAGAAAAAGAGTGGAGGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 441
DB 13325 AGAAATTAAGAAAAAGAGTGGAGGCTCTTTTGTGTGACAAAAATAAAACATCTACCT 13384
QY 442 ATTATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCATCAAGAACAAATTCACAC 501
DB 13385 ATTATATACGCTAGTGTCTATAGTCTCTGAAATCATCTGCATCAAGAACAAATTCACAC 13444
QY 502 TCTTATACCTTTTCTTTACAAGTCGTTTGGGCTTTCATCTGGATTTTTCAGGCTCTATATCTTA 561
DB 13445 TCTTATACCTTTTCTTTACAAGTCGTTTGGGCTTTCATCTGGATTTTTCAGGCTCTATATCTTA 13504
QY 562 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 621
DB 13505 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGACAGCTGGCTGTGTATA 13564
QY 622 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 681
DB 13565 AGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTAATGCGTTTGTGATGTCATTT 13624
QY 682 TCAGGCTGGCTGAGATCAGCCACTTCTTCCCGATACCGAGACCGGACACTGGCCATA 741
DB 13625 TCAGGCTGGCTGAGATCAGCCACTTCTTCCCGATACCGAGACCGGACACTGGCCATA 13684
QY 742 TCAGTGTGTATCATGCGCCAGCTTTCTATCCCGATATGACACCGGCTTAAGTTTCACGG 801
DB 13685 TCAGTGTGTATCATGCGCCAGCTTTCTATCCCGATATGACACCGGCTTAAGTTTCACGG 13744
QY 802 GAGACTTTATCTGACACGACAGTGCATCTGCCAGGGGGATCACCATCCGTCGCCGGGC 861
DB 13745 GAGACTTTATCTGACACGACAGTGCATCTGCCAGGGGGATCACCATCCGTCGCCGGGC 13804

QY 862 GTGTCAATAATATCACTCTCTGTATCATCCACAAACAGACGATACCGCTCTCTCTTTTATAG 921
DB 13805 GTGTCAATAATATCACTCTGTATCATCCACAAACAGACGATACCGCTCTCTCTTTTATAG 13864
QY 922 GTGTAAACCTTAAACTGTCATTTACCACTGTCCTCTCTCGTCAGCAAAAGAGCGCTTCAT 981
DB 13865 GTGTAAACCTTAAACTGTCATTTACCACTGTCCTCTCTCGTCAGCAAAAGAGCGCTTCAT 13924
QY 982 TTCAATAAACCGGCGAGCTCAGCAATCCCTCTCTCTGTATTTTCCGCTTTCCAGCGTTCCGC 1041
DB 13925 TTCAATAAACCGGCGAGCTCAGCAATCCCTCTCTCTGTATTTTCCGCTTTCCAGCGTTCCGC 13984
QY 1042 ACGCAGACGACGGGCTTCATCTGCATGGTGTGCTTACACAGACGGAGATATTGACATC 1101
DB 13985 ACGCAGACGACGGGCTTCATCTGCATGGTGTGCTTACACAGACGGAGATATTGACATC 14044
QY 1102 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTAAATACGTTGCTTC 1161
DB 14045 ATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACTGTCACTGTAAATACGTTGCTTC 14104
QY 1162 ATAGCAGACCTCTTTTGTGACATATCTCGGCTAGTGTGCGGATCAACGCTCTCATTTTCGCAA 1221
DB 14105 ATAGCAGACCTCTTTTGTGACATATCTCGGCTAGTGTGCGGATCAACGCTCTCATTTTCGCAA 14164
QY 1222 AAGTTGGCCCGAGGGCTTCCCGGTATCAACAGGGACACGAGATTTATTTTCTGCGAAG 1281
DB 14165 AAGTTGGCCCGAGGGCTTCCCGGTATCAACAGGGACACGAGATTTATTTTCTGCGAAG 14224
QY 1282 TGATCTTCCGTCACAGGTATTTATTTCCGCGCAAGTGTGCGGCTGATGTGCGCAACTTA 1341
DB 14225 TGATCTTCCGTCACAGGTATTTATTTCCGCGCAAGTGTGCGGCTGATGTGCGCAACTTA 14284
QY 1342 GTCCACTACAGGTCACTAATACCATCTAAAGTGTGATTCATGTGACTGCGATATGTTGT 1401
DB 14285 GTCCACTACAGGTCACTAATACCATCTAAAGTGTGATTCATGTGACTGCGATATGTTGT 14344
QY 1402 GTTTTACAGTATTAATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTT 1461
DB 14345 GTTTTACAGTATTAATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTT 14404
QY 1462 ATATCATTTTACGTTTCTGTTACAGCTTTCTTTGTACAAAGTGTGCGATTTAAGAANGCAT 1521
DB 14405 ATATCATTTTACGTTTCTGTTACAGCTTTCTTTGTACAAAGTGTGCGATTTAAGAANGCAT 14447
QY 1522 TGCTTATCAATTTTGTGCAACGACAGGTCACTATCAGTCAAAATATAAATCATTTATTCG 1581
DB 14448 ----- 14447
QY 1582 CATCCAGCTGCAAGCTCTCGAGGAATTCGGTACCCCAATTCGGTAAGGAAATAATTTATTTT 1641
DB 14448 -----TCTCGAGGAATTCGGTACC-----AAGTGTAGGAAATAATTTATTTT 14489
QY 1642 CTTTTTCTTTTACGTATAAATAGTTAAGTGTGTTAATTTAGTATGATTAATAATAAT 1701
DB 14490 CTTTTTCTTTTACGTATAAATAGTTAAGTGTGTTAATTTAGTATGATTAATAATAAT 14549
QY 1702 AGTGTGTTAATTTGCAAAAAATAATTTATAAATAATTTTATACATAAACAACATAGTA 1761
DB 14550 AGTGTGTTAATTTGCAAAAAATAATTTATAAATAATTTTATACATAAACAACATAGTA 14609
QY 1762 ATGTAAAAAATATGACAAAGTGTGTGAACGAGGAAGATATAAAGTTGAGAGTAAGTA 1821
DB 14610 ATGTAAAAAATATGACAAAGTGTGTGAACGAGGAAGATATAAAGTTGAGAGTAAGTA 14669
QY 1822 TATTATTTTATGATTAATTTGATCGAACATGTAAGATGATATACCGCGGTGAAGGTTCC 1881
DB 14670 TATTATTTTATGATTAATTTGATCGAACATGTAAGATGATATACCGCATTA----- 14721
QY 1882 AACTTTTCCATTAATGAATAAGATCACTACCGGCGGTATTTTTTTGAGTTATCGAGATTT 1941
DB 14722 ----- 14721
QY 1942 TCAGGAGCTAAGGAAGCTTAAATGGAGAAAAAATCACTGGATATACCCGCTTGATATA 2001

Db 14722 ----- 14721
QY 2002 TCCCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAGTTGCTCAATGTACCTAT 2061
Db 14722 ----- 14721
QY 2062 AACAGACGGTTCAGCTGGAATATTACGGCCCTTTTAAAGACCGTAAAGAAAAATAAGCAC 2121
Db 14722 ----- 14721
QY 2122 AAGTTTTATCGGCCCTTTTATTCACATTTCTTGCCCGCTGAUGAATGCTCATCGGAATTC 2181
Db 14722 ----- 14721
QY 2182 CGTATGGCAATGAAGACGGTGAGCTGAGCTGGTGATATGGGATAGTGTTCACCCCTGTTTACACC 2241
Db 14722 ----- 14721
QY 2242 GTTTTCCATGAGCAAACTGAACGTTTTTCATCGCTCTGGAGTGAATACCAACGACGATTC 2301
Db 14722 ----- 14721
QY 2302 CGGCAATTTTACACATATATTTCGAAGATGTGGGTGTACGGTGAAGAACTGGCCCTAT 2361
Db 14722 ----- 14721
QY 2362 TTCCCTAAAGGGTTTATGAGAAATATGTTTTTCGTCCTCAGCCAAATCCCTGGGTGAGTTTC 2421
Db 14722 ----- 14721
QY 2422 ACCAGTTTTGATTTAAACGTGGCCATATGGACAACTTCTTGCCCGCCGTTTTTCAACATG 2481
Db 14722 ----- 14721
QY 2482 GGCAAATATTATACGAAGCGGACGAAGTGTGTGANGCCGTGGCGATCAGGTTTCATCAT 2541
Db 14722 ----- 14721
QY 2542 GCGCTGTGTAGTGCTTCCATGTGCGCAGATGCTTAATGAATTACAAACAGTACTGCGAT 2601
Db 14722 ----- 14721
QY 2602 GAGTGCAGGGGGGGGTAATCGCGTGGATCGGCTTACTAAAGCCAGATAACAGTAT 2661
Db 14722 ----- 14721
QY 2662 GCCTATTGTGCGCTGATTTTTGCGGTATAGAATATATCTGATATGTGCGGCCCATTA 2721
Db 14722 ----- 14739
QY 2722 TAGTAATTTCTAGCTGTTGATCAATTAATATCAATGATAAATACTATAGTAAATAAATA 2781
Db 14740 TAGTAATTTCTAGCTGTTGATGAATTAATACTCAATGATAAATACTATAGTAAATAAATA 14799
QY 2782 AGAATAAATAAATAAATAATTTTTTATGATTAATAAGTTTATATATAATAATAATA 2841
Db 14800 AGAATAAATAAATAAATAATTTTTTATGATTAATAAGTTTATATATAATAATAATA 14859
QY 2842 TCTATACCATTACTAAATATTTTATGATTAATAAGTTTATATAATTTTGTAGAAATTTCCA 2901
Db 14860 TCTATACCATTACTAAATATTTTATGATTAATAAGTTTATATAATAATAATAATAATA 14919
QY 2902 ATCTGCTGTAATTTATCAATAAATAAATAATTAATAAATAAATAAGTTTAAAGTAATAATA 2961
Db 14920 ATCTGCTGTAATTTATCAATAAATAAATAATTAATAAATAAAGTTTAAAGTAATAATA 14979
QY 2962 ATCAAACTAATAGAAACAGTAATCTAATGTAAACAAAACATAATCTAATGTCTAATAAACA 3021
Db 14980 ATCAAACTAATAGAAACAGTAATCTAATGTAAACAAAACATAATCTAATGTCTAATAAACA 15039
QY 3022 AAGCGAAGATCTATCATTTTTATATAGTATTTTTTCAATCAACATTTCTTATTAATTTCT 3081

Db 15040 AAGCGCAAGATCTATCATTTTTATATAGTATTTTCAATCAACATTTCTTATTAATTTCT 15099
QY 3082 AAATAATACCTGTAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3141
Db 15100 AAATAATACCTGTAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15159
QY 3142 TCGAACATTAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTGTATCAATGATCTTA 3201
Db 15160 TCGAACATTAATAAACAAGGTAAACATGATAGATCATGTCAATTTGTGTATCAATGATCTTA 15219
QY 3202 CATTTGATTTGATTTACAGTTGGGAAATTTGGGTTGAAATCGATAAGCTTGGATCTCTAG 3261
Db 15220 CATTTGATTTGATTTACAGTTACTTA-----CCTTAAGCTTTGATCTCTCTAG 15265
QY 3262 AGAGCTGCAGCTGGATGGCAAAATATGATTTTTTGTGATGATGACCTGTTGCTGTTG 3321
Db 15266 A----- 15266
QY 3322 CAACAAATTTGATAAGCAATGCTTTCTTATAATGCAACTTTGTACAAGAAAGCTGAACGA 3381
Db 15267 -----CCACTTTGTACAAGAAAGCTGAACGA 15292
QY 3382 GAAACGTAATAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 3441
Db 15293 GAAACGTAATAATGATATAAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 15352
QY 3442 ACATAAATCTGTAAACACAACATATCCAGTCACTATGATCAACTACTTATGATGGTATT 3501
Db 15353 ACATAAATCTGTAAACACAACATATCCAGTCACTATGATCAACTACTTATGATGGTATT 15412
QY 3502 AGTGACCTGTAGTCACTAAAGTTGGCAGCATCACCCGAGCACATTTGGCCGGAATAATA 3561
Db 15412 AGTGACCTGTAGTCACTAAAGTTGGCAGCATCACCCGAGCACATTTGGCCGGAATAATA 15472
QY 3562 CCGTGTGACGGAGATCACTTCGCAGAAATAATAATACTCTGTGTCCTCTGTTGATACCCGG 3621
Db 15473 CCGTGTGACGGAGATCACTTCGCAGAAATAATAATACTCTGTGTCCTCTGTTGATACCCGG 15532
QY 3622 AAGCCCTGGCCCAACTTTTGGCGAAATAGACAGTTGATCGSACTACCCATTTCAACAAC 3681
Db 15533 AAGCCCTGGCCCAACTTTTGGCGAAATAGACAGTTGATCGS-----ATTTCAACAAC 15584
QY 3682 TCTTATACCTTTTCTCTTACAGTCGTTCCGCTTCACTGGAATTTTCAGCTCTATACATTA 3741
Db 15585 TCTTATACCTTTTCTCTTACAGTCGTTCCGCTTCACTGGAATTTTCAGCTCTATACATTA 15644
QY 3742 CTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 3801
Db 15645 CTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 15704
QY 3802 AGGAGCCTTGACATTTATATCCCGAGAAACATCAGGTTAATGGGTTTTTGTATGTCATTT 3861
Db 15705 AGGAGCCTTGACATTTATATCCCGAGAAACATCAGGTTAATGGGTTTTTGTATGTCATTT 15764
QY 3862 TCGCGTGTCTGAGATCAGCCTCTTCCCGAATAACGAGACCGGCACACTGGCCATA 3921
Db 15765 TCGCGTGTCTGAGATCAGCCTCTTCCCGAATAACGAGACCGGCACACTGGCCATA 15824
QY 3922 TCGGTGTCATCATGCGCCAGCTTTTCATCCCGATATGCACCAACCGGGTAAAGTTTCAACG 3981
Db 15825 TCGGTGTCATCATGCGCCAGCTTTTCATCCCGATATGCACCAACCGGGTAAAGTTTCAACG 15884
QY 3982 GAGACTTTTATCGACAGCAGCTGCACTGGCCAGGGGATCACCATCGCTCGCCCGGGC 4041
Db 15885 GAGACTTTTATCGACAGCAGCTGCACTGGCCAGGGGATCACCATCGCTCGCCCGGGC 15944
QY 4042 GTGTCAATTAATCACTCTGTATCCCAACACAGACGATTAACGGCTCTCTCTTTTATAG 4101
Db 15945 GTGTCAATTAATCACTCTGTATCCCAACACAGACGATTAACGGCTCTCTCTTTTATAG 16004
QY 4102 GTGTAAACCTTAACTGCAATTTTCCAGTCCCTGTTCTCGTCAGCAAAAAGACGGTTCAT 4161
Db 16005 GTGTAAACCTTAACTGCAATTTTCCAGTCCCTGTTCTCGTCAGCAAAAAGACGGTTCAT 16064

QY	4162	TTCAATAAACCGGGCGACCTCAGCACAATCCCTTCCTGATTTTTCGGCTTCCAGCGTTCCGC	4221
Db	16065	TTCAATAAACCGGGCGACCTCAGCACAATCCCTTCCTGATTTTTCGGCTTCCAGCGTTCCGC	16124
QY	4222	ACGCAGACGACGGGCTTCATTTCTGCATGTTGTGCTTACCAGACGGAGATATTGACATC	4281
Db	16125	ACGCAGACGACGGGCTTCATTTCTGCATGTTGTGCTTACCAGACGGAGATATTGACATC	16184
QY	4282	ATATATGCCCTTGAGCAACTGATAGCTGCGCTGTCAACTGTCACTGTAAATACGCTGCTTC	4341
Db	16185	ATATATGCCCTTGAGCAACTGATAGCTGCGCTGTCAACTGTCACTGTAAATACGCTGCTTC	16244
QY	4342	ATAGCACACCTCTTTTGTGACATACTCTGTTCTTGATCGAGATGATTTTCAGGACTATGA	4401
Db	16245	ATAGCACACCTCTTTTGTGACATACTCTGTTCTTGATCGAGATGATTTTCAGGACTATGA	16304
QY	4402	CACTAGCGTATATGAATAGGTAGATGTTTATTATTTTGTGCACACAAAAAGGCTCGGCAC	4461
Db	16305	CACTAGCGTATATGAATAGGTAGATGTTTATTATTTTGTGCACACAAAAAGGCTCGGCAC	16364
QY	4462	CTCTTTTCTCTATTCTTTTCTTTTATGATTTAATAACGCACTTTGAGGACAAATAGCGAGTAGGCT	4521
Db	16365	CTCTTTTCTCTATTCTTTTCTTTTATGATTTAATAACGCACTTTGAGGACAAATAGCGAGTAGGCT	16424
QY	4522	GGATACGACGATCCGTTTTGAGAAGAACATTTGGAAGGCTGCGTGCGACTAAGTTGGCA	4581
Db	16425	GGATACGACGATCCGTTTTGAGAAGAACATTTGGAAGGCTGCGTGCGACTAAGTTGGCA	16484
QY	4582	GCATACCCGAGAACATTTGGAAGGCTGCGTGCGACTACAGGTCACCTAATACCATCTA	4641
Db	16485	GCATACCCGAGAACATTTGGAAGGCTGCGTGCGACTACAGGTCACCTAATACCATCTA	16544
QY	4642	AGTAGTTGATTCATAGTACGATGGATATGTTGTGTTTTACAGTATTATGTAAGTCTGTTTTT	4701
Db	16545	AGTAGTTGATTCATAGTACGATGGATATGTTGTGTTTTACAGTATTATGTAAGTCTGTTTTT	16604
QY	4702	TATGCAAAATCTAAATTTAATATATGATATTTATATATCATTTTACGTTTCTCGTTACGCTT	4761
Db	16605	TATGCAAAATCTAAATTTAATATATGATATTTATATATCATTTTACGTTTCTCGTTACGCTT	16664
QY	4762	TTTTGTACAAAGTTGGC	4778
Db	16665	TTTTGTACAAACTGTG	16681

RESULT 5	
ABQ82130/c	
ID	ABQ82130 standard; DNA; 18691 BP.
XX	
AC	ABQ82130;
XX	
XX	
DT	11-DEC-2002 (first entry)
XX	
DE	Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
XX	
XX	Chimeric nucleic acid construct; recombinational cloning; silencing;
KW	recombination site; double stranded RNA; plant; ds.
KW	

OS Synthetic.
XX WO200259294-A1.
PN
XX
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-AU000073.
PF
XX
XX 26-JAN-2001; 2001US-0264067P.
PR
PR 29-NOV-2001; 2001US-0333743P.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
XX
XX Wesley S, Waterhouse P, Helliwell C;
PI

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 13; Page 62-72; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as *Escherichia coli*; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerase of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence 18691 BP: 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

Query Match	30.1%;	Score 1462.6;	DB 6;	Length 18691;
Best Local Similarity	59.4%;	Pred. No. 4.2e-194;		
Matches 2920;	Conservative	0;	Mismatches 1889;	Indels 104; Gaps 22;
QY	1	CGGGCCCCAAATAAGTATTTATTTTGACTGATAGTGAACCTGTTGCTGTGCAACAAATTGA	60	
Db	17898	CGGGCCCCAAATAAGTATTTATTTTGACTGATAGTGAACCTGTTGCTGTGCAACAAATTGA	17839	
QY	61	TGAGCAATGCTTTTTTATAATGCCAACCTTTGTACAAAAAGCTGAACGAGAAACGTAAAA	120	
Db	17838	TGAGCAATGCTTTTTTATAATGCCAACCTTTGTACAAAAAGCTGAACGAGAAACGTAAAA	17779	
QY	121	TGATATAATATCAATATATTAATTTAGATTTTGCATAAAAAACAGACTACATAATACTG	180	
Db	17778	TGATATAATATCAATATATTAATTTAGATTTTGCATAAAAAACAGACTACATAATACTG	17719	
QY	181	TAAAAACACACATATCCAGTACTATGAATCAACTACTTAGATGGTATTAGTACCTGTGA	240	
Db	17718	TAAAAACACACATATCCAGTACTATGAATCAACTACTTAGATGGTATTAGTACCTGTGA	17659	
QY	241	GTGACGCGACAGCCTTCGAAATGTTCTTCGGGTGATGCTGCCAATTAGTCGACCGACAG	300	
Db	17658	GTGACGCGACAGCCTTCGAAATGTTCTTCGGGTGATGCTGCCAATTAGTCGACCGACAG	17599	
QY	301	CCTTCCAAATGTCTTCTCAAACGGAAATCGTGGTATCCAGCCTACTCGCTATTGTCCTCA	360	
Db	17598	CCTTCCAAATGTCTTCTCAAACGGAAATCGTGGTATCCAGCCTACTCGCTATTGTCCTCA	17539	
QY	361	ATGCGGTATTAAATCATAAAAAGAATAAGAAAAAGAGTGGAGCCTCTTTTTTGTGTG	420	
Db	17538	ATGCGGTATTAAATCATAAAAAGAATAAGAAAAAGAGTGGAGCCTCTTTTTTGTGTG	17479	
QY	421	ACAAAATAAAACATCTACTCTTTCATATACGCTAGTGTCAATAGTCCTGAAAAATCATCTG	480	
Db	17478	ACAAAATAAAACATCTACTCTTTCATATACGCTAGTGTCAATAGTCCTGAAAAATCATCTG	17419	
QY	481	CATCAAGAAACAATTTCCAAACTCTTATCTTTTCTCTTACAAAGTCGTTCCGCTTCATCTG	540	

Db 17418 CATCAAGAACAGAAGTATGTCAAAAGAGAGTGTCATGAA---GCAGCGTATTACAGTG 17362
Qy 541 GATTTTCAGCCTCTATACCTTAACACGFGATAAAGTTTCTGTAAATTTCTACTGTATCGA 600
Db 17361 ACAGTTGACAGCGACGACGTATCAGTTGCTCAAGGCATATATGATGTCATATCTCCGGTC 17302
Qy 601 CCTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATATTCGCCAGAACATCAGGTTA 660
Db 17301 TGGTAAGCACACCAACATGACAGAAATGAAGCCCGCTGCTGCGTGCC---GAACGCTGGAAG 17245
Qy 661 ATGGCGTTTGTATGTCATTTTCGGCGTGGTGGATCAGCCACCTCTTTCCCGGATAACG 720
Db 17244 CGAAATTCAGAAAGGATGGCTGAGTGCAGCGGTATTTGAATGAACGCTCTTTTG 17185
Qy 721 GAGACGGGACACTGGGCATATCGGTGGTGCATCGCGGACCTTTCTATCCCGGATATGC 780
Db 17184 CTGACGAGAACAGG-----ACTGGTGAATGTCAGTTTAAGGTTTACACCTTATAAAGA 17131
Qy 781 ACCACGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGCGTGCACTGGCCAGGGGG 840
Db 17130 GAGAGCGGTTATCGTCTGTTGTGGANGTACAGAGTGATTTATTGACACGCCCCGGGCA 17071
Qy 841 ATCACCATCCGTCGCGCGCGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 900
Db 17070 CGGATGGTGATCCCTGTGCCAGTGCACGTCTGCTGCAGATAAAGTCTCCCGTGAACCT 17011
Qy 901 TAAAGCCTCTCTCTTTTATAGTGTAACCTTAACTGCACTTTTACC-----AGTCCCT 954
Db 17010 TACCGCGTGTGCATATCGGGATGAAGCTGGCGCATGATCACCACGCGATATGGCCAGT 16951
Qy 955 GTTCTGTCAGCAAAAGAGCGGTTCAATTTCAATAACCGGGGACCTCAGCCATCCCTTC 1014
Db 16950 GTGCGGCTCGTTATCGGGAGAGTGGTGATCTCAGCCACCGCGAAATGACATC 16891
Qy 1015 CTGATTTTCGGCTTTCCAGCGTTC---GGCAGCAGACGAGCGGCTTCAATCTGCAAGG- 1070
Db 16890 AAAACGCGATTAACTGATGTTCTGGGAATATAAATGTCAGGCTCCCTTATACACAGC 16831
Qy 1071 --TTGTGCTTACAGACCGGAGATATGATCATATATATGCTTGAGCACTGATAGCTG 1128
Db 16830 CAGTCTGAGGTGATACAGTAGAATATACAGAACTTTATCAGTTTGTAGTATAGA 16771
Qy 1129 TCGCTCTCACTGTCTCTGTATACGCTGTCTCATAGCACACCTCTTTTGTGACATACCTC 1188
Db 16770 GGCTGAATCCAGATGAACCGACCGACCTGTGAAGAGAAAGTATAAGAGTTGTGAAT 16711
Qy 1189 GGTAGTGGGATCAAGCTCTATTTTGGCAAAAGTTGGCCAGGCTTCCGGTATCA 1248
Db 16710 GGTAGTGGGATCAAGCTCTATTTTGGCAAAAGTTGGCCAGGCTTCCGGTATCA 16651
Qy 1249 ACAGGACACCGAGTTATTTATCTGCGAAGTGTATCTCCGTCACAGTATTTATTCG 1308
Db 16650 ACAGGACACCGAGTTATTTATCTGCGAAGTGTATCTCCGTCACAGTATTTATTCG 16591
Qy 1309 GCGCAAGTGGCTGGGTGATGCTGCCAATTTAGTGCATACAGGTCACTAATACCATCT 1368
Db 16590 GCGCAAGTGGCTGGGTGATGCTGCCAATTTAGTGCATACAGGTCACTAATACCATCT 16531
Qy 1369 AAGTAGTGTATCATAGTGCATGATGTTGTTTACAGTATATGTAAGTGTAGTCTGTTTT 1428
Db 16530 AAGTAGTGTATCATAGTGCATGATGTTGTTTACAGTATATGTAAGTGTAGTCTGTTTT 16471
Qy 1429 TTATGCAAAATCAATTTAATATATATATTTATATCAATTTTACGTTTCTCGTTACGCT 1488
Db 16470 TTATGCAAAATCAATTTAATATATATATTTATATCAATTTTACGTTTCTCGTTACGCT 16411
Qy 1489 TTCTTGTACAAAGTTGCATTTAAGAAAGCAATTTGCTTATCAATTTGTTGCAACGAAACAG 1548
Db 16410 TTCTTGTACAAAGTTGCATTTAAGAAAGCAATTTGCTTATCAATTTGTTGCAACGAAACAG 16351
Qy 1549 GTCACTATCAGTCAAAATCAATTTATTTGCCATCCAGCTGAGCTC-CTCAGGGAAT 1607
Db 16350 GTCACTATCAGTCAAAATCAATTTATTTGCCATCCAGCTGAGCTCTCTAGAGGATC 16291

Qy 1608 TCGTACCCCAATTTGGTAAGGAA-----TAATATTTTCTTTTCTCTTTTAG 1656
Db 16290 CAAGCTTATCGATTTCCGAACCCCAATTTCCCACTGTAATCAATCAATGTAAATCAAT 16231
Qy 1657 TATAAATAGTAAAGTGATGTTAAATAGTATGATTAATAAATATAGTGTATTAATGT 1716
Db 16230 GATAACACATGACATGATCTATCATGTTTACCTTTGTTTATTCATGTTCCGACTAATCAT 16171
Qy 1717 GAAAAATTAATTTAATAATATATTTGTTTACATAAACAACATAGTAATGTAAAAAAATG 1776
Db 16170 TAATTAATAGTCAATCCATTTAGAAAGTTAAATAAACTACAAGTATTAATTTAGAAATTAAT 16111
Qy 1777 ACAAGTGATGTGAAGCAAGAAAGATAAAAGTTGAGAG-----TAAAGTATATTA 1826
Db 16110 AAGAAATGTTGATTGAATAATATCTATATAAAGATAGATCTTCCGCTTTGTTATATTA 16051
Qy 1827 TTTTAAATGAATTTGATCGAACATGTAAAGATGATATACGGCGGTGAAGAGTTCCAACT 1886
Db 16050 GCATTAGATTTATGTTTGTGTTACATTTAGATTACTGTTTCTATTAGTTTGTATTTCTTT 15991
Qy 1887 TCACCAATGAATAAGATCACTACCGGCGTATTTTTCAGTTATCGAGATTTTCAGG 1946
Db 15990 ACTTTAGCTTGTAT-----TAATATTTTGTATTGATAAATTTAGTAATGATAGATTTA 15935
Qy 1947 AGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACTGATATATATCCCA 2006
Db 15934 TTCTAACAAATATTTATTAATTTTAACTAAAAATTTAGTAATGATAGATTTA 15875
Qy 2007 ATGGCATCGTAAGAACATTTTGGGCAATTTTCACTGAGTGTCTCAATGCTACTATAACCA 2066
Db 15874 ATTATATAATAACTATTAAATCATAAAAAATATTTTAAATTTTATTTTCTTTT 15815
Qy 2067 GACCTTTCAGCTGGATATTCAGCGCTTTTAAAGACCGTAAAGAAAAATAAGACAAAGT 2126
Db 15814 TACTATAGTATTTTATCATTTGATATTTAATTTCTCAACACAGCTAGATTTACTATATGG 15755
Qy 2127 TTATCCGCGCTTTATTTCACTTTTCCCGCTGTAGTAAATGCTCATCCGGAATTCGTTAT 2186
Db 15754 GCCCGACATATCAGTATATATTTCTTATACCGCAAAATCAGCGCGCAAAATACGCATCTG 15695
Qy 2187 GCAATGAAGACGCTGAGCTGTATATGGATAGTGTTCACCGTTGTTA--CACCCTT 2244
Db 15694 TTATCTGGCTTTTAGTAAGCGGATCCAGCGATTAOGCCCGCTCCCATCTATCGCA 15635
Qy 2245 TTCCATGACAACTGAAACGTTTTTATCGCTCTGAGTGAATACACACAGCAATTTCCGG 2304
Db 15634 GTACTGTTGATTTCAATTAAGCAATTTCCGACATGGAGCCATCACAGACGGCATGATG 15575
Qy 2305 CAGTTTCTACATATATTTCCGAAGTGTGGCGGTGTACGGTGAATAAACCCTGGCTATTTC 2364
Db 15574 AACCTGAATCGCCAGCGCATCAGCACCTTTGCGCTTCCGTATATATTTGCCCATGTT 15515
Qy 2365 CTTAAGGCTTTATGAGAAATATGTTTTTCGCTCAGCCCAATCCCTGGGTGAGTTTCACC 2424
Db 15514 GAAAAAGCGGCGAAGAGTTGTCCATATGGCCAGTTTAAATCAAACTGTTGAACT 15455
Qy 2425 AGTTTGTATTTAAACGTCGCAATATGGAACAACCTTTCGCCCCGCTTTTCCACATGGGC 2484
Db 15454 CACCCAGGATTTGGCTGAGACGCAAAACATATTTCAATAAACCTTTTAGGGAATATGCG 15395
Qy 2485 AAATATTAACGCAAGCGGACAGGTTGCTGTATGTCGCTGGGATTCAGGTTTCAATGCGC 2544
Db 15394 CAGGTTTTCCCGTAACACGCCACATCTTTGCGAATATATGTGTAGAACTCCGGAATC 15335
Qy 2545 GTCTGTATGCTTCCATCTCGGCAGATGCTTAATGAATTAACAAGTACTGCGATGAG 2604
Db 15334 GTCGGTATTTCACTCCAGAGCGATGAAACGTTTTCAGTTTGTCTATGGAACG--GTG 15277
Qy 2605 TGGCAGGCGGGCGTAATCGGTGGATCCGGCTTACTAAAAAGCCAGATAACAGTATGCG 2664
Db 15276 TAACAAGGTTGAACATCTATCCCATATCACCAGCTCACCCTTTCATTTCGCATACGGAAT 15217

QY 2665 TATTTGCGGTGATTTTTCGGGTATAAGAAATATATACTGATATATGTCGGGCCCAATAATAG 2724
Db 15216 TCCGATGAGCATTTCAATCAGCGCGGCAAGAAATGTAATAAGCGCGGATAAAATCTGTC 15157
QY 2725 TAAATCTAGCTGGTTTGATGAATTAATAATCAATGATAAATACTATAGTAAAAATAAGA 2784
Db 15156 TTAATTTTCTTTACGGTCTTTAAAAAGCGGTAATATCCAGCTGAACGGTCTGGTTATAG 15097
QY 2785 ATAAATAAATTAATAATATTTTATGATTAATAGTTTATTAATAATTAATAATCT 2844
Db 15096 GTACATTTAGCAACTGACTGAATGCTCAAAATGTTCTTTAGATGCCATTTGGGATATA 15037
QY 2845 ATACCAATTAATAATATTTTAGTTTAAAAAGTTAAATAAATATTTTGTGAAAAATCCAATC 2904
Db 15036 TCAACGGTGGTATATCCAGTGATTTTCTCCATTTTAGCTTCTCTAGCTCTCTGAAAT 14977
QY 2905 TGTCTGTAATTTATCAATAAACAATAATTA---ATAACAAGCTAAAGTAACAAATAA 2960
Db 14976 CTGATAAATCTCAAAAAATAGCCCGGTAGTGATCTTTATTTCAATATGTTGGTGAAGTTGGAA 14917
QY 2961 TATCAAACTAATAGAACAGTAACTTAATGTAAACAAAACATAATCAATCAATGCTAAATAAC 3020
Db 14916 CTTCTTACCGCGGTATATCACTTACATGTTGATCGATCAAAATTCATTAAAAATAATATACT 14857
QY 3021 AAAGCGCAAGATCATCATTTTATATAGTATTAATTTCAATCAACATCTTATTAATTTT 3080
Db 14856 TA-----CTCTCAACTTTTATCTTCTCGTCTTACACATCACTTTGTCAATATTTT 14807
QY 3081 TAAATAATCTCTAGTTTATTAATCTTAAATGATGATGACTTATTAATTAATGAATTA 3140
Db 14806 TTAATTTATCTATGTTTGTATGAACAATAATATTTTAATAATTTATTTTCAAAATATA 14747
QY 3141 GTCGAACATGAATAAACAAGGTAAACATGATGATCATGTCATTTGTGTATCATGATCTT 3200
Db 14746 ACACTATATTTATTAATCAATACTAATTAACATCACTTAACTATTTTATCTAAAAAGGA 14687
QY 3201 ACATTTGGATGATTAAGTTGGGAATTTGGTTGGAATCGATAAGCTTGGATCTCTTA 3260
Db 14686 AAAAAGAAAATAAT-----ATTTCTTACCAATTTGGGGTACCGAAATCTCTCGA 14638
QY 3261 GAGAGCTGACCTGGATGGCAATAATGATTTTATTTTACTGATGATGACCTGTTCTGTT 3320
Db 14637 G-GAGCTGACCTGGATGGCAATAATGATTTTATTTTACTGATGATGACCTGTTCTGTT 14579
QY 3321 GCAACAAATTTGATAAGCAATGCTTTCTTATATGCCAACTTTGTACAAAGAAAGCTGAACG 3380
Db 14578 GCAACAAATTTGATAGCAATGCTTTCTTATATGCCAACTTTGTACAAAGAAAGCTGAACG 14519
QY 3381 AGAAACGTAAATGATATTAATATCAATATTAATTAATTAATTTGATTAATAAACAAGAC 3440
Db 14518 AGAAACGTAAATGATATTAATATCAATATTAATTAATTTGATTAATAAACAAGAC 14459
QY 3441 TACATAATCTGTTAAACACAACTATCCAGTCACTATGATGAATCACTACTTTAGATGGTAT 3500
Db 14458 TACATAATCTGTTAAACACAACTATCCAGTCACTATGATGAATCACTACTTTAGATGGTAT 14399
QY 3501 TAGTGACCTGATGCTAGCTAAGTTGGAGCAATCACCGGACGATCTTCGGCGGCAATTAAT 3560
Db 14398 TAGTGACCTGATGCTAGCTAAGTTGGAGCAATCACCGGACGATCTTCGGCGGCAATTAAT 14339
QY 3561 ACCTGTGACGGAGATCACTTCGAGATAAATAATCTGTGTGCTGCTGTTGATACCGG 3620
Db 14338 ACCTGTGACGGAGATCACTTCGAGATAAATAATCTGTGTGCTGCTGTTGATACCGG 14279
QY 3621 GAAGCCCTGGGCAACTTTTGGGCAAAATGAGACGTTGATCGGCACTACCCATTTCAAA 3680
Db 14278 GAAGCCCTGGGCAACTTTTGGGCAAAATGAGACGTTGATCGGCACTACCCAGATGT 14219
QY 3681 CTCTTATCTTTCTCTTACAAGTCTGCGGCTTCACTGGAATTTTACGCTCTTACTT 3740
Db 14218 CAAAAGAGGTGTGCTATGAA---GCAGCGTATTAACAGTGACAGTTGACAGCAGCTA 14162
QY 3741 ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGAGACTGGCTGTAT 3800

Db 14161 TCATTTGCTCAAGCAATATATGATGTCAATATCTCCGGTCTGGTAAGCAACAACCATCGAG 14102
QY 3801 AAGGAGCCTGACATTTATATTTCCCAAGAACATCAGGTTAATGCGGTTTTTGTATGTCAAT 3860
Db 14101 AATGAAGCCGCTCTCTGCGTGCC---GAACGCTGGAAGCGGAAATCAGGAAGGGATG 14045
QY 3861 TTCCGGGTGCTGAGATCAGCACTTTCTTCCCGATAACGAGAGCCGCACTTGGCCAT 3920
Db 14044 GCTGAGGTCGCGCGGTTTATTGAATAAGAACGGCTCTTTTGTCTGAGAGAACAGGG----- 13990
QY 3921 ATCGTGTGTCATCATGCGCCAGCTTTTCATCCCGATATGCAACCCAGGTTAAAGTTACG 3980
Db 13989 -ACTGTTGAATGCAAGTTTAAAGTTTACACCTATAAAGAGAGAGCCGCTTATCGTCTGT 13931
QY 3981 GGAGACTTTTATCTGACAGACAGCTGCTGCGCAGGGGATACCATCTCGTCCGCCGG 4040
Db 13930 TGTGATGTACAGAGTGATATTTATTGACACGCCCGCGGCGAGGGATGATCCCCCTCGC 13871
QY 4041 CGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATA 4100
Db 13870 CAGTCCACGCTGCTGTGTCAGATAAAGTCTCCCGTGAACTTTACCGGTGGTGATATCGG 13811
QY 4101 GGTGTAAACCTTAAACTGCAATTTCAACCA-----GTCCCTGTTCTCGTCAGCAAAAGAGC 4154
Db 13810 GGATGAAGCTGGCGCATGATGACCAACGATATGCCAGTGTGCCGCTCTCCGTTATCGG 13751
QY 4155 CTTTCAATTTAAATAAAGCGGGGACCTCAGCCATCCCTTCTGATTTTCCGCTTTCCAGC 4214
Db 13750 GGAAGAAGTGGCTGATCTCAGCCACCGGAAATGACATCAAAAACGCCATTAACCTGAT 13691
QY 4215 GTTC---GSCACGACAGACGCGGCTTCATTTCTGATGG---TTGTGCTTACCAGACCGG 4268
Db 13690 GTTCTGGGAATTAATGTTGAGGCTCCCTTATACACSCCAGTCTGCAAGTCTGATACAG 13631
QY 4269 AGATATTTGATCATATATATGCTTTGAGCAACTGATAGCTGTGCTGTCACTGTCACTGT 4328
Db 13630 TAGAAATTTACAGAAACTTTTATCAGCTTTAGTAAGTATAGAGGCTGAAAAATCCAGATGAAG 13571
QY 4329 AATACGCTGCTCATAGACACCTCTTTTGTGACATCTTCTGTTCTTGTATGAGATGAT 4388
Db 13570 CCGAACGACTTGTGAAGAGAAAAGTATAAGAGTTGTGAAATGTTCTTGTATGAGATGAT 13511
QY 4389 TTCAGGACTATGACACTAGCTATATGAATAGTAGATGCTTTTATTTTGTCACAAAA 4448
Db 13510 TTCAGGACTATGACACTAGCTATATGAATAGTAGATGCTTTTATTTTGTCACAAAA 13451
QY 4449 AAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATTAATACGGCATTTGAGGACAA 4508
Db 13450 AAGAGGCTCGACCTCTTTTCTTATTTCTTTTATGATTAATACGGCATTTGAGGACAA 13391
QY 4509 TAGCGAGTGGCTGGATACGACGATTTCCGTTTTCAGAAAGAACATTTTGGAGGCTGTCCGTC 4568
Db 13390 TAGCGAGTGGCTGGATACGACGATTTCCGTTTTCAGAAAGAACATTTTGGAGGCTGTCCGTC 13331
QY 4569 GACTAAGTTGGCAGCACTACCCGAAAGAACATTTTGGAGGCTGTCCGTCAGCTACAGTCA 4628
Db 13330 GACTAAGTTGGCAGCACTACCCGAAAGAACATTTTGGAGGCTGTCCGTCAGCTACAGTCA 13271
QY 4629 CTAATACCATTAAGTAGTTGATTCATAGTGATGCTGGATGTTGTTGTTTACAGATTTAT 4688
Db 13270 CTAATACCATTAAGTAGTTGATTCATAGTGATGCTGGATGTTGTTGTTTACAGATTTAT 13211
QY 4689 GTAGTCTGTTTTTATGCAAAATCTAAATTTAATATATTTATATTTATATCATTTTACGTT 4748
Db 13210 GTAGTCTGTTTTTATGCAAAATCTAAATTTAATATATTTATATTTATCATTTTACGTT 13151
QY 4749 TCTCGTTAGCTTTTTTGTACAAAGTTGGCAATTAATAAAGCAATTCGCTCATCAATTTGT 4808
Db 13150 TCTCGTTAGCTTTTTTGTACAAAGTTGGCAATTAATAAAGCAATTCGCTCATCAATTTGT 13091
QY 4809 TGCACGACAGGTCATCATCATCAATTAATAAATCAATTTTTCGGGCCCGAG 4861

Db 13090 TGAACGAAAGTCTACTATGTCGATCAAAATTAATCAATTTTGGGGCCGAG 13038

RESULT 6
AAC55521
ID AAC55521 standard; DNA; 4470 BP.
XX
AC AAC55521;
XX
DT 11-JAN-2001 (first entry)
XX
DE Donor plasmid pDONR201 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO20052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005432.
XX
PR 02-MAR-1999; 99US-0122389P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GP, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
PS Example 9; Fig 49; 459pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
Query Match 24.5%; Score 1193; DB 3; Length 4470;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CGGGCCCCCAATATGATTTTATTTGACTGATAGTACCTGTTCGATGCAACAATTGA 60
|||||

Db 21 CGGGCCCCCAATATGATTTTATTTGACTGATAGTACCTGTTCGATGCAACAATTGA 80
QY 61 TGAGCAATGCTTTTATTAATGCGCAACTTTGTGACAAAAGCTGAAACGAGAAACGTAAAA 120
Db 81 TGAGCAATGCTTTTATTAATGCGCAACTTTGTGACAAAAGCTGAAACGAGAAACGTAAAA 140
QY 121 TGATATTAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
Db 141 TGATATTAATATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 200
QY 181 TAAACACACACATATCCAGTCACTATGAATCAACTTACCTTAGATGCTATTTAGTACCTGTA 240
Db 201 TAAACACACACATATCCAGTCACTATGAATCAACTTACCTTAGATGCTATTTAGTACCTGTA 260
QY 241 GTGACCGACAGCGCTTCCAAATGTTCTTCGAGTGTAGTGTGCAACTTAGTGTGACCGACAG 300
Db 261 GTGACCGACAGCGCTTCCAAATGTTCTTCGAGTGTAGTGTGCAACTTAGTGTGACCGACAG 320
QY 301 CTTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACTCGCTATTTGTCCTCA 360
Db 321 CTTTCCAAATGTTCTTCTCAACGGAATCGTGTATCCAGCTACTCGCTATTTGTCCTCA 380
QY 361 ATGCGGTATTAATCATATAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTTGTGTG 420
Db 381 ATGCGGTATTAATCATATAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTTGTGTG 440
QY 421 ACATAATTAACATCTACCTATTATATAGCTAGTGTGATAGTGTGCAACTTAGTGTGACCTG 480
Db 441 ACATAATTAACATCTACCTATTATATAGCTAGTGTGATAGTGTGCAACTTAGTGTGACCTG 500
QY 481 CATCAAGAACCAATTTCACAACTCTTATATCTTCTTACAAAGTCTTTCGGCTTTCATCTG 540
Db 501 CATCAAGAACCAATTTCACAACTCTTATATCTTCTTACAAAGTCTTTCGGCTTTCATCTG 560
QY 541 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGA 600
Db 561 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAGTTTCTGTAATTTCTACTGTATCGA 620
QY 601 CTGACAGACTGGCTGTGTATTAAGGAGGCTGACATTTATATTTCCCGAGAACATCAGTTA 660
Db 621 CTGACAGACTGGCTGTGTATTAAGGAGGCTGACATTTATATTTCCCGAGAACATCAGTTA 680
QY 661 ATGGCGTTTTCATGCTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACG 720
Db 681 ATGGCGTTTTCATGCTCAATTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGGATAACG 740
QY 721 GAGACCGGCACACTGGCCATATCGGTGTGTCATCTGCGCAGCTTTCATCCCGGATATGC 780
Db 741 GAGACCGGCACACTGGCCATATCGGTGTGTCATCTGCGCAGCTTTCATCCCGGATATGC 800
QY 781 ACCACCGGTAAAGTTTCAGGGAGACTTTTATCTGACAGCAGACGTGCACTGGCCAGGGGG 840
Db 801 ACCACCGGTAAAGTTTCAGGGAGACTTTTATCTGACAGCAGCAGTGCATGGCCAGGGGG 860
QY 841 ATCACCATCCGTCGCGCGGGGTGTCAATAATATCACTGTATATCCCAACACAGACGA 900
Db 861 ATCACCATCCGTCGCGCGGGGTGTCAATAATATCACTGTATATCCCAACACAGACGA 920
QY 901 TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGATTTTACAGTCTCTCTCTCTC 960
Db 921 TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGATTTTACAGTCTCTCTCTCTC 980
QY 961 GTGACGAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 981 GTGACGAAAGAGCGGTTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1040
QY 1021 TTCCGCTTTCCAGCGTTTCGGCACGACGAGCGGCTTCATTTCTGATGTTGTGCTTAC 1080
Db 1041 TTCCGCTTTCCAGCGTTTCGGCACGACGAGCGGCTTCATTTCTGATGTTGTGCTTAC 1100
QY 1081 CAGACCGGAGATTTGACATCATATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACT 1140
Db 1101 CAGACCGGAGATTTGACATCATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACT 1160

QY 1141 GTCACCTGAATACGCTCTTCATAGCACACCTCTTTTGTGACATATTCGGGTA 1193
DB 1161 GTCACCTGAATACGCTCTTCATAGCACACCTCTTTTGTGACATATTCGGGTA 1213

RESULT 7
ABZ58767
ID ABZ58767 standard; DNA; 4470 BP.
XX
XX ABZ58767;
AC
XX 01-MAY-2003 (first entry)
DT
XX
XX Destination plasmid pDONR201 nucleotide sequence.
DE
XX
XX Nucleic acid insertion; recombination; nucleic acid selection;
KW Nucleic acid isolation; ds.
XX
XX Synthetic.
OS
XX
XX WO200295055-A2.
PN
XX
XX 28-NOV-2002.
PD
XX
XX 21-MAY-2002; 2002WO-US015947.
PF
XX
XX 21-MAY-2001; 2001US-0291973P.
PR
XX
XX (INVI-) INVITROGEN CORP.
PA
XX
XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
PI
XX
XX WPI; 2003-129436/12.
DR
XX
XX Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
XX Disclosure; Fig 26B-C; 273pp; English.
PS
XX
XX The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR201 nucleotide sequence
XX
SQ Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match 24.5%; Score 1193; DB 7; Length 4470;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAATGATTTTATTTGACTGATGACCTCTTCGTTGCCACAAATGA 60
DB 21 CGGGCCCCAAATAATGATTTTATTTGACTGATGACCTCTTCGTTGCCACAAATGA 80
QY 61 TGAGCAATGCTTTTATATGCCAATTTGTGACAAAAAGCTGAACGAGAAACGTAAAA 120
DB 81 TGAGCAATGCTTTTATATGCCAATTTGTGACAAAAAGCTGAACGAGAAACGTAAAA 140
QY 121 TGATATAATATCAATATATTAATAGATTTTGTGATAAAAAACAGCTACATATCTG 180
DB 141 TGATATAATATCAATATATTAATAGATTTTGTGATAAAAAACAGCTACATATCTG 200
QY 181 TAAACACACATATCCAGTCACTATGAATCAACTACTTGTAGTGGTATTAGTGACCTGTA 240

RESULT 8

ADAS0329 standard; DNA; 4892 BP.

XX

AC ADAS0329;

PD 08-SEP-2000.
XX 02-MAR-2000; 2000WO-US005432.
XX 02-MAR-1999; 99US-0122389P.
PR 23-MAR-1999; 99US-0126049P.
PR 28-MAY-1999; 99US-0136744P.
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX Example 10; Fig 53; 459pp; English.
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (I) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX att recombination site. (I), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning. (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is used
XX in the exemplification of the present invention
SQ Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;
Query Match 24.5%; Score 1193; DB 3; Length 4939;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCCCAAATAATGATTTTATTTTACTGATAGTACCTGTTCTGTCACAAATGA 60
Db 3555 CGGGCCCCAAATAATGATTTTATTTTACTGATAGTACCTGTTCTGTCACAAATGA 3614
QY 61 TGAGCAATGCTTTTATTAATGCCAACCTTTGTACAAAAGCTGAACGAAACGTAAAA 120
Db 3615 TGAGCAATGCTTTTATTAATGCCAACCTTTGTACAAAAGCTGAACGAAACGTAAAA 3674
QY 121 TGATATAATATCAATATATTAATTAATTTTGTATATTTTGTATATTAATATCTG 180
Db 3675 TGATATAATATCAATATATTAATTAATTTTGTATATTTTGTATATTAATATCTG 3734
QY 181 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 240
Db 3735 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 3794
QY 241 GTGACCGGACAGCTTCCAAAATGTTCTTCGGGTGATGCTGCCAATTAATCGACGACAG 300
Db 3795 GTGACCGGACAGCTTCCAAAATGTTCTTCGGGTGATGCTGCCAATTAATCGACGACAG 3854
QY 301 CCTTCCAAATGTTCTTCAACGGGAATCGTGTATCCAGGCTTACTCGCTATTGCTCTCA 360
Db 3855 CCTTCCAAATGTTCTTCAACGGGAATCGTGTATCCAGGCTTACTCGCTATTGCTCTCA 3914

QY 361 ATGCGGTATTAATCATATAAAGAAATAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 420
Db 3915 ATGCGGTATTAATCATATAAAGAAATAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 3974
QY 421 ACAAATAAACAATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAATCAATCTG 480
Db 3975 ACAAATAAACAATCTACCTATTATATACGCTAGTGTATAGTCTCTGAAATCAATCTG 4034
QY 481 CATCAAGAACAAATTTACAACTCTTATATCTTCTTCAAGTGTCTTGGCTTCACTG 540
Db 4035 CATCAAGAACAAATTTACAACTCTTATATCTTCTTCAAGTGTCTTGGCTTCACTG 4094
QY 541 GATTTTCAGCTCTATATCTTACTTAAACGCTGATAAAGTTTCTGTAATTTCTATGTA 600
Db 4095 GATTTTCAGCTCTATATCTTACTTAAACGCTGATAAAGTTTCTGTAATTTCTATGTA 4154
QY 601 CTTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATTTCCCGACATCAGGTTA 660
Db 4155 CTTGCAGACTGGCTGTGTATTAAGGAGCGCTGACATTTATTTCCCGACATCAGGTTA 4214
QY 661 ATGCGGTATTAATCATATAAAGAAATAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 720
Db 4215 ATGCGGTATTAATCATATAAAGAAATAGAAAAAGAGGTGCGAGCTCTTTTGTGTG 4274
QY 721 GAGACCGGCACACTGGCCATATCGGTGGTCAATCATGCGCAGCTTTTATCCCGATATGC 780
Db 4275 GAGACCGGCACACTGGCCATATCGGTGGTCAATCATGCGCAGCTTTTATCCCGATATGC 4334
QY 781 ACCACCGGTAAAGTTTCAOOGGAGACTTTATCTGACAGAGAGCTGACCTGGCCAGGGG 840
Db 4335 ACCACCGGTAAAGTTTCAOOGGAGACTTTATCTGACAGAGAGCTGACCTGGCCAGGGG 4394
QY 841 ATCAACATCGTCCCGCGGCTGTCAATAATATCACTCTGTATCATCCACAAACAGACGA 900
Db 4395 ATCAACATCGTCCCGCGGCTGTCAATAATATCACTCTGTATCATCCACAAACAGACGA 4454
QY 901 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGAATTTCAACAGTCCCTGTTCTC 960
Db 4455 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGAATTTCAACAGTCCCTGTTCTC 4514
QY 961 GTACGAAAAGACCGTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 4515 GTACGAAAAGACCGTTCATTTCAATAAACCGGGGACCTCAGCCATCCCTTCTGATT 4574
QY 1021 TTCCGCTTTCCAGCGTTTCGGCACGACAGACGCGGCTTCATTCTGCAATGTTGCTTAC 1080
Db 4575 TTCCGCTTTCCAGCGTTTCGGCACGACAGACGCGGCTTCATTCTGCAATGTTGCTTAC 4634
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGAAGCAACTGATAGCTGCTGCTCAACT 1140
Db 4635 CAGACCGGAGATATTGACATCATATATGCTTGAAGCAACTGATAGCTGCTGCTCAACT 4694
QY 1141 GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTACATATCTCGGGTA 1193
Db 4695 GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTACATATCTCGGGTA 4747
RESULT 10
AAC55632/c
ID AAC55632 standard; DNA; 5584 BP.
XX AAC55632;
XX 11-JAN-2001 (first entry)
XX Donor plasmid pDONR207 nucleotide sequence.
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.
XX Bacteriophage lambda.
OS Synthetic.

XX WO20052027-A1.
XX PD 08-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US005432.
XX PR 02-MAR-1999; 99US-0122389P.
XX PR 23-MAR-1999; 99US-0126049P.
XX PR 28-MAY-1999; 99US-0136744P.
XX PA (LIFE-) LIFE TECHNOLOGIES INC.
XX PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
XX attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
XX recombinational cloning of polypeptides.
XX
XX Disclosure; Fig 97; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
XX encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
XX nucleotide sequence. Also described are: (1) an isolated nucleic acid
XX molecule (II) comprising one or more att recombination sites comprising
XX at least one mutation in its core region that increases the specificity
XX of interaction between the recombination site and a second att
XX recombination site; and (2) an isolated nucleic acid molecule (III)
XX comprising one or more mutated att recombination sites comprising at
XX least one mutation in its core region that enhances the efficiency of
XX recombination between a first nucleic acid molecule comprising the
XX mutated att recombination site and a second nucleic acid molecule
XX comprising a second recombination site that interacts with the mutated
XX recombination site. (1), (II), (III), primers, vectors and methods
XX from the present invention are used for the recombinational cloning of
XX nucleic acid molecules. They can be used for changing vectors, targeting
XX gene products to intracellular locations, cleaving fusion tags from
XX desired proteins, operably linking nucleic acid molecules of interest to
XX regulatory genetic sequences, constructing genes for fusion proteins,
XX changing copy number, changing replicons, cloning into phages and
XX cloning. (I), (II), (III), host cells and vectors can be used in the
XX production of polypeptides and antibodies. The present sequence is used
XX in the exemplification of the present invention
XX
XX Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;
XX
XX Query Match 24.5%; Score 1193; DB 3; Length 5584;
XX Best Local Similarity 100.0%; Pred. No. 1e-156;
XX Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CGGGCCCCAAATGATTTTATTTTGGTCTGATGACCTGTTGGTTCGACCAAAATTGA 60
XX 5564 CGGGCCCCAAATGATTTTATTTTGGTCTGATGACCTGTTGGTTCGACCAAAATTGA 5505
XX
XX 61 TGAGCAATGCTTTTATAAAGCCAACTTTGTAACAAAAGCTGAACGAGAAAAGCTTAAA 120
XX 5504 TGAGCAATGCTTTTATAAAGCCAACTTTGTAACAAAAGCTGAACGAGAAAAGCTTAAA 5445
XX
XX 121 TGATATAATATCAATATATTAATTTAGTATTTTGCATATAAAGCACTACATATATCTG 180
XX 5444 TGATATAATATCAATATATTAATTTAGTATTTTGCATATAAAGCACTACATATATCTG 5385
XX
XX 181 TAAACACACATATCCAGTCTACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGTA 240
XX 5384 TAAACACACATATCCAGTCTACTATGAATCAACTACTTAGATGGTATTAGTGAACCTGTA 5325
XX
XX 241 GTGACCGCAGAGCTTCCAAATGTTCTTGGGTGATGCTGCGCAACTTAGTCGACCGACAG 300
XX 5324 GTGACCGCAGAGCTTCCAAATGTTCTTGGGTGATGCTGCGCAACTTAGTCGACCGACAG 5265
XX 301 CCTTCCAAATGTTCTTCTCAACGGGAATCGTGGTATCCAGCCCTACTCGCTATTGTCTCA 360
XX

DB 5264 CTTCCAAATGTTCTTCTCAACGGGAATCGTGGTATCCAGCTACTCGCTATTGTCCTCA 5205
QY 361 ATGCCGTATTAAATCATATAAAGAAATAGAAAAAGAGTGGAGCCCTCTTTTGTGTG 420
DB 5204 ATGCCGTATTAAATCATATAAAGAAATAGAAAAAGAGTGGAGCCCTCTTTTGTGTG 5145
QY 421 ACATAATAAAAACATCTACCTATTATATACCTTCTTCTTACAAAGTCTGTCGCTTCAATCTG 480
DB 5144 ACATAATAAAAACATCTACCTATTATATACCTTCTTCTTACAAAGTCTGTCGCTTCAATCTG 5085
QY 481 CATCAAGAAACAATTTCAACAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
DB 5084 CATCAAGAAACAATTTCAACAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5025
QY 541 GATTTTCAAGCTCTATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
DB 5024 GATTTTCAAGCTCTATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4965
QY 601 CTGCGAGACTGCTGTATATAGGGAGCTGACATTTATATCCCGCAGAACATCAGGTTA 660
DB 4964 CTGCGAGACTGCTGTATATAGGGAGCTGACATTTATATCCCGCAGAACATCAGGTTA 4905
QY 661 ATGGCGCTTTTGTATGTCATTTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 720
DB 4904 ATGGCGCTTTTGTATGTCATTTTTCGGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 4845
QY 721 GAGACCGGCACACTGGCCATATCGGTGGTCTATCATCGCCAGCTTCTTCTTCTTCTTCTTCTTCT 780
DB 4844 GAGACCGGCACACTGGCCATATCGGTGGTCTATCATCGCCAGCTTCTTCTTCTTCTTCTTCT 4785
QY 781 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGGG 840
DB 4784 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGACGTGACCTGGCCAGGGGG 4725
QY 841 ATCACCATCCGTCGCGCGGCGGTCTCAATAATATCACTGTATCAATCCCAAAACAGACGA 900
DB 4724 ATCACCATCCGTCGCGCGGCGGTCTCAATAATATCACTGTATCAATCCCAAAACAGACGA 4665
QY 901 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTTACCCAGTCCCTGTTCTC 960
DB 4664 TAACGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTTACCCAGTCCCTGTTCTC 4605
QY 961 GTCAGCAAAAGAGCGCTTCAATTTCAATAAAGCGGGCGACCTCAGCCATCCCTTCTGATT 1020
DB 4604 GTCAGCAAAAGAGCGCTTCAATTTCAATAAAGCGGGCGACCTCAGCCATCCCTTCTGATT 4545
QY 1021 TTCCGCTTTCCAGCGTTTCGGCAGCAGACGAGCGGCTTCAATTTGCAATGGTGTGCTTAC 1080
DB 4544 TTCCGCTTTCCAGCGTTTCGGCAGCAGACGAGCGGCTTCAATTTGCAATGGTGTGCTTAC 4495
QY 1081 CAGACCGGAGATTTGACATCATATATGCTTGAAGCACTGATAGCTGTGCTGTCAACT 1140
DB 4484 CAGACCGGAGATTTGACATCATATATGCTTGAAGCACTGATAGCTGTGCTGTCAACT 4425
QY 1141 GTCACTGTAATACGCTGCTTCATAGCAGACACCTCTTTTGAATATCTTCCGGTA 1193
DB 4424 GTCACTGTAATACGCTGCTTCATAGCAGACACCTCTTTTGAATATCTTCCGGTA 4372

RESULT 11
ABZ58766/c
ID ABZ58766 standard; DNA; 5584 BP.
XX
AC ABZ58766;
XX
DT 01-MAY-2003 (first entry)
XX
DE Donor plasmid pDONR207 nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
XX nucleic acid isolation; ds.
XX

OS	Synthetic.	
XX	WO200295055-A2.	
PN	28-NOV-2002.	
XX	21-MAY-2002; 2002WO-US015947.	
XX	21-MAY-2001; 2001US-0291973P.	
PF	(INVI-) INVITROGEN CORP.	
XX	Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;	
XX	WPI; 2003-129436/12.	
XX	Inserting a population of nucleic acids into a second target molecule for	
PT	selecting and isolating nucleic acid molecules by mixing the second	
PT	population of nucleic acid with a second target nucleic acid.	
XX	Disclosure; Fig 18B-C; 273pp; English.	
XX	The invention relates to inserting a population of nucleic acids into a	
XX	second target molecule. The method involves (a) mixing a first population	
CC	of nucleic acid comprising one or more recombination sites with a target	
CC	nucleic acid; (b) causing some or all of the nucleic acid molecules of	
CC	the first population to recombine with the first target nucleic acid	
CC	molecules to form a second population; (c) mixing the second population	
CC	of nucleic acid with a second target nucleic acid; and (d) causing some	
CC	or all of the nucleic acid molecules of the second population to	
CC	recombine with some or all of the second target nucleic acid molecules to	
CC	form a third population of nucleic acid. The method is useful for	
CC	selecting and isolating nucleic acid molecules. The present sequence	
CC	represents the donor plasmid pDONR207 nucleotide sequence	
XX	Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other;	
SQ	Query Match 24.5%; Score 1193; DB 7; Length 5584;	
	Best Local Similarity 100.0%; Pred. No. 1e-156;	
	Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGGGCCCCCAATATGATTTTATTTTGAATGACTGATGACTGCTGTTGCGTTCGCAACAAATTGA 60	
DB	5564 CGGGCCCCCAATATGATTTTATTTTGAATGACTGATGACTGCTGTTGCGTTCGCAACAAATTGA 5505	
QY	61 TGAGCAATGCTTTTATTAATGCCAACTTTGTACAAAAGCTGAACGAAACCTTAAAA 120	
DB	5504 TGAGCAATGCTTTTATTAATGCCAACTTTGTACAAAAGCTGAACGAAACCTTAAAA 5445	
QY	121 TGATATAATATCAATATATTAATTAATTTAGATTTTGCATAAAAACAGACTACATAATCTG 180	
DB	5444 TGATATAATATCAATATATTAATTAATTTAGATTTTGCATAAAAACAGACTACATAATCTG 5385	
QY	181 TAAACACACATATCCAGTCACTATGAATCAACTACTTTAGATGGTATTTAGTGCCTGTA 240	
DB	5384 TAAACACACATATCCAGTCACTATGAATCAACTACTTTAGATGGTATTTAGTGCCTGTA 5325	
QY	241 GTGACCGCAGCCTTCCAAATGTTCTCGGGTGATGCTGCCAACTTTAGTCGACGACAG 300	
DB	5324 GTGACCGCAGCCTTCCAAATGTTCTCGGGTGATGCTGCCAACTTTAGTCGACGACAG 5265	
QY	301 CCTTCCAAATGTTCTTCTCAACGGGAATGTCGTATCCAGCCTACTCTCGTATTTGTCCTCA 360	
DB	5264 CCTTCCAAATGTTCTTCTCAACGGGAATGTCGTATCCAGCCTACTCTCGTATTTGTCCTCA 5205	
QY	361 ATCCCGTATTAATCAATAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTG 420	
DB	5204 ATCCCGTATTAATCAATAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTG 5145	
QY	421 ACAAAATAAAACATCTACCTATTATATACGCTAGTGCATAGTCTGGAATCATCTG 480	
DB	5144 ACAAAATAAAACATCTACCTATTATACGCTAGTGCATAGTCTGGAATCATCTG 5085	

QY	481 CATCAGAACAAATTCACAACTCTTATACCTTTTCTTTTCAAGTCGTTCCGGGTTCACTG 540	
DB	5084 CATCAGAACAAATTCACAACTCTTATACCTTTTCTTTTCAAGTCGTTCCGGGTTCACTG 5025	
QY	541 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600	
DB	5024 GATTTTCAGCCTCTATACCTTACTTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA 4965	
QY	601 CTGCGAGACTGGCTGTGTATAGGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA 660	
DB	4964 CTGCGAGACTGGCTGTGTATAGGGAGCCTGACATTTATATTTCCCGAGAACATCAGGTTA 4905	
QY	661 ATGGCGTTTGTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 720	
DB	4904 ATGGCGTTTGTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG 4845	
QY	721 GAGACCGGCACACTGGCCATATCGTGTGTCATCATGCGCCAGCTTTTCATCCCGATATGC 780	
DB	4844 GAGACCGGCACACTGGCCATATCGTGTGTCATCATGCGCCAGCTTTTCATCCCGATATGC 4785	
QY	781 ACCACCGGTAAAGTTTCAGGGAGACTTTTATCTGACAGCAGCTGCACCTGGCCAGGGG 840	
DB	4784 ACCACCGGTAAAGTTTCAGGGAGACTTTTATCTGACAGCAGCTGCACCTGGCCAGGGG 4725	
QY	841 ATCACCATCCGTCGCGCGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 900	
DB	4724 ATCACCATCCGTCGCGCGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGA 4665	
QY	901 TAAGCGTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTTACCCAGTCCCTGTTCTC 960	
DB	4664 TAAGCGTCTCTCTTTTATAGGTGTAAACCTTAACTGCAATTTACCCAGTCCCTGTTCTC 4605	
QY	961 GTCAGAAAAAGAGCCGTTTCATTTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT 1020	
DB	4604 GTCAGAAAAAGAGCCGTTTCATTTTCAATAAACCGGGCGACCTCAGCCATCCCTTCTGATT 4545	
QY	1021 TTCGCTTTCCAGGTTTCGCGACGACAGACGAGCGGCTTCATCTGCAATGTTGTGCTTAC 1080	
DB	4544 TTCGCTTTCCAGGTTTCGCGACGACAGACGAGCGGCTTCATCTGCAATGTTGTGCTTAC 4485	
QY	1081 CAGACCGGAGATATGACATCATATATGCTTGGAGCACTGATAGCTGTGCTCTCAACT 1140	
DB	4484 CAGACCGGAGATATGACATCATATATGCTTGGAGCACTGATAGCTGTGCTCTCAACT 4425	
QY	1141 GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCCGGTA 1193	
DB	4424 GTCACTGTAAATACGCTGCTTCATAGCACACCTCTTTTGTGACATCTTCCGGTA 4372	
	RESULT 12	
	ABZ59768	
ID	ABZ59768 standard; DNA; 4428 BP.	
XX	AC ABZ58768;	
XX	01-MAY-2003 (first entry)	
XX	Destination plasmid pDONR212 nucleotide sequence.	
XX	Nucleic acid insertion; recombination; nucleic acid selection;	
XX	nucleic acid isolation; ds.	
XX	Synthetic.	
XX	WO200295055-A2.	
XX	28-NOV-2002.	
XX	21-MAY-2002; 2002WO-US015947.	
XX	21-MAY-2001; 2001US-0291973P.	
XX	(INVI-) INVITROGEN CORP.	

XX PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN; 720
XX XX
XX DR WPI; 2003-129436/12. 1518
XX XX
XX PT Inserting a population of nucleic acids into a second target molecule for 780
XX PT selecting and isolating nucleic acid molecules by mixing the second 1577
XX PT population of nucleic acid with a second target nucleic acid. 1637
XX XX
XX PS Disclosure; Fig 27B-C; 273pp; English. 840
XX XX
XX CC The invention relates to inserting a population of nucleic acids into a 1638
XX CC second target molecule. The method involves (a) mixing a first population 1697
XX CC of nucleic acid comprising one or more recombination sites with a target 900
XX CC nucleic acid; (b) causing some or all of the nucleic acid molecules of 1757
XX CC the first population to recombine with the first target nucleic acid 1757
XX CC molecules to form a second population; (c) mixing the second population 960
XX CC of nucleic acid with a second target nucleic acid; and (d) causing some 1817
XX CC or all of the nucleic acid molecules of the second population to 1817
XX CC recombine with some or all of the second target nucleic acid molecules to 1020
XX CC form a third population of nucleic acid. The method is useful for 1877
XX CC selecting and isolating nucleic acid molecules. The present sequence 1080
XX CC represents the destination plasmid pDONR212 nucleotide sequence 1937
XX SQ Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other; 1143
Query Match 24.4%; Score 1186.6; DB 7; Length 4428;
Best Local Similarity 99.7%; Pred. No. 7.9e-156;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGGGCCCCAATATGATTTTATTTTGTGATGATGACCTGTCGTTGCAACAAATTGA 60
Db 858 CGGGCCCCAATATGATTTTATTTTGTGATGATGACCTGTCGTTGCAACAAATTGA 917
QY 61 TGAGCAATGCTTTTATTAATGCTTGTACAAAAAGCTGAACGAGAAAGCTTAAA 120
Db 918 TGAGCAATGCTTTTATTAATGCTTGTACAAAAAGCTGATATCGAAGCTTAAA 977
QY 121 TGATATAATATCATATATATTAATGATTTTGTGATTAATAAAGAGCTATCATATCTG 180
Db 978 TGATATAATATCATATATATTAATGATTTTGTGATTAATAAAGAGCTATCATATCTG 1037
QY 181 TAAACACACATATCCAGTACATGATGATGATGATGATGATGATGATGATGATGATG 240
Db 1038 TAAACACACATATCCAGTACATGATGATGATGATGATGATGATGATGATGATGATG 1097
QY 241 GTGACCGACAGCTTCCAAATGTTCTTGGGTGATGCTGCAACTAGTGCAGCGACAG 300
Db 1098 GTGACCGACAGCTTCCAAATGTTCTTGGGTGATGCTGCAACTAGTGCAGCGACAG 1157
QY 301 CTTTCCAAATGTTCTTCCAAACGGAATGCTGATCCAGCTACTCGCTATGTCCTCA 360
Db 1158 CTTTCCAAATGTTCTTCCAAACGGAATGCTGATCCAGCTACTCGCTATGTCCTCA 1217
QY 361 ATGCGGTATTAATCATATAAAGAAATAGAAAGAGGTGCGAGCTCTTTTGTGTG 420
Db 1218 ATGCGGTATTAATCATATAAAGAAATAGAAAGAGGTGCGAGCTCTTTTGTGTG 1277
QY 421 ACAAAATAAAACATCTACTATTCATATACGCTAGTGCATAGCTGCTGAAATCATCTG 480
Db 1278 ACAAAATAAAACATCTACTATTCATATACGCTAGTGCATAGCTGCTGAAATCATCTG 1337
QY 481 CATCAAGAACATTTTCAACATCTTATCTTTTCTTTTCAAGTCTGTCGCTTATCTG 540
Db 1338 CATCAAGAACATTTTCAACATCTTATCTTTTCTTTTCAAGTCTGTCGCTTATCTG 1397
QY 541 GATTTTCAGCTCTATCTACTTACTTAAAGCTGATTAAGTTTCTGTAAATTTCTACTGTATCGA 600
Db 1398 GATTTTCAGCTCTATCTACTTACTTAAAGCTGATTAAGTTTCTGTAAATTTCTACTGTATCGA 1457
QY 601 CTGACAGCTGGCTGTATAGGGAGCTGACATTTATATCCCGAGAACATCAGGTTA 660
Db 1458 CTGACAGCTGGCTGTATAGGGAGCTGACATTTATATCCCGAGAACATCAGGTTA 1517

QY 661 ATGGCGTTTGTATGTCATTTTCGGCTGGCTGAGATCAGCCACTTCTTCCCGATAACG 720
Db 1518 ATGGCGTTTGTATGTCATTTTCGGCTGGCTGAGATCAGCCACTTCTTCCCGATAACG 1577
QY 721 GAGACCGGCACACTGCGCCATATCGGTGGTCAATCATCGCGAGCTTTTCATCCCGATATGC 780
Db 1578 GAGACCGGCACACTGCGCCATATCGGTGGTCAATCATCGCGAGCTTTTCATCCCGATATGC 1637
QY 781 ACCACCGGTAAAGTTTCAAGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGG 840
Db 1638 ACCACCGGTAAAGTTTCAAGGAGACTTTATCTGACAGCAGCTGCACTGGCCAGGGG 1697
QY 841 ATACCATCGTCCCGGCGGTCAATAATATCACTCTGTATCATCCCAAAACAGACGA 900
Db 1698 ATACCATCGTCCCGGCGGTCAATAATATCACTCTGTATCATCCCAAAACAGACGA 1757
QY 901 TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTTACAGTCCCTGTCTC 960
Db 1758 TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAACTGCAATTTACAGTCCCTGTCTC 1817
QY 961 GTACGMAAAGAGCGGTTCATTTCAATAAACCAGGCGAGCTCAGCATCCCTTCTGATT 1020
Db 1818 GTACGMAAAGAGCGGTTCATTTCAATAAACCAGGCGAGCTCAGCATCCCTTCTGATT 1877
QY 1021 TTCCGCTTTCCAGGTTTCGGCACGACGACGAGCTTCACTTCTGATGCTGTGTCTTAC 1080
Db 1878 TTCCGCTTTCCAGGTTTCGGCACGACGACGAGCTTCACTTCTGATGCTGTGTCTTAC 1937
QY 1081 CAGACCGGAGATATGACATCATATATATGCTTGAAGCAACTGATAGCTGCTGCTCACT 1140
Db 1938 CAGACCGGAGATATGACATCATATATATGCTTGAAGCAACTGATAGCTGCTGCTCACT 1997
QY 1141 GTCACTGATACGCTCTTCATAGCACACCTCTTTTGTGACATCTTCCGGTA 1193
Db 1998 GTCACTGATACGCTCTTCATAGCACACCTCTTTTGTGACATCTTCCGGTA 2050
RESULT 13
ABZ58769
ID ABZ58769 standard; DNA; 4627 BP.
XX AC ABZ58769;
XX AC
XX DT 01-MAY-2003 (first entry)
XX DE Destination plasmid pDONR212 (P) nucleotide sequence.
XX KW Nucleic acid insertion; recombination; nucleic acid selection;
XX KW nucleic acid isolation; ds.
XX OS Synthetic.
XX XX WO200295055-A2.
XX PN 28-NOV-2002.
XX XX 21-MAY-2002; 2002WO-US015947.
XX PF 21-MAY-2001; 2001US-0291973P.
XX PR (INVI-) INVITROGEN CORP.
XX PA
XX XX Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX PI WPI; 2003-129436/12.
XX DR
XX PT Inserting a population of nucleic acids into a second target molecule for
XX PT selecting and isolating nucleic acid molecules by mixing the second
XX PT population of nucleic acid with a second target nucleic acid.
XX PS Disclosure; Fig 28B-C; 273pp; English.
XX XX

CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence
CC represents the destination plasmid pDONR212(F) nucleotide sequence
XX
SQ Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;

Query Match 24.4%; Score 1186.6; DB 7; Length 4627;
Best Local Similarity 99.7%; Pred. No. 7.9e-156;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATATGATTTTATTTGACCTGATAGTCACTGTTCTGTTGCAACAAATGTA 60
Db 9 CGGGCCCCAAATATGATTTTATTTGACCTGATAGTCACTGTTCTGTTGCAACAAATGTA 68
QY 61 TGAGCAATGCTTTTATATAGTCCAACTTTGTACAAAAAGCTGACGAGAAAGTAA 120
Db 69 TGAGCAATGCTTTTATATAGTCCAACTTTGTACAAAAAGCTGATATGAGAAAGTAA 128
QY 121 TGATATAATATCAATATATTAATTAATGATTTTGCATAAAAAAGACATCAATATCTG 180
Db 129 TGATATAATATCAATATATTAATTAATGATTTTGCATAAAAAAGACATCAATATCTG 188
QY 181 TAAACACAAACATATCCAGTCACTATGATGAATCAACTACTTAGATGATAGTACCTGTA 240
Db 189 TAAACACAAACATATCCAGTCACTATGATGAATCAACTACTTAGATGATAGTACCTGTA 248
QY 241 GTGACGACGAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATAGTGTAGTCGCGACAG 300
Db 249 GTGACGACGAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATAGTGTAGTCGCGACAG 308
QY 301 CCTTCCAAATGTTCTTCGAAACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCA 360
Db 309 CCTTCCAAATGTTCTTCGAAACGGAATCGTGTATCCAGCCTACTCGCTATTGTCCTCA 368
QY 361 ATGCGGTATTAATCATAAAAAGAAATAGAAAAAGAGTGGAGCCTCTTTTGTGTG 420
Db 369 ATGCGGTATTAATCATAAAAAGAAATAGAAAAAGAGTGGAGCCTCTTTTGTGTG 428
QY 421 ACATAATAAACATCTACCTATTCATATACGCTAGTGTCACTAGTCTGAAAAATCATCTG 480
Db 429 ACATAATAAACATCTACCTATTCATATACGCTAGTGTCACTAGTCTGAAAAATCATCTG 488
QY 481 CATCAAGAACAAATTCACAACTCTTATACATTTTCTCTTACAGTGTTCGGCTTATCTG 540
Db 489 CATCAAGAACAAATTCACAACTCTTATACATTTTCTCTTACAGTGTTCGGCTTATCTG 548
QY 541 GATTTTCAGCTCTATCTACTTAACCGTGAATAGTCTTCTGTAATTTCTACTGTATCGA 600
Db 549 GATTTTCAGCTCTATCTACTTAACCGTGAATAGTCTTCTGTAATTTCTACTGTATCGA 608
QY 601 CCTGACAGCTGGTGTATATAGGAGCCTGACATTTATATCCCGAGAACATCAGGTGA 660
Db 609 CCTGACAGCTGGTGTATATAGGAGCCTGACATTTATATCCCGAGAACATCAGGTGA 668
QY 661 ATGCGGTTTTGATGTCATTTTCGGGTGCTGAGATCAGCACTTCTTCCCGATAACG 720
Db 669 ATGCGGTTTTGATGTCATTTTCGGGTGCTGAGATCAGCACTTCTTCCCGATAACG 728
QY 721 GAGACCGGACACTGGCCATATCGTGGTTCATATGCGCAGCTTTCATCCCGATATGC 780
Db 729 GAGACCGGACACTGGCCATATCGTGGTTCATATGCGCAGCTTTCATCCCGATATGC 788
QY 781 ACCACCGGTAAGTTTCAACGGGACATTTATCTGACAGCAGAGCTGCACTGGCCAGGGG 840

Db 789 ACCACCGGTAAGTTTCAACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGG 848
QY 841 ATCACCATCGTGGCCCGGGGTGTCAATATATACATCTGTACATCCACAAACAGACGA 900
Db 849 ATCACCATCGTGGCCCGGGGTGTCAATATATACATCTGTACATCCACAAACAGACGA 908
QY 901 TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTACCAAGTCCCTTCTC 960
Db 909 TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCATTTACCAAGTCCCTTCTC 968
QY 961 GTACAGAAAGAGCGCTTCAATTTCAATAAACGGGCGACCTCAGCATCCCTTCTGATT 1020
Db 969 GTACAGAAAGAGCGCTTCAATTTCAATAAACGGGCGACCTCAGCATCCCTTCTGATT 1028
QY 1021 TTCGGCTTCCAGCGTTCGGCACGACGACGCGCTTCATCTGATGGTTGTGCTTAC 1080
Db 1029 TTCGGCTTTCACGCGTTCGGCACGACGACGCGCTTCATCTGATGGTTGTGCTTAC 1088
QY 1081 CAGACCGGAGATATGACATCATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACT 1140
Db 1089 CAGACCGGAGATATGACATCATATATGCTTTGAGCAACTGATAGTGTGCTGTCAACT 1148
QY 1141 GTCACTGTAAATAGCGTTCATAGCACACCTCTTTTGCATACATCTCGGGTA 1193
Db 1149 GTCACTGTAAATAGCGTTCATAGCACACCTCTTTTGCATACATCTCGGGTA 1201

RESULT 14
ABZ58770
ID ABZ58770 standard; DNA; 4627 BP.
XX
AC ABZ58770;
XX
DT 01-MAY-2003 (first entry)
XX
DE Destination plasmid pDONR212(R) nucleotide sequence.
XX
KW Nucleic acid insertion; recombination; nucleic acid selection;
KW Nucleic acid isolation; ds.
XX
OS Synthetic.
XX
PN WO200295055-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US015947.
XX
PR 21-MAY-2001; 2001US-0291973P.
XX
PA (INVI-) INVITROGEN CORP.
XX
PI Brasch MA, Cheo D, Li X, Esposito D, Byrd DRN;
XX
DR WPI; 2003-129436/12.
XX
PT Inserting a population of nucleic acids into a second target molecule for
PT selecting and isolating nucleic acid molecules by mixing the second
PT population of nucleic acid with a second target nucleic acid.
XX
PS Disclosure; Fig 29B-C; 273pp; English.
XX
CC The invention relates to inserting a population of nucleic acids into a
CC second target molecule. The method involves (a) mixing a first population
CC of nucleic acid comprising one or more recombination sites with a target
CC nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC the first population to recombine with the first target nucleic acid
CC molecules to form a second population; (c) mixing the second population
CC of nucleic acid with a second target nucleic acid; and (d) causing some
CC or all of the nucleic acid molecules of the second population to
CC recombine with some or all of the second target nucleic acid molecules to
CC form a third population of nucleic acid. The method is useful for
CC selecting and isolating nucleic acid molecules. The present sequence

CC	represents the destination plasmid pDONR212(R) nucleotide sequence			
XX	Sequence	4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other;		
XX	Query Match	24.4%; Score 1186.6; DB 7; Length 4627;		
XX	Best Local Similarity	99.7%; P: 0; Mismatches 4; Indels 0; Gaps 0;		
XX	Matches 1189; Conservative			
QY	1	CGGGCCCCAAATATGATTTTATTTTGTACATGATAGTACCTGTGCTGTTGCAACAAATGA	60	
DB	9	CGGGCCCCAAATATGATTTTATTTTGTACATGATAGTACCTGTGCTGTTGCAACAAATGA	68	
QY	61	TGAGCAATGCTTTTATTAATGCCCCAATCTTTGACAAAAGAGTGAACGAGAAACGTAAAA	120	
DB	69	TGAGCAATGCTTTTATTAATGCCCCAATCTTTGACAAAAGAGTGAATATCGAAACGTAAAA	128	
QY	121	TGATATAATATCAATATATTAATTTAGATTTTGCATATAAAGAGAGTACATATACTG	180	
DB	129	TGATATAATATCAATATATTAATTTAGATTTTGCATATAAAGAGAGTACATATACTG	188	
QY	181	TAAACACAAATATCCAGTCACTATGATCAATCACTATTAGATGTTATTTAGTACCTGTA	240	
DB	189	TAAACACAAATATCCAGTCACTATGATCAATCACTATTAGATGTTATTTAGTACCTGTA	248	
QY	241	GTGACCGGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATTTAGTCCACGACAG	300	
DB	249	GTGACCGGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAATTTAGTCCACGACAG	308	
QY	301	CTTCCCAATGTTCTTCTCAAGCGGAATCGTGTATCCAGCCTTACCTGCTATTTGCTCTCA	360	
DB	309	CTTCCCAATGTTCTTCTCAAGCGGAATCGTGTATCCAGCCTTACCTGCTATTTGCTCTCA	368	
QY	361	ATGCCCTATTAATATCAATAAAGAAATAGAAAAGAGTGGCAGCCTCTTTTGTGTG	420	
DB	369	ATGCCCTATTAATATCAATAAAGAAATAGAAAAGAGTGGCAGCCTCTTTTGTGTG	428	
QY	421	ACAAATATAAATCACTATCTATTAATACGTAGTGTGTCATAGTCTGAAATCATCTG	480	
DB	429	ACAAATATAAATCACTATCTATTAATACGTAGTGTGTCATAGTCTGAAATCATCTG	488	
QY	481	CATCAGAAACAAATTCACAACTCTTATCTTTCTTCTTCAAGTCTGCTGCTTCATCTG	540	
DB	489	CATCAGAAACAAATTCACAACTCTTATCTTTCTTCTTCAAGTCTGCTGCTTCATCTG	548	
QY	541	GATTTTCAGCCTCTATCTTACTTAAAGTGAATAAAGTTTCTGTAATTTCTACTGTATCGA	600	
DB	549	GATTTTCAGCCTCTATCTTACTTAAAGTGAATAAAGTTTCTGTAATTTCTACTGTATCGA	608	
QY	601	CTTGACAGCTGGTGTATTAAGGAGCCTGACATTTATATCCCAAGAACATCAGGTTA	660	
DB	609	CTTGACAGCTGGTGTATTAAGGAGCCTGACATTTATATCCCAAGAACATCAGGTTA	668	
QY	661	ATGCGCTTTTGTATGTCATTTTCCGGTGGCTGAGATCAGCCTTCTTCCCGGATTAACG	720	
DB	669	ATGCGCTTTTGTATGTCATTTTCCGGTGGCTGAGATCAGCCTTCTTCCCGGATTAACG	728	
QY	721	GAGACCGGACACCTGGCCATATCGGTGTATCATGTCGCGAGCTTTTATCCCGGATATGC	780	
DB	729	GAGACCGGACACCTGGCCATATCGGTGTATCATGTCGCGAGCTTTTATCCCGGATATGC	788	
QY	781	ACCACCGGTAAGTTTCACGGAGACTTTTATCTGACAGCAGCAGTGTGCTGCGCGGGG	840	
DB	789	ACCACCGGTAAGTTTCACGGAGACTTTTATCTGACAGCAGCAGTGTGCTGCGCGGGG	848	
QY	841	ATCACCATCTCGTGGCGGGGCTGTCAATAATATCACTCTGTATATCCCAAAACAGACGA	900	
DB	849	ATCACCATCTCGTGGCGGGGCTGTCAATAATATCACTCTGTATATCCCAAAACAGACGA	908	
QY	901	TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAACTGATTTACACAGTCCCTGTTCTC	960	
DB	909	TAAAGGCTCTCTCTTTTATAGTGTAAACCTTAAACCTGATTTACACAGTCCCTGTTCTC	968	
QY	961	GTACAGAAAAGAGCGCTTCAATTTCAATAAACCGGGGACCTTCAGCCATCCCTTCTCTGATT	1020	

Db 969 GTACAGAAAAGAGCGCTTCAATTTCAATAAACCGGGGACCTTCAGCCATCCCTTCTCTGATT 1028

QY 1021 TTCCGCTTTCCAGCGTTTCGGCAGCAGACGACGAGGCTTCATTCTGCAATGTTGTGCTTAC 1080

Db 1029 TTCCGCTTTCCAGCGTTTCGGCAGCAGCAGCAGGCTTCATTCTGCAATGTTGTGCTTAC 1088

QY 1081 CAGACCGGAGATTTGACATCATATATGCTTTCAGCAACTGATAGCTGTGCTGCTCAACT 1140

Db 1089 CAGACCGGAGATTTGACATCATATATGCTTTCAGCAACTGATAGCTGTGCTGCTCAACT 1148

QY 1141 GTCACTGTAAATACCGCTCTTCATAGCACACCTCTTTTTCAGCATCTTCGGGTA 1193

Db 1149 GTCACTGTAAATACCGCTCTTCATAGCACACCTCTTTTTCAGCATCTTCGGGTA 1201

RESULT 15

AAC55524

ID AAC55524 standard; DNA; 4165 BP.

XX AAC55524;

XX 11-JAN-2001 (first entry)

XX Donor plasmid pDONR204 nucleotide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

KW mutant; recombinational cloning; entry vector; destination vector;

KW gene product targeting; fusion tag cleavage; ds.

XX Bacteriophage lambda.

OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

XX 02-MAR-2000; 2000WO-US005432.

XX 02-MAR-1999; 99US-0122389P.

PR 23-MAR-1999; 99US-0126049P.

PR 28-MAY-1999; 99US-0136744P.

XX (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch WA, Temple GF, Cheo D;

XX WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.

Example 9; Fig 52; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins,

CC	changing copy number, changing replicons, cloning into phages and	
CC	cloning (I), (II), (III), host cells and vectors can be used in the	
CC	production of polypeptides and antibodies. The present sequence is used	
CC	in the exemplification of the present invention	
XX		
SQ	Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 0 U; 1 Other;	
	Query Match 22.0%; Score 1068.2; DB 3; Length 4165;	
	Best Local Similarity 98.8%; Pred. No. 2e-139;	
	Matches 1088; Conservative 0; Mismatches 8; Indels 5; Gaps 1;	
QY	3278 GGCAAAATATGATTTATTTAGTACATGATGACCTGTTGGTGCACAAATGATAAGC 3337	
DB	2108 GGCAAAATATGATTTATTTAGTACATGATGACCTGTTGGTGCACAAATGATAAGC 2167	
QY	3338 AATGCTTTCTTATAATGCCAACTTTTGACAAAGAGCTGAACGAGAAACGTTAAATGATA 3397	
DB	2168 AATGCTTTCTTATAATGCCAACTTTTGACAAAGAGCTGAACGAGAAACGTTAAATGATA 2227	
QY	3398 TAAATATCAATATATTAATTTAGATTTTGCATATAAAACAGACTACATAATACCTGTAAAA 3457	
DB	2228 TAAATATCAATATATTAATTTAGATTTTGCATATAAAACAGACTACATAATACCTGTAAAA 2287	
QY	3458 CACAAATATCCAGTACTATGAATCAACTTACTTAGATGGTATTAGTGAAGCTGTAGTCGA 3517	
DB	2288 CACAAATATCCAGTACTATGAATCAACTTACTTAGATGGTATTAGTGAAGCTGTAGTCGA 2347	
QY	3518 CTAAAGTTGGCAGCATCACCCGACGACCTTTGCGCGGCAATAAATACCTGTGACGGAAGATC 3577	
DB	2348 CTAAAGTTGGCAGCATCACCCGACGACCTTTGCGCGGCAATAAATACCTGTGACGGAAGATC 2407	
QY	3578 ACTTGGCAGAAATAAATAATCCTGGTGCCCTGTGTGATACCGGGAAGCCCTGGGCCCACT 3637	
DB	2408 ACTTGGCAGAAATAAATAATCCTGGTGCCCTGTGTGATACCGGGAAGCCCTGGGCCCACT 2467	
QY	3638 TTGGCGGAAATAGACGCTTGTATCGGCACTACCCCACTTTTCAAACTCTTTATACCTTTCTCT 3697	
DB	2468 TTGGCGGAAATAGACGCTTGTATCGGCACTACCCCACTTTTCAAACTCTTTATACCTTTCTCT 2522	
QY	3698 TACAAGTCGTTGGCTTCATCTGGATTTTTCAGCCTCTTACTTACTAAACGTGATAAAGT 3757	
DB	2523 TACAAGTCGTTGGCTTCATCTGGATTTTTCAGCCTCTTACTTACTAAACGTGATAAAGT 2582	
QY	3758 TTCTGTAAATTTCTATGTATGACCTGACACTGCTGTGTATAGGAGGCTGACATTT 3817	
DB	2583 TTCTGTAAATTTCTATGTATGACCTGACACTGCTGTGTATAGGAGGCTGACATTT 2642	
QY	3818 ATATTCCCGACAGACATCAGGTTAATGCGGTTTTTGTATGTCATTTTCGCGGTGGCTGAGAT 3877	
DB	2643 ATATTCCCGACAGACATCAGGTTAATGCGGTTTTTGTATGTCATTTTCGCGGTGGCTGAGAT 2702	
QY	3878 CAGCCACTTTCTCCCGATAACGGAGACCGGACACTGGCCCATATCGGTGGTCAATGC 3937	
DB	2703 CAGCCACTTTCTCCCGATAACGGAGACCGGACACTGGCCCATATCGGTGGTCAATGC 2762	
QY	3938 GCGAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTACGGGAGACTTTTATCTGACA 3997	
DB	2763 GCGAGCTTTTCATCCCGATATGACACCGGTTAAAGTTTACGGGAGACTTTTATCTGACA 2822	
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QY	4058 TCTGTATACATCCAAACAGACGATAAGCGCTCTCTCTTTTATAGGTGTAACCTTAACT 4117	
DB	2883 TCTGTATACATCCAAACAGACGATAAGCGCTCTCTCTTTTATAGGTGTAACCTTAACT 2942	
QY	4118 GCATTTCCAGTCCCTGTTCTGTCAGCAAGAGCGCTTCTATTTCAATAAACCAGGCG 4177	
DB	2943 GCATTTCCAGTCCCTGTTCTGTCAGCAAGAGCGCTTCTATTTCAATAAACCAGGCG 3002	
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Search completed: May 7, 2004, 18:27:12
Job time : 1223.77 secs

ATTACHMENTS

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	759.2	15.6	5938	2	US-08-850-890-3	Sequence 3, Appl
C 2	759.2	15.6	5838	2	US-08-944-916-3	Sequence 3, Appl
C 3	759.2	15.6	5838	2	US-08-814-877-3	Sequence 3, Appl
C 4	759.2	15.6	5838	4	US-09-272-432A-3	Sequence 3, Appl
C 5	759.2	15.6	9737	4	US-09-479-122-22	Sequence 22, Appl
C 6	759.2	15.6	9737	4	US-09-479-122-22	Sequence 23, Appl
C 7	759.2	15.6	9737	4	US-09-479-122-28	Sequence 28, Appl
C 8	759.2	15.6	9737	4	US-09-484-987-22	Sequence 22, Appl
C 9	759.2	15.6	9737	4	US-09-484-997-23	Sequence 23, Appl
C 10	759.2	15.6	9737	4	US-09-484-997-28	Sequence 28, Appl
C 11	759.2	15.6	9737	4	US-09-481-355-22	Sequence 22, Appl
C 12	759.2	15.6	9737	4	US-09-481-355-23	Sequence 23, Appl
C 13	759.2	15.6	9737	4	US-09-481-355-28	Sequence 28, Appl
C 14	759.2	15.6	9737	4	US-09-481-282-22	Sequence 22, Appl
C 15	759.2	15.6	9737	4	US-09-481-282-23	Sequence 23, Appl
C 16	759.2	15.6	9737	4	US-09-481-284-28	Sequence 28, Appl
C 17	759.2	15.6	9737	4	US-09-481-284-28	Sequence 28, Appl
C 18	759.2	15.6	9737	4	US-09-455-659A-22	Sequence 22, Appl
C 19	759.2	15.6	9737	4	US-09-455-659A-23	Sequence 23, Appl
C 20	759.2	15.6	9737	4	US-09-455-659A-28	Sequence 28, Appl
C 21	759.2	15.6	9737	4	US-09-484-996-22	Sequence 22, Appl
C 22	759.2	15.6	9737	4	US-09-484-996-23	Sequence 23, Appl
C 23	759.2	15.6	9737	4	US-09-484-996-28	Sequence 28, Appl
C 24	759.2	15.6	9737	4	US-09-479-123-22	Sequence 22, Appl
C 25	759.2	15.6	9737	4	US-09-479-123-23	Sequence 23, Appl
C 26	759.2	15.6	9737	4	US-09-479-123-28	Sequence 28, Appl
C 27	759.2	15.6	9737	4	US-09-479-122-24	Sequence 24, Appl
C 28	759.2	15.6	9737	4	US-09-484-997-24	Sequence 24, Appl

SUMMARY

RESULT 2

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Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1852 TAAGATGATATACGGCGGTAAAGAGTTCCAACTTTCCACATAAATAAGATCACTA 1911
Db 3071 TGAGACGTTGATCGGCAGTAGAGGTTCCAACTTTCCACATAAATAAGATCACTA 3012
QY 1912 CCGGCGGTATTTTGGATTATCGAGATTTCAGAGCTTAAGAGCTAAATGGAGAAA 1971
Db 3011 CCGGCGGTATTTTGGATTATCGAGATTTCAGAGCTTAAGAGCTAAATGGAGAAA 2952
QY 1972 AAAATCACTGGATATACCGCTTGATATATCCATGGCAGCTTAAGAGCAATTTTGG 2031
Db 2951 AAAATCACTGGATATACCGCTTGATATATCCATGGCAGCTTAAGAGCAATTTTGG 2892
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QY 2452 GACAACTCTTCGCGCCCGTTTCCACATGGGCAATATATACGCAAGCGCAAGGTG 2511
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QY 2572 ATGCTTAATGAATTACACAGTACTGCGATGAGTGGCGAGCGGGCGGCGTAAT 2623
Db 2351 ATGCTTAATGAATTACACAGTACTGCGATGAGTGGCGAGCGGGCGGCGTAAT 2300
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RESULT 3

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US-08-814-877-3/c
; Sequence 3, Application US/08814877
; Patent No. 5965443
; GENERAL INFORMATION:
; APPLICANT: Goryshin, Igor V
; APPLICANT: Reznikoff, William S
; TITLE OF INVENTION: System for In Vitro Transposition
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814.877
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.94142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Plasmid DNA"
IMMEDIATE SOURCE:
CLONE: PRZTL1
FEATURE:
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LOCATION: 1..19
FEATURE:
NAME/KEY: CDS
LOCATION: 77..1267
OTHER INFORMATION: /function= "tetracycline resistance"
FEATURE:
NAME/KEY: CDS
LOCATION: 2301..2960
OTHER INFORMATION: /function= "chloramphenicol resistance"
FEATURE:
NAME/KEY: insertion_seq
LOCATION: 4564..4582
FEATURE:
NAME/KEY: CDS
LOCATION: 4715..5530
OTHER INFORMATION: /function= "kanamycin resistance"
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US-08-814-877-3

Query Match 15.6%; Score 759.2; DB 2; Length 5838;
Best Local Similarity 99.0%; Pred. No. 1.2e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1852 TAAGATGATATACGGCGGTAAAGAGTTCCAACTTTCCACATAAATAAGATCACTA 1911
Db 3071 TGAGACGTTGATCGGCAGTAGAGGTTCCAACTTTCCACATAAATAAGATCACTA 3012
QY 1912 CCGGCGGTATTTTGGATTATCGAGATTTCAGAGCTTAAGAGCTAAATGGAGAAA 1971
Db 3011 CCGGCGGTATTTTGGATTATCGAGATTTCAGAGCTTAAGAGCTAAATGGAGAAA 2952
QY 1972 AAAATCACTGGATATACCGCTTGATATATCCATGGCAGCTTAAGAGCAATTTTGG 2031
Db 2951 AAAATCACTGGATATACCGCTTGATATATCCATGGCAGCTTAAGAGCAATTTTGG 2892
QY 2032 GCATTTCACTGAGTTCCTCAATGATCCTATATACAGACAGCTTCAGCTGGATATTACGGCC 2091
Db 2891 GCATTTCACTGAGTTCCTCAATGATCCTATATACAGACAGCTTCAGCTGGATATTACGGCC 2832
QY 2092 TTTTAAAGACCGTAAAGAAAATAAGACACAGCTTTTATCCGGCCTTTTATTCACATCTT 2151
Db 2831 TTTTAAAGACCGTAAAGAAAATAAGACACAGCTTTTATCCGGCCTTTTATTCACATCTT 2772
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Db 2771 GCCGCGCTGATGATGCTATCCGGAATTCGATGCGCAATGAAGACAGCTGAGCTGGTG 2712
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QY 2272 TCGCTCTGGAGTGAATACCAAGAGATTTCCGGGAGTTTCTACACATATATTCGCAAGAT 2331
Db 2651 TCGCTCTGGAGTGAATACCAAGAGATTTCCGGGAGTTTCTACACATATATTCGCAAGAT 2592
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RESULT 4

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US-09-272-432A-3/c
; Sequence 3, Application US/09272432A
; Patent No. 6437109
; GENERAL INFORMATION:
; APPLICANT: Reznikoff, William S
; APPLICANT: Zhou, Hong
; APPLICANT: Goryshin, Igor Y
; TITLE OF INVENTION: System for In Vitro Transposition
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,432A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296.96277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608/251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5838 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pr2TL1
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; LOCATION: 1..19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77..1267
; OTHER INFORMATION: /function= "tetracycline resistance"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2301..2960)
; OTHER INFORMATION: /function= "chloramphenicol resistance"
; FEATURE:
; NAME/KEY: insertion_seq
; LOCATION: 4564..4582
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4715..5530
; OTHER INFORMATION: /function= "kanamycin resistance"
; US-09-272-432A-3

Query Match 15.6%; Score 759.2; DB 4; Length 5838;
Best Local Similarity 99.0%; Pred. No. 1.2e-141;
Matches 764; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1852 TAAGATGATATACGGCGGTAAAGAGTTCCAACTTTCCACATATGAAATGAATCACTA 1911
Db 3071 TGAGACGTTGATCGGCACGTAAAGAGTTCCAACTTTCCACATATGAAATGAATCACTA 3012
QY 1912 CCGGGCGTATTTTGTAGTTATCGAGATTTTCAGGAGCTAAGAGCTAAATGGAGAA 1971
Db 3011 CCGGGCGTATTTTGTAGTTATCGAGATTTTCAGGAGCTAAGAGCTAAATGGAGAA 2952
QY 1972 AAATCACTGGATATACCACTGTTGATATATCCATGGCATCGTAAAGAACATTTTGAG 2031
Db 2951 AAATCACTGGATATACCACTGTTGATATATCCATGGCATCGTAAAGAACATTTTGAG 2892
QY 2032 GCATTTTCAGTCAGTTGCTCAATGTACCTATAAACCAGACCGTTTCAGTGGATATTACGGCC 2091
Db 2891 GCATTTTCAGTCAGTTGCTCAATGTACCTATAAACCAGACCGTTTCAGTGGATATTACGGCC 2832
QY 2092 TTTTAAAGACCGTAAAGAAAATTAAGCAAGTTTTCATCGGCTTTTATTCACATTTCTT 2151
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QY 2152 GCCCGCTGTGATGAATGCTCATCCGAAATTCGATGCGCAATGGAAGACGGTGAOCTGTG 2211
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Db 2711 ATATGGGATAGTGTTCACCGCTTGTTCACCGCTTGTTCACCGCTTGTTCACCGCTTGTTC 2652
QY 2272 TCGCTCTGGAGTGAATACCAAGAGATTTCCGGGAGTTTCTACACATATATTCGCAAGAT 2331
Db 2651 TCGCTCTGGAGTGAATACCAAGAGATTTCCGGGAGTTTCTACACATATATTCGCAAGAT 2592
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Db 2591 GTGCGCTGTACGGTGAATACCAAGAGATTTCCGGGAGTTTCTACACATATATTCGCAAGAT 2532
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Db 2531 TTCGCTCTCAGCAATCCCTGGGTGAGTTTCCACAGTTTTCAGTTTAAACGTTGGCAATATG 2472
QY 2452 GACAACTTCTTCGCGCGGTTTCCACCATGGGCAAAATATATACGCAAGGCGCAAGGTG 2511
Db 2471 GACAACTTCTTCGCGCGGTTTCCACCATGGGCAAAATATATACGCAAGGCGCAAGGTG 2412
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Db 2411 CTGATGCGCTGGGAGTTTCCAGTTTCATCATCCGCTCTGTGATGGTTTCCATGTCGGCAGA 2352
QY 2572 ATGCTTAATGAATACAAAGTACTGCGATGAGTGGCGAGGGCGGGCGGTAAAT 2623
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2332 GTGGCGGTGTACCGTGAAGAAACCTGGGCTATTTCCCTAAAGGTTTATTTGAGAATATGTTT 2391
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RESULT 6
US-09-479-122-23/c
; Sequence 23, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-479-122-23

Query Match 15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Query Match 15.6%; Score 759.2; DB 4; Length 9737;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 2434 CTGATGCGCTGGCGATTCAGCTTCATCATGCGCTGTGTGCTTCCATGCTGGCAGA 2375
Qy 2572 ATGCTTAATGAATTAACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2623
Db 2374 ATGCTTAATGAATTAACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2323
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RESULT 7

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US-09-479-122-28/c
; Sequence 28, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/359,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-28
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Query Match

Best Local Similarity 15.6%; Score 759.2; DB 4; Length 9737;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 3034 CCGGCGCTATTTTGTAGTTATCGAGATTTTTCAGGAGCTAAGAGCTAAATGGAGAAA 2975
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Db 2914 GCATTTTCAGTCACTGCTCAATGATACCTATAACAGACCGTTTTCAGCTGGATATTTACGGCC 2855
Qy 2092 TTTTAAAGACCGTAAAGAAAATAAGCACAAAGTTTATCCGGCTTTATTCACATCTT 2151
Db 2854 TTTTAAAGACCGTAAAGAAAATAAGCACAAAGTTTATCCGGCTTTATTCACATCTT 2795
Qy 2152 GCGGCGCTGATGATGCTCATCCGGAATTCGGTATGCAATGAAGACCGTGGAGCTGTG 2211
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Qy 2392 TCGCTCTGAGTGAATACCAAGCATTTCCAGTGTGTGTACAGTTTGTATTAAGCTGGCCAAATG 2451
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Db 2374 ATGCTTAATGAATTAACAGTACTGCGATGAGTGGCGGGGGCGGCGTAAT 2323
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RESULT 8

US-09-484-997-22/c
; Sequence 22, Application US/09484997

Wed May 12 08:20:57 2004

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Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 2974 AAAATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAAATTTTCAG 2915
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RESULT 14
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; Sequence 22, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-481-355-28
; Query Match 15.6%; Score 759.2; DB 4; Length 9737;

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4	2563.2	52.7	17476	15	US-10-385-546-7
5	2528	52.0	17681	15	US-10-055-001A-26
6	2510.6	51.6	17458	15	US-10-055-001A-25
7	1462.6	30.1	18691	15	US-10-055-001A-13
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9	1193	24.5	4892	16	US-10-357-268-1
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C 37	759.2	15.6	9737	15	US-10-331-329-23
C 38	759.2	15.6	9737	15	US-10-331-329-28
C 39	759.2	15.6	9871	15	US-10-331-329-24
C 40	759.2	15.6	10060	15	US-10-331-329-25
C 41	757.6	15.6	5750	13	US-10-270-176-32
C 42	757.6	15.6	5812	13	US-10-270-176-48
C 43	757.6	15.6	6205	13	US-10-270-176-33
C 44	757.6	15.6	8500	12	US-10-296-947-7
C 45	757.6	15.6	14468	15	US-10-295-362-19

ALIGNMENTS

RESULT 1

US-10-055-001A-13

; Sequence 13, Application US/10055001A

; Publication No. US20030049835A1

; GENERAL INFORMATION:

; APPLICANT: Wesley, Susan V.

; APPLICANT: Waterhouse, Peter

; APPLICANT: Halliwell, Christopher A.

; TITLE OF INVENTION: Method and means for producing efficient silencing constructs

; TITLE OF INVENTION: using recombinational cloning

; FILE REFERENCE: HELICA

; CURRENT APPLICATION NUMBER: US/10/055,001A

; CURRENT FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 18691

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: acceptor vector pHELLSGATE

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (7922)..(9985)

; OTHER INFORMATION: spectinomycin resistance

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (10706)..(11324)

; OTHER INFORMATION: right T-DNA border fragment

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (11674)..(13019)

; OTHER INFORMATION: CamV35S promoter fragment

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (17890)..(17659)

; OTHER INFORMATION: attP1 recombination site (complement)

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NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: codb selection marker (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron 2
FEATURE:
NAME/KEY: misc feature
LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
FEATURE:
NAME/KEY: misc feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
FEATURE:
NAME/KEY: misc feature
LOCATION: (13675)..(13980)
OTHER INFORMATION: codb selection marker (complement)
FEATURE:
NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
FEATURE:
NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
FEATURE:
NAME/KEY: misc feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: (497)..(1442)
OTHER INFORMATION: nptII coding region
FEATURE:
NAME/KEY: misc feature
LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
FEATURE:
NAME/KEY: misc feature
LOCATION: (2149)..(2706)
OTHER INFORMATION: a left T-DNA border region
US-10-055-001A-13
Query Match 100.0%; Score 4861; DB 15; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGGCCCCAAATAATGATTTTATTTTGAATGATGACCTGTTTCGTTGCAACAAATGA 60
Db 13040 CGGGCCCCAAATATGATTTTATTTGACATGATGACCTGTTTCGTTGCAACAAATGA 13099
Qy 61 TGAGCAATGCTTTTATATATGCAACTTTGTCACAAAAGCTGAAAGAGAAAGTAA 120
Db 13100 TGAGCAATGCTTTTATATATGCAACTTTGTCACAAAAGCTGAAAGAGAAAGTAA 13159
Qy 121 TGATATAATATCAATATATTAATTAATTTGATATAAAAAACAGACTACATAACTG 180
Db 13160 TGATATAATATCAATATATTAATTTGATATAAAAAACAGACTACATAACTG 13219
Qy 181 TAAACACAAACATATCCAGTCACTATGAATCAACTTCTAGATGGTATTAAGTACCTGTA 240
Db 13220 TAAACACAAACATATCCAGTCACTATGAATCAACTTCTAGATGGTATTAAGTACCTGTA 13279
Qy 241 GTGACCCGACAGCCCTCCAAATGTTCTTCGGGTGATGCTGCCAATAGTGCAGCCGACAG 300
Db 13280 GTGACCCGACAGCCCTCCAAATGTTCTTCGGGTGATGCTGCCAATAGTGCAGCCGACAG 13339
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QY 1381 CATAGTACTGATATGTTGTGTTTATACAGTATATATGATGCTGTTTTTATGCAAAATC 1440
DB 14420 CATAGTACTGATATGTTGTGTTTATACAGTATATATGATGCTGTTTTTATGCAAAATC 14479
QY 1441 TAAATTAATATATGAT 1500
DB 14480 TAAATTAAT 14539
QY 1501 GTTGCAATATATAGAAAGCAATGCTTATCAATTTGTGCAACGAAACAGATCTATCAGT 1560
DB 14540 GTTGCAATATATAGAAAGCAATGCTTATCAATTTGTGCAACGAAACAGATCTATCAGT 14599
QY 1561 GAAATTAAT 1620
DB 14600 GAAATTAAT 14659
QY 1621 TGGTAAGGAAAT 1680
DB 14660 TGGTAAGGAAAT 14719
QY 1681 TTAGTATGAT 1740
DB 14720 TTAGTATGAT 14779
QY 1741 GTTACATTAACCAATAGTAT 1800
DB 14780 GTTACATTAACCAATAGTAT 14839
QY 1801 GATAAAGTTGAGAGTAAGTAT 1860
DB 14840 GATAAAGTTGAGAGTAAGTAT 14899
QY 1861 ATACGCGCGTAAAGGTTCCAACTTTCCAACTTTCCAACTTTCCAACTTTCCAACTTTCCAA 1920
DB 14900 ATACGCGCGTAAAGGTTCCAACTTTCCAACTTTCCAACTTTCCAACTTTCCAACTTTCCAA 14959
QY 1921 TTTTTTGTAGTTATCGAGATTTTTCAGAGCTTAAGGAGCTTAAAGTAAAGTAAAGTAAAGTAAAG 1980
DB 14960 TTTTTTGTAGTTATCGAGATTTTTCAGAGCTTAAGGAGCTTAAAGTAAAGTAAAGTAAAGTAAAG 15019
QY 1981 GGATATACACCGTTGAT 2040
DB 15020 GGATATACACCGTTGAT 15079
QY 2041 TCAGTTGCTCAATGACCTATACACGAGTTCAGCTGATATATATATATATATATATATATATAT 2100
DB 15080 TCAGTTGCTCAATGACCTATACACGAGTTCAGCTGATATATATATATATATATATATATAT 15139
QY 2101 ACCGTAAGAAATTAAGCAACAGTATATATATATATATATATATATATATATATATATATAT 2160
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DB 15200 ATGAATGCTATCCGGAAATTCGGTATGGCAATGAAGAGAGCTGGTATATATATATATATAT 15259
QY 2221 AGTGTTCACCCCTGTTACACCGTTTTCATAGCAACAGTATATATATATATATATATATATAT 2280
DB 15260 AGTGTTCACCCCTGTTACACCGTTTTCATAGCAACAGTATATATATATATATATATATATAT 15319
QY 2281 AGTGAATACCAACAGATTTCCGGCAGTTTCTACATATATATATATATATATATATATATATAT 2340
DB 15320 AGTGAATACCAACAGATTTCCGGCAGTTTCTACATATATATATATATATATATATATATATAT 15379
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DB 15380 TACGGTGAACACCTGGCCTAT 15439
QY 2401 GCCAATCCCTGGGTGAGTTTCCAGAGTTTGTATATATATATATATATATATATATATATATATAT 2460
DB 15440 GCCAATCCCTGGGTGAGTTTCCAGAGTTTGTATATATATATATATATATATATATATATATATAT 15499
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DB 15500 TTGCGCCCGCTTTTACCATGGGCAAT 15559
QY 2521 CTGGCGATTCAGGTTTCATCATGCGCGTCTGTGATGCTTCCATGTGCGGAGATGCTTAAAT 2580
DB 15560 CTGGCGATTCAGGTTTCATCATGCGCGTCTGTGATGCTTCCATGTGCGGAGATGCTTAAAT 15619
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DB 15620 GAAATTAACAGTACTCGGATGAGTGGCAGGCGGGGGGTAAATCGCGTGGATCCGGCTTA 15679
QY 2641 CTAAAGCGCAGATACAGTATGCGTATTTGCGCGTGAATTTTGGCGGTATAAGATATAT 2700
DB 15680 CTAAAGCGCAGATACAGTATGCGTATTTGCGCGTGAATTTTGGCGGTATAAGATATAT 15739
QY 2701 ACTGATATGTCGGGCCATAATAGTAAATCTAGCTGGTGTGATGAATTAATATCAATGA 2760
DB 15740 ACTGATATGTCGGGCCATAATAGTAAATCTAGCTGGTGTGATGAATTAATATCAATGA 15799
QY 2761 TAAATATCTATAGTAAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2820
DB 15800 TAAATATCTATAGTAAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 15859
QY 2821 AGTTTATTTAT 2880
DB 15860 AGTTTATTTAT 15919
QY 2881 AATATTTTGTAGAAATTCATCTGCTGTAAATTTATCAATTAATTAATTAATTAATTAATTAAT 2940
DB 15920 AATATTTTGTAGAAATTCATCTGCTGTAAATTTATCAATTAATTAATTAATTAATTAATTAAT 15979
QY 2941 CAAGCTAAAGTAAACAAATATATCAAACTAAATAGAAACAGTAATCTATATATATATATATATAT 3000
DB 15980 CAAGCTAAAGTAAACAAATATATCAAACTAAATAGAAACAGTAATCTATATATATATATATAT 16039
QY 3001 TAAATCTAT 3060
DB 16040 TAAATCTAT 16099
QY 3061 TCATATCTTAT 3120
DB 16100 TCATATCTTAT 16159
QY 3121 ACTATTAATTAATGAATTTAGTCGAACATGAAATTAACAAAGTAAACATGATAGATCATGTC 3180
DB 16160 ACTATTAATTAATGAATTTAGTCGAACATGAAATTAACAAAGTAAACATGATAGATCATGTC 16219
QY 3181 ATTGTGTTATCATCTTACATTTGGATTTACAGTTGGGAAATTTGGGTTTGGAAAT 3240
DB 16220 ATTGTGTTATCATCTTACATTTGGATTTACAGTTGGGAAATTTGGGTTTGGAAAT 16279
QY 3241 CGATAGCTTGGATCTCTAGAGCTGCGAGTGGTGAATTAATTAATTAATTAATTAATTAATTAAT 3300
DB 16280 CGATAGCTTGGATCTCTAGAGCTGCGAGTGGTGAATTAATTAATTAATTAATTAATTAATTAAT 16339
QY 3301 CTGATAGTGACCTGTTGTTGCAACAAATGATAAGCAATGCTTTCTTATATATATATATATATAT 3360
DB 16340 CTGATAGTGACCTGTTGTTGCAACAAATGATAAGCAATGCTTTCTTATATATATATATATATAT 16399
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QY 3781 CTTGACAGCTGGCTGTGTATTAAGGAGCCTGACATTTATATTTCCCGAACAATCAGGTTA 3840
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QY 3841 ATGGCGTTTGTATGTCATTTTTCGGGTGCTGAGATCAGCCTCTCTTCCCGATAACG 3900
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QY 3961 ACCACGGGTAAAGTTACCGGGAGACTTATCTGACAGCAGCGTGCCTGCGCCAGGGG 4020
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QY 4021 ATCACCATCGTCCCGCGGTGTCATTAATATCACTCTGTACATCCCAAAACAGACGA 4080
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Db 17240 TTCGGCTTTCAGGTTTCGGCCAGCAGCGGCTTCTATCTGATGTTGCTTAC 17299
QY 4261 CAGACCGGAGATATGACATATATGCTTTGAGCAACTGATAGCTGTGCTTCACT 4320
Db 17300 CAGACCGGAGATATGACATATATGCTTTGAGCAACTGATAGCTGTGCTTCACT 17359
QY 4321 GTCACTGTATACGCTGCTCATAGCACACCTCTTTTGACATACTTCTGTTCTGATGC 4380
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QY 4441 ACACAAAAGAGGCTCGCACTCTTTTCTTATTTCTTTTATGATTAATACGGATT 4500
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QY 4501 GAGGCAATACGGATAGGCTGGATACGACGATTCGGTTTTCAGAGAACATTTGGAAGG 4560
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QY 4861 G 4861
Db 17900 G 17900

RESULT 2

US-10-055-001A-23
; Sequence 23, Application US/10055001A
; Publication No. US20030049H35A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17862
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23

Query Match 64.9%; Score 3154.4; DB 15; Length 17862;
Best Local Similarity 82.6%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 16; Indels 831; Gaps 2;

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QY 61 TGAGCAATGCTTTTATATGATGCTTGTACAAAGCTGAAACGAGAAACGTAAAA 120
Db 13100 TGAGCAATGCTTTTATATGATGCTTGTACAAAGCTGAAACGAGAAACGTAAAA 13159
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Db 13340 CCTTCGAAATGTTCTTCTCAACGGATCGTCCTATCCAGCTACTCGCTATTGTCCTCA 13399
QY 361 ATGCGGTATTAAATCAATAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTG 420
Db 13400 ATGCGGTATTAAATCAATAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTGTGTG 13459

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QY |||||
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13640 CCTCGACACTGGCTGTCTAAGGAGCCTGACATTTATATCTCCGAGACATCAGGTTA 13699
QY |||||
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Db |||||
13700 ATGGCGTTTTTGATGTCTATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCGGATTAACG 13759
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Db |||||
13820 ACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGGG 13879
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841 ATCAACCATTCGTCGCCCGGGCTGCAATATATCACTCTGTATCATCCACAAACAGACGA 900
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13880 ATCAACCATTCGTCGCCCGGGCTGCAATATATCACTCTGTATCATCCACAAACAGACGA 13939
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13940 TAAGGCTCTCTCTTTATAGGTGTAACCTTAACTGCAATTCACAGTCCCTGTTCTC 13999
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961 GTACAGAAAGAGCGGTTCAATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATT 1020
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14000 GTACAGAAAGAGCGGTTCAATTTCAATAAACCAGGCGACCTCAGCCATCCCTTCTGATT 14059
QY |||||
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Db |||||
14060 TTCGCTTTTCAGCGTTTCGGCAGCAGACGCGGCTTCATTTCTGCATGTTGTGCTTAC 14119
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14120 CAGACCGGAGATATGACATCATATATGCTTGGACCACTGATAGCTGTCCTGTCACT 14179
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Db |||||
14540 GTTGGCATATATAAGAAAGCAATTCCTTATCAATTTGTTCACAAACAGGTCACATCAGT 14599
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14780 TGTTTACATAAAACAAACATAGTAATGTAAAAAAATATGACAAAGTGTGTGTAAGACGAAGA 14839
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1800 AGATAAAGTTGAGAGTAAGTATATTTTATGAAATTTGATCGAACATGTAAGATGA 1859
Db |||||
14840 AGATAAAGTTGAGAGTAAGTATATTTTATGAAATTTGATCGAACATGTAAGATGA 14899
QY |||||
1860 TATACGCGCGGTAAAGAGTTTCCAACTTTCACCATATGAATAAGATCACTACCGGCGT 1919
Db |||||
14900 TATACGCAATTA----- 14913
QY |||||
1920 ATTTTGTAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAAGTGAAGAAATAAATCAAC 1979
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QY |||||
1980 TGGATATACCAACCGTTGATATATCCCAATGCGCATCGTAAGAACATTTTCGAGGCAATTC 2039
Db |||||
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QY |||||
2040 GTCAGTTGCTCAATGTACTATTAACCAAGCCGTTTCCAGCTGGAATATACGCGCTTTTAA 2099
Db |||||
14914 ----- 14913
QY |||||
2100 GACGTAAGAAAAATAAGCACAAAGTTTATCCGGCTTTTATTCACATTTCTGCGCGCCT 2159
Db |||||
14914 ----- 14913
QY |||||
2160 GATGAATGCTCATCCGGAATTCGATGSCAATGAAAGACGCTGAGCTGCTGATATGGA 2219
Db |||||
14914 ----- 14913
QY |||||
2220 TAGTGTTCACCCCTTGTATACACCGTTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTG 2279
Db |||||
14914 ----- 14913
QY |||||
2280 GAGTGAATACACGACGATTTCCGGCAGTTTCTACATATATTCGCAAGATGTCGCGCTG 2339
Db |||||
14914 ----- 14913
QY |||||
2340 TTACGCTGAAAAACCTGCGCTTATTTCCCTAAAGGTTTATTTGAGAAATATGTTTTTCGCTC 2399
Db |||||
14914 ----- 14913
QY |||||
2400 AGCCAATCCCTGGGTGAGTTTCCAGTTTGTATTTTAAACGTGGCCAATATGGAACAAT 2459
Db |||||
14914 ----- 14913
QY |||||
2460 CTTGCGCCCGGTTTTCACCATGGGCAATATATATACCAAGGCGACAGGTCGTGATGCC 2519
Db |||||
14914 ----- 14913
QY |||||
2520 GCTGGCGATTTCAGGTTTCATCATGCGGCTCTGTGATGGCTTCCATGTCCGACAGATGCTTAA 2579
Db |||||
14914 ----- 14913
QY |||||
2580 TGAATTAACAACAGTACTGCGATGAGTGCGAGGGCGGGCGTAAATCGCGTGGATCCGCGTT 2639

Db	14914	-----	14913
Qy	2640	ACTAAAGCCAGATAACAGATATCGTATTTTGGCGCTGATTTTGGCGTATAAGATATA	2699
Db	14914	-----	14913
Qy	2700	TACTGATATGTCGGGCGCCATAATAGTAATCTTAGCTGGTTGATGAATTAATAATCAATG	2759
Db	14914	-----	14913
Qy	2760	ATRAAATACATAGTAAAAATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAA	2819
Db	14970	ATRAAATACATAGTAAAAATAAGATAAATAAATAAATAAATAAATAAATAAATAAATAA	15029
Qy	2820	TAGTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	2879
Db	15030	TAGTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	15089
Qy	2880	AAATATTTTCTAGAAATTCGAATCTGCTGTAATTTATCAATAAACAATAAATAAATAA	2939
Db	15090	AAATATTTTCTAGAAATTCGAATCTGCTGTAATTTATCAATAAACAATAAATAAATAA	15149
Qy	2940	ACAAGCTAAAGTAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	2999
Db	15150	ACAAGCTAAAGTAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	15209
Qy	3000	ATAATCTAATGCTAAATAAATAAACAAGCGAAGATCTATCTATTTATATAGTATTTTCA	3059
Db	15210	ATAATCTAATGCTAAATAAATAAACAAGCGAAGATCTATCTATTTATATAGTATTTTCA	15269
Qy	3060	ATCAACATCTCTTAAATTTCTTAATAATATCTTCTAGTTTATTTATTTAACTCTTAATG	3119
Db	15270	ATCAACATCTCTTAAATTTCTTAATAATATCTTCTAGTTTATTTATTTAACTCTTAATG	15329
Qy	3120	GACTATTTAAATGAAATGATGCGAATGAAATGAAATGAAATGAAATGAAATGAAATG	3179
Db	15330	GACTATTTAAATGAAATGATGCGAATGAAATGAAATGAAATGAAATGAAATGAAATG	15389
Qy	3180	CATTGCTGATCATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	3239
Db	15390	CATTGCTGATCATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	15449
Qy	3240	TCGATAGCTGGATCTCTAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3299
Db	15450	TCGATAGCTGGATCTCTAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	15509
Qy	3300	ACTGATAGTACCTGTTTGGTTCGAAATGAAATGAAATGAAATGAAATGAAATGAAAT	3359
Db	15510	ACTGATAGTACCTGTTTGGTTCGAAATGAAATGAAATGAAATGAAATGAAATGAAAT	15569
Qy	3360	TTTGTACAGAAAGCTGAAACGAGAAACGTAATAATGATATAATCAATATATTAATA	3419
Db	15570	TTTGTACAGAAAGCTGAAACGAGAAACGTAATAATGATATAATCAATATATTAATA	15629
Qy	3420	GATTTTGCATAAAAACAGACTACATAATCTGTAATAACCAACATATCCAGTCACTAT	3479
Db	15630	GATTTTGCATAAAAACAGACTACATAATCTGTAATAACCAACATATCCAGTCACTAT	15689
Qy	3480	AATCAACTACTTAGATGATTTAGTACCTGCTGATGCTGATGCTGATGCTGATGCTG	3539
Db	15690	AATCAACTACTTAGATGATTTAGTACCTGCTGATGCTGATGCTGATGCTGATGCTG	15749
Qy	3540	CGCACTTTTGGCGGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAT	3599
Db	15750	CGCACTTTTGGCGGAATAAATACCTGTGACGGAAGATCACTTCGAGAAATAAATAAT	15809
Qy	3600	TGGTGTCCCTGTTGATACCGGAAGCCCTGGGCCAACTTTTGGCGAAATAGAGCGTTGA	3659
Db	15810	TGGTGTCCCTGTTGATACCGGAAGCCCTGGGCCAACTTTTGGCGAAATAGAGCGTTGA	15869
Qy	3660	TGGGCACTACCATTCACAACTCTATATCTTTCTTACAAAGTGGCTTCGCTTCATCT	3719
Db	15870	TGGGCACTACCATTCACAACTCTATATCTTTCTTACAAAGTGGCTTCGCTTCATCT	15929
Qy	3720	GGATTTTCAGCTCTATATCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCG	3779
Db	15930	GGATTTTCAGCTCTATATCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCG	15989
Qy	3780	ACCTCAGACTGGCTGTGTATAAGGAGCCTGACATTTTATATTTCCCCAGAACATCAGGTT	3839
Db	15990	ACCTCAGACTGGCTGTGTATAAGGAGCCTGACATTTTATATTTCCCCAGAACATCAGGTT	16049
Qy	3840	AATGCGTTTTTGTATGTCTATTTTCCGGTGGCTGAGATCAGCCACTTCTTCCCGATAC	3899
Db	16050	AATGCGTTTTTGTATGTCTATTTTCCGGTGGCTGAGATCAGCCACTTCTTCCCGATAC	16109
Qy	3900	GGAGACCGCACACATGGCCCATATCGTGTGTATCATGCGCCAGCTTTCATCCCCCATATG	3959
Db	16110	GGAGACCGCACACATGGCCCATATCGTGTGTATCATGCGCCAGCTTTCATCCCCCATATG	16169
Qy	3960	CACACCGGGTAAAGTTTCAACGGGAGATTTTATCTGACAGACAGCTGCACTGGCCAGGG	4019
Db	16170	CACACCGGGTAAAGTTTCAACGGGAGATTTTATCTGACAGACAGCTGCACTGGCCAGGG	16229
Qy	4020	GATCACCATCGCTCGCCCGGGCTGTCAATATATCACTCTGTACATCCACAAACAGACG	4079
Db	16230	GATCACCATCGCTCGCCCGGGCTGTCAATATATCACTCTGTACATCCACAAACAGACG	16289
Qy	4080	ATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAATTCACAGTCCCTGTTCT	4139
Db	16290	ATAACGGCTCTCTCTTTTATAGTGTAAACCTTAAACTGCAATTCACAGTCCCTGTTCT	16349
Qy	4140	CGTCAGCAAAAGAGCCGTTTCAATTTAAACCGGGCGACCTCAGCCATCCCTTCTGTAT	4199
Db	16350	CGTCAGCAAAAGAGCCGTTTCAATTTAAACCGGGCGACCTCAGCCATCCCTTCTGTAT	16409
Qy	4200	TTTCCGCTTTCAGCGCTCGGCACGACGAGCGGCTTCACTTCTCATGTTGTTGCTTA	4259
Db	16410	TTTCCGCTTTCAGCGCTCGGCACGACGAGCGGCTTCACTTCTCATGTTGTTGCTTA	16469
Qy	4260	CCAGACCGGAGATTTGACATCATATATGCTTGTGACCACTGATAGTGTGCTGTCAAC	4319
Db	16470	CCAGACCGGAGATTTGACATCATATATGCTTGTGACCACTGATAGTGTGCTGTCAAC	16529
Qy	4320	TGTCACGTAAATACGCTGCTTCAAGACACCTCTTTTGTGACATCTCTGTTCTTGATG	4379
Db	16530	TGTCACGTAAATACGCTGCTTCAAGACACCTCTTTTGTGACATCTCTGTTCTTGATG	16589
Qy	4380	CAGATGATTTTCCAGGACTATGACATGATGCTGATGATGATGATGATGATGATGATG	4439
Db	16590	CAGATGATTTTCCAGGACTATGACATGATGCTGATGATGATGATGATGATGATGATG	16649
Qy	4440	CACAAAAAAGAGGCTCGCACCTCTTTTCTTTTATGATTTTATGATTTTATGCGCAT	4499
Db	16650	CACAAAAAAGAGGCTCGCACCTCTTTTCTTTTATGATTTTATGATTTTATGCGCAT	16709
Qy	4500	TGAGGACATAGCGGTAGGCTGATACGAGATTCGTTTGTGAGAGAAATTTGGAAGG	4559
Db	16710	TGAGGACATAGCGGTAGGCTGATACGAGATTCGTTTGTGAGAGAAATTTGGAAGG	16769
Qy	4560	CTGTGCGTCCGACTAAGTTGGCAGCATCACCCGAGAACTTTGGAAGGCTGTGCGTCA	4619
Db	16770	CTGTGCGTCCGACTAAGTTGGCAGCATCACCCGAGAACTTTGGAAGGCTGTGCGTCA	16829
Qy	4620	TACAGGTCATTAATACCATCTAGTAGTGTGATTCATGATGATGATGATGATGATGAT	4679
Db	16830	TACAGGTCATTAATACCATCTAGTAGTGTGATTCATGATGATGATGATGATGATGAT	16889
Qy	4680	CAGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4739
Db	16890	CAGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	16949
Qy	4740	TTTTACGCTTCTCGCTCAGCTTTTTTGTACAAAGTGGCAATTAATAAAGCATGCTCA	4799
Db	16950	TTTTACGCTTCTCGCTCAGCTTTTTTGTACAAAGTGGCAATTAATAAAGCATGCTCA	17009

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Qy 1761 AATGTAAAAAATATGACAAAGTGAATGTGTAAGACGAAGAATAAAGATTGAGAGTAAGT 1820
Db 14613 AATGTAAAAAATATGACAAAGTGAATGTGTAAGACGAAGAATAAAGATTGAGAGTAAGT 14672
Qy 1821 ATATTATTTTAAATGTAATGTCGAACATGTGAAGATGATATACGGCGGTAAGAGGTTTC 1880
Db 14673 ATATTATTTTAAATGTAATGTCGAACATGTGAAGATGATATACGGCATTA----- 14725
Qy 1881 CAACCTTACCATAAATGAATAAGATCACTACCGGGCGTATTTTTTGGAGTTATCGAGATT 1940
Db 14726 ----- 14725
Qy 1941 TTCAGGAGCTAAGAAAGCTAAAAATGGAGAAAAAATACTGAGATATACCAACCGTTGATAT 2000
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Qy 2001 ATCCCAATGCGATCGTAAGAAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTA 2060
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Qy 2061 TAACCAAGACCGTTTCAGCTGGATATATACGGCCTTTTAAAGACCGTAAGAAAAATAAGCA 2120
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Qy 2121 CAAGTTTATCCGGCCTTTATTCACATCTTGCCCGCCTGATGAATGCTCATCCGGAATT 2180
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Qy 2241 CGTTTCCATGAGCAAACTGAAAGCTTTTCATCGCTCTGAGTGAATPACCAACGCGATT 2300
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Qy 2301 CCGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAAAACTGGCCTA 2360
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Qy 2361 TTTCCCTAAAGGTTTATGAGAATATGTTTTTCTGCTCAGCCAAATCCCTGGGTGAGTTT 2420
Db 14726 ----- 14725
Qy 2421 CACAGTTTGTATTAACCGTGGCCAAATATGGACAACCTTCTCGCCCCCGTTTTCACCAT 2480
Db 14726 ----- 14725
Qy 2481 GGGCAATATATACGCAAGCGGACAGGTGCTGATGCCGCTGGCGATTCCAGTTTCATCA 2540
Db 14726 ----- 14725
Qy 2541 TGCGCTCTGATGGCTTCCATGTCGGCAGAAATGCTTAATGAATTAACAACAGTACTCGGA 2600
Db 14726 ----- 14725
Qy 2601 TGAGTGGCAGGGCGGGCGGTAATCGCGTGGATCCGGCTTACTAAAGCCGAGATAACAGTA 2660
Db 14726 ----- 14725
Qy 2661 TGGCTATTTGCGCGCTGATTTTTTCCGGTATAGAATATATATCATGATGTCGGGCCCAT 2720
Db 14726 ----- 14725
Qy 2721 ATAGTAATCTAGCTGGTTGATGAATTAATAATCAATGAFAAAATACTATAGFAAAAAAT 2780
Db 14743 ATAGTAATCTAGCTGGTTGATGAATTAATAATCAATGAFAAAATACTATAGFAAAAAAT 14802
Qy 2781 AAGAATAAATAAATAAATAAATAATTTTTTATGATTAATAGTTTATATATATTAAT 2840
Db 14803 AAGAATAAATAAATAAATAAATAATTTTTTATGATTAATAGTTTATATATATTAAT 14862

Qy 2841 ATCTATACCATTTACTAAATATTTTAGTTTAAAGTTAAATAATAATTTTGTGTAGAATTCC 2900
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Qy 2901 AATCTGCTGTAAATTTATCATAAACAATAATTAATAACAAGCTAAAGTAACAATAA 2960
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Qy 2961 TATCAAACTTAATAGAAAACAGTAATCTAATGTAAACAAAACATAATCTAATGCTAAATAAC 3020
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Qy 3141 GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTGTCATTTGTGTATCATTCATT 3200
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Qy 3621 GAAGCCTTGGGCGCACTTTTGGCGAAAAATGAGAGCTGTGATCGGCACTACCCATTTCAACA 3680
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QY 4641 AAGTAGTTGATTCATAGTGAATGATGTTGTTTATGATGATGATGATGATGATGATGATGAT 4700
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QY 4701 TTATGMAAATCTAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4760
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RESULT 4

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US-10-385-546-7
; Sequence 7, Application US/10385546
; Publication No. US20030175783A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Wesley, Susan
; APPLICANT: Hellmell, Chris
; TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
; FILE REFERENCE: COLINA-US2
; CURRENT APPLICATION NUMBER: US/10/385,546
; CURRENT FILING DATE: 2003-03-12
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; PRIOR APPLICATION NUMBER: US 60363852
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 17476
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7
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Query Match 52.7%; Score 2563.2; DB 15; Length 17476;

Best Local Similarity 77.7%; Pred. No. 0; Mismatches 23; Indels 1024; Gaps 5; Matches 3651; Conservative 0;

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Qy	1042	ACGACAGACGCGGCTTCATTTCTGCAATGTTGCTTACAGACCGGAGATATTGACATC	1101	Qy	2121	CAAGTTTTATCGGCTTTTATTCACATTTCTGCGCGCTGATGAATGCTCATCCGGAATT	2180
Db	13985	ACGACAGACGCGGCTTCATTTCTGCAATGTTGCTTACAGACCGGAGATATTGACATC	14044	Db	14726	-----	14725
Qy	1102	ATATATGCTTGAAGAACTGATAGCTGCTGCTCACTGCTCACTGATTAACGCTGCTTC	1161	Qy	2181	CGGTATGGCAATGAAGAAGCGGTAGCTGGTGATATGGGATAGTGTTCACCCCTGTTACAC	2240
Db	14045	ATATATGCTTGAAGAACTGATAGCTGCTGCTCACTGCTCACTGATTAACGCTGCTTC	14104	Db	14726	-----	14725
Qy	1162	ATAGCACACCTCTTTTGAATATCTCGGTAGTGGCGATCAACGCTCACTTTTCGCCAA	1221	Qy	2241	CGTTTTCCATGAGCAAACTGAACGTTTTTCATCGCTCTCGAGTGGAATACCAAGACGATTT	2300
Db	14105	ATAGCACACCTCTTTTGAATATCTCGGTAGTGGCGATCAACGCTCACTTTTCGCCAA	14164	Db	14726	-----	14725
Qy	1222	AAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACGAGATTTATTTATTTCTGCGAAG	1281	Qy	2301	CGGCGAGTTTTCACACATATTTCGCAAGATGTGGGTGTTTACGGTGAAGAACTCGGCCCTA	2360
Db	14165	AAGTTGGCCAGGCTTCCCGGTATCAACAGGGACACACGAGATTTATTTATTTCTGCGAAG	14224	Db	14726	-----	14725
Qy	1282	TGATCTTCCGTCACAGGTATTTATTCGCGCAAGTGCCTGCGGTGATGCTGCCAACTTA	1341	Qy	2361	TTTCCCTAAAGGTTTTATTGAGAAATGTTTTTCGTCTCAGCCATCCCTGGGTGAGTTT	2420
Db	14225	TGATCTTCCGTCACAGGTATTTATTCGCGCAAGTGCCTGCGGTGATGCTGCCAACTTA	14284	Db	14726	-----	14725
Qy	1342	GTCGACTACAGGTCACATAACCATCTAAGTAGTGTGATTCATAGTGAAGTGTGTTGT	1401	Qy	2421	CACCGTTTTGATTTAAACGTGGCCCAATATGGACAACCTTCTTCGCCCCCGTTTTCCACCAT	2480
Db	14285	GTCGACTACAGGTCACATAACCATCTAAGTAGTGTGATTCATAGTGAAGTGTGTTGT	14344	Db	14726	-----	14725
Qy	1402	GTTTTACGATTAATGATGCTGCTTTTATGCAAAATCTAATTTAATATATATGATATTT	1461	Qy	2481	GGGCAAAATATTATACGCAAGGCGACAAGGTGCTGTATCGCGCTGGCGATTCAGGTTCAATCA	2540
Db	14345	GTTTTACGATTAATGATGCTGCTTTTATGCAAAATCTAATTTAATATATATGATATTT	14404	Db	14726	-----	14725
Qy	1462	ATATCAATTTACGTTCTCGTTTCAGCTTCTCTGTACAAAAGTTGGCAATTTAAGAAAGCAT	1521	Qy	2541	TGCGCTGTGATGGCTTCCATGTCGGCAGAAATGCTTTAATGAATTAACAACAGTACTGCGA	2600
Db	14405	ATATCAATTTACGTTCTCGTTTCAGCTTCTCTGTACAAAAGTTGGCAATTTAAGAAAGCAT	14447	Db	14726	-----	14725
Qy	1522	TGCTTATCAATTTGTTGCAAGCAAGAGTCTATACGTCACTATACGTCAAAATAAATCATTTTGC	1581	Qy	2601	TGAGTGGCAGGGGGGGCGTAATCGCGTGGATCCGGCTTACTAAAAGCCAGATAACAGTA	2660
Db	14448	-----	14447	Db	14726	-----	14725
Qy	1592	CATCCAGCTGCAGCTCTCGGAGATTCGGTACCCCA-ATTGGTAAGAAATAATTATTT	1640	Qy	2661	TGCGTATTTGGCGCTGATTTTTCGGGTATAAGAAATATATCTGATATATGTCGGGCCCATTA	2720
Db	14448	-----TCTCGAGGAATTCGGTACCCAGCTTGGTAAGGAATTAATTATTT	14492	Db	14726	-----TATTTGTTTTAATCATTA	14742
Qy	1641	TCTTTTTTCTTTAGTATAAAATAGTTAAGTATGTTTAAATPAGTATGATTAATAATA	1700	Qy	2721	ATAGTAATTTCTAGCTGGTTTGATGAATTAATATCAATGAATTAATATAGTAAAAAT	2780
Db	14493	TCTTTTTTCTTTAGTATAAAATAGTTAAGTATGTTTAAATPAGTATGATTAATAATA	14552	Db	14743	ATAGTAATTTCTAGCTGGTTTGATGAATTAATATCAATGAATTAATATAGTAAAAAT	14802
Qy	1701	TAGTTGTTATATTTGTAATAATAATTTATATAATATATGTTTACATAAACAACATAGT	1760	Qy	2781	AAGTAATAATAATAATAATAATAATTTTTTTATGATTAATAGTTTATATATAATTAAT	2840
Db	14553	TAGTTGTTATATTTGTAATAATAATTTATATAATATATGTTTACATAAACAACATAGT	14612	Db	14803	AAGTAATAATAATAATAATAATAATTTTTTTATGATTAATAGTTTATATATAATTAAT	14862
Qy	1761	AATGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	1820	Qy	2841	ATCTATACCATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	2900
Db	14613	AATGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	14672	Db	14863	ATCTATACCATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	14922
Qy	1821	ATATTATTTTAAATGAATTTGATCGAACATGTAAGATGATATACGGCCGGTAAAGGTTTC	1880	Qy	2901	AATCTGCTTGTAAATTTTATCAATAAACAATAATAATAATAATAATAATAATAATAATA	2960
Db	14673	ATATTATTTTAAATGAATTTGATCGAACATGTAAGATGATATACGGCCGGTAAAGGTTTC	14725	Db	14923	AATCTGCTTGTAAATTTTATCAATAAACAATAATAATAATAATAATAATAATAATAATA	14982
Qy	1881	CAACTTTCACCAATGAATTAAGTACATCTACCGGCGGTATTTTGTAGTTATCGAGATT	1940	Qy	2961	TATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACAATAATCTAATGTAATATAAC	3020
Db	14726	-----	14725	Db	14983	TATCAAACTAATAGAAAACAGTAATCTAATGTAACAAAACAATAATCTAATGTAATATAAC	15042
Qy	1941	TTCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATAT	2000	Qy	3021	AAAGGCGAAGATCTCATTTTTTATATAGTATATATTTTCAATCAATCTTTTATTAATTTTC	3080
Db	14726	-----	14725	Db	15043	AAAGGCGAAGATCTCATTTTTTATATAGTATATATTTTCAATCAATCTTTTATTAATTTTC	15102
Qy	2001	ATCCCAATGGCATCGTAAAGAACATTTTGGAGCAATTTTCAGTCAGTTGCTCAATGTACCTA	2060	Qy	3081	TAAATAATCTAGTTGTTTATTAATTAATCTTAAATGGAATGTAATTAATTAATTAATTAATTA	3140
Db	14726	-----	14725	Db	15103	TAAATAATCTAGTTGTTTATTAATTAATCTTAAATGGAATGTAATTAATTAATTAATTAATTA	15162

3141 GTCCGACATGAATAAACAAGTAATCATGATAGATCATGTCATGTTGTTATCATTCATTT 3200
15163 GTCCGACATGAATAAACAAGTAATCATGATAGATCATGTCATGTTGTTATCATTCATTT 15222
3201 ACATTTGANTTGAATACAGTTGGGAAATTTGGTTGGAATCGAATAGCTTGGATCCCTCTA 3260
15223 ACATTTGANTTGAATACAGTTGGGAAATTTGGTTGGAATCGAATAGCTTGGATCCCTCTA 15282
3261 GAGAGCTGACGTGATGGCAAAATGAATGATTTATTTTGAATGATGATGACCTGTTGCTT 3320
15283 GA----- 15284
3321 GCAACAAATTTGATGAACAACTGTTCTTTATAATGCAACTTTTGTATCAAGAAAGCTGAACG 3380
15285 -----CCACTTTGTACAAGAAAGCTGAACG 15309
3381 AGAAACGTAAATGATATAAATATCAATATATTAATTTAGATTTTGTGATATAAATAACAGAC 3440
15310 AGAAACGTAAATGATATAAATATCAATATATTAATTTAGATTTTGTGATATAAATAACAGAC 15369
3441 TACATAAATCTGTAATAACACAAATATCCAGTCACTATGAATCAACTACTTAGATGGTAT 3500
15370 TACATAAATCTGTAATAACACAAATATCCAGTCACTATGAATCAACTACTTAGATGGTAT 15429
3501 TAGTGACCTGTAGTCGATTAAGTTGGCAGCATCACCGACGACTTTGGCGCGAATAAAT 3560
15430 TAGTGACCTGTAGTCGATTAAGTTGGCAGCATCACCGACGACTTTGGCGCGAATAAAT 15489
3561 ACCTGTGAGGAGATCACTTCGAGATAAATAATCTGTTGTCCTGTTGATACCGG 3620
15490 ACCTGTGAGGAGATCACTTCGAGATAAATAATCTGTTGTCCTGTTGATACCGG 15549
3621 GAAGCCCTGGGCCAACTTTTGGCGAAATGAGACGTTGATCGGCACTACCCATTTCAAA 3680
15550 GAAGCCCTGGGCCAACTTTTGGCGAAATGAGACGTTGATCGG-----ATTTCACAA 15601
3681 CTCCTAATCTTTCTTACAGTCGTTGGCTTCACTCGGATTTTACGCTCTATCTT 3740
15602 CTCCTAATCTTTCTTACAGTCGTTGGCTTCACTCGGATTTTACGCTCTATCTT 15661
3741 ACTTAACGTGATAAAGTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGAT 3800
15662 ACTTAACGTGATAAAGTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGAT 15721
3801 AAGGGAGCCTGACATTTATTTCCCGAACAATCAGGTTAATGCGCTTTTGTGATGTCATT 3860
15722 AAGGGAGCCTGACATTTATTTCCCGAACAATCAGGTTAATGCGCTTTTGTGATGTCATT 15781
3861 TTGCGGCTGCTGAGATCAGCACTTTCTCCCGATAACGAGACCGGACACTGGCCAT 3920
15782 TTGCGGCTGCTGAGATCAGCACTTTCTCCCGATAACGAGACCGGACACTGGCCAT 15841
3921 ATCGGTGGTCAATCATGCGCCAGCTTTTATCCCGATATGACACCGGGTAAAGTTCAAG 3980
15842 ATCGGTGGTCAATCATGCGCCAGCTTTTATCCCGATATGACACCGGGTAAAGTTCAAG 15901
3981 GGAGACTTTTATCTGACAGCAGAGTGTCAGTGGCCAGGGGATCACCATCGCTGCCCGGG 4040
15902 GGAGACTTTTATCTGACAGCAGAGTGTCAGTGGCCAGGGGATCACCATCGCTGCCCGGG 15961
4041 CGTGTCAATTAATCACTCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTTATA 4100
15962 CGTGTCAATTAATCACTCTGTATCATCCAAACAGACGATTAACGGCTCTCTCTTTTATA 16021
4101 GGTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAAGACGCTTCA 4160
16022 GGTGTAAACCTTAACTGCAATTTTACAGTCCCTGTTCTGTCAGCAAAAAGACGCTTCA 16081
4161 TTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCGTGATTTTCCGCTTTCAGGCTTCGG 4220
16082 TTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCGTGATTTTCCGCTTTCAGGCTTCGG 16141

4221 CACGACGACGCGCTTCATTCGTGCTTACGACCGGAGATATTGACAT 4280
16142 CACGACGACGCGCTTCATTCGTGCTTACGACCGGAGATATTGACAT 16201
4281 CATATATGCTTTGAGCAACTGATAGCTGTCGCTCACTGCTCACTGCTTAATACGCTGCTT 4340
16202 CATATATGCTTTGAGCAACTGATAGCTGTCGCTCACTGCTCACTGCTTAATACGCTGCTT 16261
4341 CATAGCACCTCTTTTGGACATACCTTCTGTTGATGCGAGATGATTTTCAGGACTATG 4400
16262 CATAGCACCTCTTTTGGACATACCTTCTGTTGATGCGAGATGATTTTCAGGACTATG 16321
4401 ACCTAGCTATATGAATAGTAGATCTTTTATTTTGTGCACACAAAGAGGCTCGCA 4460
16322 ACCTAGCTATATGAATAGTAGATCTTTTATTTTGTGCACACAAAGAGGCTCGCA 16381
4461 CCTCTTTTCTTATTTCTTTTATGATTAATACGCAATTCAGGCAATTCGCGAGTAGGC 4520
16382 CCTCTTTTCTTATTTCTTTTATGATTAATACGCAATTCGCGAGTAGGC 16441
4521 TGGATACGACGATTCCTGTTTGGAGAAACATTTTGGAGGCTGTCGTCGACTAAAGTTGGC 4580
16442 TGGATACGACGATTCCTGTTTGGAGAAACATTTTGGAGGCTGTCGTCGACTAAAGTTGGC 16501
4581 AGCATCACCCGAAAGAACATTTTGGAGGCTGTCGTCGACTAAAGTTGGC 4640
16502 AGCATCACCCGAAAGAACATTTTGGAGGCTGTCGTCGACTAAAGTTGGC 16561
4641 AAGTAGTTGATTCATGAGTACGATGATGTTGTTTACAGTATTAAGTCTGTTT 4700
16562 AAGTAGTTGATTCATGAGTACGATGATGTTGTTTACAGTATTAAGTCTGTTT 16621
4701 TTATGCAAAATCTAATTAATATTTATATTTATATCATTTTACGTTTCTGTTTCACT 4760
16622 TTATGCAAAATCTAATTAATATTTATATTTATATCATTTTACGTTTCTGTTTCACT 16681
4761 TTTTGTACAAAGTTGGC 4778
16682 TTTTGTACAAAGTTGGC 16699

RESULT 5

US-10-055-001A-26
; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELIGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 17681
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE12
US-10-055-001A-26

Query Match 52.0%; Score 2528; DB 15; Length 17681;

Best Local Similarity 76.5%; Pred. No. 0;

Matches 3682; Conservative 0; Mismatches 85; Indels 1043; Gaps 6;

QY 82 GCCAACTTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATT 141

Db 13025 GACAAGTTTGTACAAAAGCTGACGAGAAACGTAATAATGATATAAATATCAATATATT 13084

QY 142 AAATTAGATTTGCAATAAAAAACAGACTACATAATCTGTAAAAACACACATATCCAGTC 201

13085 AAATTAGATTTTGCNATAAAACAGACTACATAAATCTGTATAAACAACATATCCAGTC 13144
202 ACTATGAATCAACTACTTAGATGGTATTAGTAGCACTGTAGTCGACCGACAGCCCTCCAAA 261
13145 ACTATGAATCAACTACTTAGATGGTATTAGTAGCACTGTAGTCGACCGACAGCCCTCCAAA 13204
262 TGTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGAGCCCTCCAAAATGTTCTCTCAA 321
13205 TGTTCTCTCGGGTGATGCTGCCAACTTAGTCGACCGAGCCCTCCAAAATGTTCTCTCAA 13264
322 ACGGAATCGTCGTATCCAGCCTACTCTGCTATGTCCTCAATGCGGTATTAAATCATATAAA 381
13265 ACGGAATCGTCGTATCCAGCCTACTCTGCTATGTCCTCAATGCGGTATTAAATCATATAAA 13324
382 AGAATAAGAAAAGAGTGGAGCCCTCTTTTGTGTGCAAAAATAAAACATCTACCT 441
13325 AGAATAAGAAAAGAGTGGAGCCCTCTTTTGTGTGCAAAAATAAAACATCTACCT 13384
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13385 ATTCAATACCGTAGTGTCTAGTCTGCTGAAATCATCTGATCAAGAACTTCAAC 13444
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13445 TCTTATACCTTTCTTTTACAGTCGTTCCGCTTCTATCTGATTCGAGCTCTATCTTA 13504
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13505 CTAAAGCTGATAAAGTTTCTGTAATTTCTGATTCGATTCGACCTGCGCTGTGATA 13564
622 AGGAGCCCTGACATTTATATCCAGACACATCATGCTTAATGGCTTTTGTATGTCATTT 681
13565 AGGAGCCCTGACATTTATATCCAGACACATCATGCTTAATGGCTTTTGTATGTCATTT 13624
682 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACCGGAGACCGGACACATCGGCCATA 741
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742 TCGGTGGTCATCAGCGCCAGCTTTCATCCCGATATGACACACCGGGTAAAGTTTCAGG 801
13685 TCGGTGGTCATCAGCGCCAGCTTTCATCCCGATATGACACACCGGGTAAAGTTTCAGG 13744
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13745 GAGACTTTATCTGACAGCAGCTGCACTGCGCAGGGGATCAACATCCGTCGCCCGGC 13804
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13805 GTGTCAATATATCACTCTGTATATCCAAACAGACGATAACCGCTCTCTCTTTTATAG 13864
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13865 GTGTAAACCTTAACTGCAATTCACAGTCCCTGTTCTGTCAGCAAAAGAGCCGTTTCA 13924
982 TTCAATAAACCGGGCGACTCAGCCATCCCTTCTGATTTTCCGCTTTCAGGTTTCGGC 1041
13925 TTCAATAAACCGGGCGACTCAGCCATCCCTTCTGATTTTCCGCTTTCAGGTTTCGGC 13984
1042 ACGCAGACGAGCGGCTTCAATCTGATGTTGTGCTTACAGACCGGAGATTTGACATC 1101
13985 ACGCAGACGAGCGGCTTCAATCTGATGTTGTGCTTACAGACCGGAGATTTGACATC 14044
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14045 ATATATGCTTGTAGCAACTGATAGCTGCTGTCATCTGATCTGATCTGATCTGCTTTC 14104
1162 ATAGCACACCTCTTTTGTGACATCTTCCGGGTAGTCCGATCAACGTCATTTTCGCCAA 1221
14105 ATAGCACACCTCTTTTGTGACATCTTCCGGGTAGTCCGATCAACGTCATTTTCGCCAA 14164
1222 AAGTTGGCCCGAGCTTCCGGTATCAACAGGACACCGAGATTTATTTATCTCGGAAG 1281

14165 AAGTTGGCCCGAGCTTCCGGTATCAACAGGACACACAGGATTTATTTATCTCGGAAG 14224
1282 TGATCTTCCGTCCACAGCTATTTATTCGGCGCAAGTCGTCGGTGATGCTGCCAATTA 1341
14225 TGATCTTCCGTCCACAGCTATTTATTCGGCGCAAGTCGTCGGTGATGCTGCCAATTA 14284
1342 GTCGACTACAGGTCACATACCATCTAAGTAGTCTGATTCATGACCTGGATATGTTGT 1401
14285 GTCGACTACAGGTCACATACCATCTAAGTAGTCTGATTCATGACCTGGATATGTTGT 14344
1402 GTTTTACAGTATTTAGTAGTCTGTTTATGCAAAATCTAATTTAATATATGATATTT 1461
14345 GTTTTACAGTATTTAGTAGTCTGTTTATGCAAAATCTAATTTAATATATGATATTT 14404
1462 ATATCATTTTACGTTTCTCGTTTTCAGCTTCTGTTTACAAAGTTGGCATTAAGAAGCAT 1521
14405 ATATCATTTTACGTTTCTCGTTTTCAGCTTCTGTTTACAAAGTTGGCATTAAGAAGCAT 1521
1522 TCGTTATCAATTTGTTGCAACGAAAGGTCATATCATCTCAAAATATAAATCATTTATTCG 1581
14448 ----- 14447
1582 CATCCAGCTGACAGCTCTCGAGGAATTCGGTACCCCA--ATTGGTAAGGAAATAAATTT 1640
14448 -----TCTCGAGGAATTCGGTACCCCAAGTTGGTAAGGAAATAAATTT 14492
1641 TCTTTTTCCTTTAGTATAAAATAGTTAAGTAGTCTGTTAATTAATGATTAATAATA 1700
14493 TCTTTTTCCTTTAGTATAAAATAGTTAAGTAGTCTGTTAATTAATGATTAATAATA 14552
1701 TAGTGTGTTAATTTGTGAAAATAAATTTAATAATAATTTTACATAAACAACATAGT 1760
14553 TAGTGTGTTAATTTGTGAAAATAAATTTAATAATAATTTTACATAAACAACATAGT 14612
1761 AATGTAAAAATAATGACAAAGTGTGTAAAGCAAGAGAGATAAAGTTGAGAGTAAGT 1820
14613 AATGTAAAAATAATGACAAAGTGTGTAAAGCAAGAGAGATAAAGTTGAGAGTAAGT 14672
1821 ATATTTTATTAATTTGATCGAACATGTAAGATGATATACGGCGCTGACAGGTTTC 1880
14673 ATATTTTATTAATTTGATCGAACATGTAAGATGATATACGGCGCTGACAGTAA-- 14725
1881 CAATTTTCACTTAATGAATAAGATCACTACCGGGCTATTTTGTGTTATCGAGATT 1940
14726 ----- 14725
1941 TCCAGGAGCTAAGGAAGCTAAATGAGAAAAAATCACTGGATATACCACTGTTGATAT 2000
14726 ----- 14725
2001 ATCCCAATGGCTCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTA 2060
14726 ----- 14725
2061 TAACCAGACCGTTCAGTGGATTTACGGCTTTTAAAGACCGTAAAGAAAAATAAGCA 2120
14726 ----- 14725
2121 CAAGTTTATCCGGCTTTTATTCACATTTCTTCCCGCTGATGATGCTCATCCGGAATT 2180
14726 ----- 14725
2181 CGGTATGCAATGAAGACCGTGAGTGGTATGAGGATAGTGTTCACCTCTGTACAC 2240
14726 ----- 14725
2241 CGTTTCCATGAGCAAACTGAACGTTTTCATCGCTCTGGAGTGAATACACAGCAGATT 2300
14726 ----- 14725
2301 CCGGAGCTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCTA 2360
14726 ----- 14725

QY	2361	TTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTT	2420
Db	14726	-----	14725
QY	2421	CACCAGTTTTGATTTAAACGTGGCCAAATATGGACAACCTTCTCGCCCCGGTTTTTCACCAT	2480
Db	14726	-----	14725
QY	2481	GGGCAAAATATTATACGCAAGCGACACAGGTGCTGATGCCGTGGCGATTCCAGGTTCATCA	2540
Db	14726	-----	14725
QY	2541	TGCCGTCTGTGATGGCTTCCATGTCGGCAGAAATGCTTTAAATGAATTAACAAGTACTGCGA	2600
Db	14726	-----	14725
QY	2601	TGAGTGGCAGGGCGGGCGTAATTCGCGTGGATCCGGCTTACTAAAGCCAGATAACAGTA	2660
Db	14726	-----	14725
QY	2661	TGCGTATTTGCGGCTGATTTTTTTCGGGTATAAGAAATATATCTGATATGTCGGGCCCATTA	2720
Db	14726	-----TATTTGTTTTTAATCATA	14742
QY	2721	ATAGTAATTTCTAGCTGGTTTGATGAATTAATTAATCAATGATAAATACTATAGTAAAAAT	2780
Db	14743	ATAGTAATTTCTAGCTGGTTTGATGAATTAATTAATCAATGATAAATACTATAGTAAAAAT	14802
QY	2781	AAGAATAAATAAATAAATAAATTTTTTTATGATTAATAGTTTATTAATTAATTAAT	2840
Db	14803	AAGBATAAATAAATAAATAAATTTTTTTATGATTAATAGTTTATTAATTAATTAAT	14862
QY	2841	ATCTATACCAATTAATAAATAATTTTATAGTTTAAAGTTAAATAATTTTTTGTAGAAATTC	2900
Db	14863	ATCTATACCAATTAATAAATAATTTTATAGTTTAAAGTTAAATAATTTTTTGTAGAAATTC	14922
QY	2901	AATCTGCTTGTAAATTAATAAACAATAATTTAAATAACAAGCTAAAGTAACAATAA	2960
Db	14923	AATCTGCTTGTAAATTAATAAACAATAATTTAAATAACAAGCTAAAGTAACAATAA	14982
QY	2961	TATCAAACTAATAAGAAACAGTAATCTAATGTAACAAACATAATCTAATGCTAATAAAC	3020
Db	14983	TATCAAACTAATAAGAAACAGTAATCTAATGTAACAAACATAATCTAATGCTAATAAAC	15042
QY	3021	AAAGCGAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTC	3080
Db	15043	AAAGCGAAGATCTATCATTTTATATAGTATTTTCAATCAACATTTCTTATTAATTC	15102
QY	3081	TAAATATCTTGTAGTTTATTAACCTCTAAATGGATTCGACTATTAATTAATGAATTA	3140
Db	15103	TAAATATCTTGTAGTTTATTAACCTCTAAATGGATTCGACTATTAATTAATGAATTA	15162
QY	3141	GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTATTTGTTTATCAATGATCTT	3200
Db	15163	GTCGAACATGAATAAACAAGGTAAACATGATAGATCATGTCTATTTGTTTATCAATGATCTT	15222
QY	3201	ACATTTGGATTAAGTACAGTTGGAAATTTGGTTTGGAAATCGAATCGAATGTTG-----GAT	3254
Db	15223	ACATTTGGATTAAGTACAGTTGGAAATTTGGTTTGGAAATCGAATCGAATGTTG-----GAT	15282
QY	3255	CTCTAGAGAGCTGCAGCTGGATGGCAAAATAATGATTTTATTTTGTACTGATAGTACCTG	3314
Db	15283	TATCATCATCATATAGACACAGCAATAAAGTAATCAGATTATCAGTTAAAGCTATGTA	15342
QY	3315	TTCGTTGCAACAAA-----	3328
Db	15343	ATATTTGGCCATAACCAATCAATTAATAAATAATAGATCAGTTTAAAGAAATCAAGCTC	15402
QY	3329	-----	3328
Db	15403	AAAAAAATAAAGAGAAAGGGTCTTAACCAAGAAATAAGAGAGAAAACTAGAAATT	15462

QY	3329	TTGATAAGCAATGCTTTCTTTATAATGCCAACTTTGTGTACAAGAAAGCTGAACGAGAAACGCT	3388
Db	15463	TACCTGCACAAGCTTGGATCCTCTAGACCACCTTTGTACAAGAAAGCTGAACGAGAAACGCT	15522
QY	3389	AAAAATGATATAAATAATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3448
Db	15523	AAAAATGATATAAATAATCAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	15582
QY	3449	ACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC	3508
Db	15583	ACTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC	15642
QY	3509	TGTAGTCGACTTAAGTTGGCAGCATACCCGACGCACTTTGGCGCGAATAAATACTCTGTGA	3568
Db	15643	TGTAGTCGACTTAAGTTGGCAGCATACCCGACGCACTTTGGCGCGAATAAATACTCTGTGA	15702
QY	3569	CGGAAGATCACTTTGCGCAGAAATAAATACTCTGCTGTCTGCTGTGATACCGGGAAGCCCT	3628
Db	15703	CGGAAGATCACTTTGCGCAGAAATAAATACTCTGCTGTCTGCTGTGATACCGGGAAGCCCT	15762
QY	3629	GGGCCAACTTTTGGCGGAAATAGAGAGTTGATCGGCACTACCCATTTTCACAACTCTTATA	3688
Db	15763	GGGCCAACTTTTGGCGGAAATAGAGAGTTGATCGGCACTACCCATTTTCACAACTCTTATA	15814
QY	3689	CTTTTCTCTTACAAGTCGTTTGGCTTCACTCGAATTTTCAAGCTCTATCTACTTAAACG	3748
Db	15815	CTTTTCTCTTACAAGTCGTTTGGCTTCACTCGAATTTTCAAGCTCTATCTACTTAAACG	15874
QY	3749	TGATAAAGTTTCTGTAAATTTCTACTGTATCGACTCGCAGACTGCTGTGTATAAGGAGC	3808
Db	15875	TGATAAAGTTTCTGTAAATTTCTACTGTATCGACTCGCAGACTGCTGTGTATAAGGAGC	15934
QY	3809	CTGACATTTATATTTCCCGGAAACATCAGGTTAATGGGTTTTTGTATGTCAATTTTCGCGT	3868
Db	15935	CTGACATTTATATTTCCCGGAAACATCAGGTTAATGGGTTTTTGTATGTCAATTTTCGCGT	15994
QY	3869	GGCTGAGATCAGCACTTCTTCCCGGATTAACGAGACCGGCACTTGGCCATATCCGTTGG	3928
Db	15995	GGCTGAGATCAGCACTTCTTCCCGGATTAACGAGACCGGCACTTGGCCATATCCGTTGG	16054
QY	3929	TCATCATGCGCCAGCTTTTATCCCGGATTAACGAGACCGGCACTTGGCCATATCCGTTGG	3988
Db	16055	TCATCATGCGCCAGCTTTTATCCCGGATTAACGAGACCGGCACTTGGCCATATCCGTTGG	16114
QY	3989	TATCTGACAGCAGCGTGCACTGGCGAGGGGATCAACATCCGTCGCGCGGGGGTGTCAA	4048
Db	16115	TATCTGACAGCAGCGTGCACTGGCGAGGGGATCAACATCCGTCGCGCGGGGGTGTCAA	16174
QY	4049	TAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAA	4108
Db	16175	TAATATCACTCTGTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAA	16234
QY	4109	CTTTAAACTGCAATTTCAACAGTCCCTGTCTCTGTCAGCAAAAGAGCGGTTTCAATTTCAATA	4168
Db	16235	CTTTAAACTGCAATTTCAACAGTCCCTGTCTCTGTCAGCAAAAGAGCGGTTTCAATTTCAATA	16294
QY	4169	AACCGGGGAGCTCAGGCATCCCTTCTGATTTTTTCCGCTTTCCAGGTTCCGCGACGAG	4228
Db	16295	AACCGGGGAGCTCAGGCATCCCTTCTGATTTTTTCCGCTTTCCAGGTTCCGCGACGAG	16354
QY	4229	CGACGGCTTCACTTCTGCAATGTTGTCTTACAGACCGGAGATATTGACATCATATATG	4288
Db	16355	CGACGGCTTCACTTCTGCAATGTTGTCTTACAGACCGGAGATATTGACATCATATATG	16414
QY	4289	CCTTGAGCAACTGATAGTGTCTGCTGTCAACTGTCTGTCTGTCTCTTTTATAGGTGTAAA	4348
Db	16415	CCTTGAGCAACTGATAGTGTCTGCTGTCAACTGTCTGTCTGTCTCTTTTATAGGTGTAAA	16474
QY	4349	ACCTCTTTTGTACATCTCTGTTGTGATGAGATGATTTTTCAGGACTATGACCTAGC	4408
Db	16475	ACCTCTTTTGTACATCTCTGTTGTGATGAGATGATTTTTCAGGACTATGACCTAGC	16534
QY	4409	GTATATGAATAGGTAGTGTTTTTTATTTTGTGTACACAAAAAGAGGCTTCGACCTCTTTT	4468

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Db 16535 GTATATGAATAGTAGATGTTTTTATTTTGTGCACAAAAAGAGGCTCGACCTCTTTT 16594
QY 4469 TCTTATTTCTTTTATGATTTAATACGGCAATGAGGACAATAGCGAGTAGGCTGGATACG 4528
Db 16595 TCTTATTTCTTTTATGATTTAATACGGCAATGAGGACAATAGCGAGTAGGCTGGATACG 16654
QY 4529 AGATTCGGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCAC 4588
Db 16655 ACATTTCCGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCAC 16714
QY 4589 CCGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCAC 4648
Db 16715 CCGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCGAGCATCAC 16774
QY 4649 GATTCATAGTACTGATATGTTGTGTTTACAGTATTAATGATGCTGTTTATGCAA 4708
Db 16775 GATTCATAGTACTGATATGTTGTGTTTACAGTATTAATGATGCTGTTTATGCAA 16834
QY 4709 AATCTAATTAATATGATATTAATGATATTAATGATGCTGTTTATGCAA 4768
Db 16835 AATCTAATTAATATGATATTAATGATATTAATGATGCTGTTTATGCAA 16894
QY 4769 CAAAGTTGGC 4778
Db 16895 CAAACTGTGC 16904

RESULT 6
US-10-055-001A-25
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Wesley, Susan V.
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell, Christopher A.
; TITLE OF INVENTION: Method and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELICA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 17458
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25

Query Match 51.6%; Score 2510.6; DB 15; Length 17458;
Best Local Similarity 77.2%; Pred. No. 0;
Matches 3628; Conservative 0; Mismatches 29; Indels 1040; Gaps 6;

QY 82 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAATATATT 141
Db 13025 GACAAGTTTGACAAAAAGCTGAACGAGAAACGTAATAATGATATAATCAATATATT 13084
QY 142 AAATTAGATTTGCAATAAAAAACAGACTACATATACCTGTAATAACAGACATATCCAGTC 201
Db 13085 AAATTAGATTTGCAATAAAAAACAGACTACATATACCTGTAATAACAGACATATCCAGTC 13144
QY 202 ACTATGAATCAACTTACATAGATGTTATGATGACTGTAGTCGACCGACGACCTTCACAA 261
Db 13145 ACTATGAATCAACTTACATAGATGTTATGATGACTGTAGTCGACCGACGACCTTCACAA 13204
QY 262 TGTCTTCGGGTGATGCTGCCAATCTAGTCGACCGACGACCTTCACAAATGTTCTTCCAA 321
Db 13205 TGTCTTCGGGTGATGCTGCCAATCTAGTCGACCGACGACCTTCACAAATGTTCTTCCAA 13264
QY 322 ACGAATCGTGTATCCAGGCTACTCGCTATGTTGCTCAATGCGGTATTAATCATAAAA 381
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Db 13265 ACGGAATCGTGTATCCAGGCTACTCGCTATTTGCTCAATGCCGTATTAATCATAAAA 13324
QY 382 AGAAATAAGAAAAAGAGTGGAGGCTCTTTTGTGTGACAAAAATAAAAAATCTACTCT 441
Db 13325 AGAAATAAGAAAAAGAGTGGAGGCTCTTTTGTGTGACAAAAATAAAAAATCTACTCT 13384
QY 442 ATTGATATACGCTAGTGTCTGATAGTCTGAAATCATCTGCAATCAAGAACAAATTTCCACAC 501
Db 13385 ATTGATATACGCTAGTGTCTGATAGTCTGAAATCATCTGCAATCAAGAACAAATTTCCACAC 13444
QY 502 TCTTATACCTTTCTCTTACAGTCTGCGGCTTCACTGGATTTTTCAGCTCTTACTACTTA 561
Db 13445 TCTTATACCTTTCTCTTACAGTCTGCGGCTTCACTGGATTTTTCAGCTCTTACTACTTA 13504
QY 562 CTAACCGTGAATAAGTTCTGTAAATTTCTACGTATCGACCTGACAGACTGGCTGTGTATA 621
Db 13505 CTAACCGTGAATAAGTTCTGTAAATTTCTACGTATCGACCTGACAGACTGGCTGTGTATA 13564
QY 622 AGGAGGCTGACATTTATATATCCCCAGAACATCAAGTTAAATGGCGTTTTTGTGTCATTT 681
Db 13565 AGGAGGCTGACATTTATATATCCCCAGAACATCAAGTTAAATGGCGTTTTTGTGTCATTT 13624
QY 682 TCGCGGTGCTGAGATCAGACCACTTTCTCCCGATAACGAGACCGGACACCTGACCATTA 741
Db 13625 TCGCGGTGCTGAGATCAGACCACTTTCTCCCGATAACGAGACCGGACACCTGACCATTA 13684
QY 742 TCGGTGCTCATCATGGCCAGGCTTTTCATCCCGATATGACCAACCGGTAAAGTTACGG 801
Db 13685 TCGGTGCTCATCATGGCCAGGCTTTTCATCCCGATATGACCAACCGGTAAAGTTACGG 13744
QY 802 GAGACTTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCGGGC 861
Db 13745 GAGACTTTTATCTGACAGCAGAGCTGACCTGGCCAGGGGATCACCATCCGTCGCCGGGC 13804
QY 862 GTGTCAAATAATATCACTCTGTATCATCCAAACAGACGATACGGCTCTCTCTTTATAG 921
Db 13805 GTGTCAAATAATATCACTCTGTATCATCCAAACAGACGATACGGCTCTCTCTTTATAG 13864
QY 922 GTGTAAACCTTAAACCTGCAATTTCCAGGTCCTGTTCTGTCAGAAAAGACCGTTCAAT 981
Db 13865 GTGTAAACCTTAAACCTGCAATTTCCAGGTCCTGTTCTGTCAGAAAAGACCGTTCAAT 13924
QY 982 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGGTTCCGGC 1041
Db 13925 TTCAATAAACCGGGGACCTCAGCCATCCCTTCTCTGATTTTCCGCTTTCCAGGTTCCGGC 13984
QY 1042 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTTGCTTACAGACCGGAGATTTGACATC 1101
Db 13985 ACGCAGACGACGGGCTTCAATCTGCAATGTTGTTGCTTACAGACCGGAGATTTGACATC 14044
QY 1102 ATATATGCTTGTAGCAACTGATAGCTGTCAACTGTCACTGTCACTGTAAATAGCTCTTC 1161
Db 14045 ATATATGCTTGTAGCAACTGATAGCTGTCAACTGTCACTGTAAATAGCTCTTC 14104
QY 1162 ATAGCACACCTCTTTTGTACATACCTTCGGGTAGTGCCGATCAACGCTCTCATTTTCCCAA 1221
Db 14105 ATAGCACACCTCTTTTGTACATACCTTCGGGTAGTGCCGATCAACGCTCTCATTTTCCCAA 14164
QY 1222 AAGTTGGCCCGGCTTCCGGGTATCAACAGGACACACAGGATTTTATTTTCTGCGAAG 1281
Db 14165 AAGTTGGCCCGGCTTCCGGGTATCAACAGGACACACAGGATTTTATTTCTGCGAAG 14224
QY 1282 TGATCTTCGCTCAGAGTATTTTATTCGGGCAAGGTCGCTCGGGTGATGCTGCCAATCTTA 1341
Db 14225 TGATCTTCGCTCAGAGTATTTTATTCGGGCAAGGTCGCTCGGGTGATGCTGCCAATCTTA 14284
QY 1342 GTCGACTACAGGTCACTAATAACCTAAGTAGTTGATTCATAGTACCTGGATATGTTGT 1401
Db 14285 GTCGACTACAGGTCACTAATAACCTAAGTAGTTGATTCATAGTACCTGGATATGTTGT 14344
QY 1402 GTTTTACAGTATTTAGTCTGTTTATGCAAAATCTAATTTAATATATTGATATT 1461
Db 14345 GTTTTACAGTATTTAGTCTGTTTATGCAAAATCTAATTTAATATATTGATATT 14404
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; NAME/KEY: misc feature
; LOCATION: (17922)..(18687)
; OTHER INFORMATION: octopine synthase gene terminator region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (264)..(496)
; OTHER INFORMATION: nopaline synthase gene promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (497)..(1442)
; OTHER INFORMATION: nptII coding region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1443)..(2148)
; OTHER INFORMATION: nopaline synthase gene terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2149)..(2706)
; OTHER INFORMATION: a left T-DNA border region
US-10-055-001A-13

Query Match      30.1%; Score 1462.6; DB 15; Length 18691;
Best Local Similarity 59.4%; Pred. No. 7.5e-233;
Matches 2920; Conservative 0; Mismatches 1889; Indels 104; Gaps 22;

QY      1  CGGGCCCCAAATATGATTTTATTTTGGACTGATGACCTGTTGGTTCGCAACAAATTGA 60
DB      17898  CGGGCCCCAAATATGATTTTATTTTGGACTGATGACCTGTTGGTTCGCAACAAATTGA 17839

QY      61  TGAGCAATGCTTTTATAATGCCAATTTGTACATGATGACCTGTTGGTTCGCAACAAATTGA 120
DB      17838  TGAGCAATGCTTTTATAATGCCAATTTGTACATGATGACCTGTTGGTTCGCAACAAATTGA 17779

QY      121  TGATATAAATATCAATATATTAATATAGATTTTGATATAAATAAAGACACTACATAACTG 180
DB      17778  TGATATAAATATCAATATATTAATATAGATTTTGATATAAATAAAGACACTACATAACTG 17719

QY      181  TAAACACACACATATCCAGTCACATGATGAATCACTACTAGATGGTATAGTACCTGTA 240
DB      17718  TAAACACACACATATCCAGTCACATGATGAATCACTACTAGATGGTATAGTACCTGTA 17659

QY      241  GTCGACGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTTCGACCGACAG 300
DB      17658  GTCGACGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTTCGACCGACAG 17599

QY      301  CCTTCCAAATGTTCTTCTCAACCGGATCGTCGTATCCAGCTACTGCTATTGCTCTCA 360
DB      17598  CCTTCCAAATGTTCTTCTCAACCGGATCGTCGTATCCAGCTACTGCTATTGCTCTCA 17539

QY      361  ATCCCGTATTAAATCATATAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTGTGTG 420
DB      17538  ATCCCGTATTAAATCATATAAAGAAATAAGAAAGAGGTGCGAGCCTCTTTTGTGTG 17479

QY      421  ACAAATAAATAACATCTACCTTTCATATACGCTAGTGTGATAGTCTGAAATATCATCTG 480
DB      17478  ACAAATAAATAACATCTACCTTTCATATACGCTAGTGTGATAGTCTGAAATATCATCTG 17419

QY      481  CATCAAGAACAAATTCACAACTCTTATACCTTTCTCTTCAAGTCGTTCCGCTTCATCTG 540
DB      17418  CATCAAGAACAAAGTATGTCAAAAGAGGTGTGCTGTAAGAA---GCAGCGTATTACAGTG 17362

QY      541  GATTTTCAGCCTCTATACCTTACTTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600
DB      17361  ACAGTTGACAGCGACAGCTATCAGTTGCTCAAGSCATATATGATGTCATATCTCCGGTC 17302

QY      601  CTTGACACTGGCTGTGTATTAAGGAGCGCTGACATTTATATATCCCAAGAACATCAGGTTA 660
DB      17301  TGSTAAGCACAAACCATCAGAAATGAAGCCGCTGCTGCGTGCC---GAACGCTGGAAG 17245

QY      661  ATGCGCTTTTGTATGTCATTTTCGCGTGGCTGAGATCAGCCACTCTCTCCCGATACG 720
DB      17244  CGGAAATCAGGAAGGATGGCTGAGGTGCGCCCGGTTATTGAAATGAACGGCTCTTTTG 17185
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QY      721  GAGACCGGCACACTGCGCCCATATCGGTGGTCATCATGCGGCAGCTTTATATCCCGATATGC 780
DB      17184  CTGACGAGAACACAGG-----ACTGGTGAATGCACTTTTAAGGTTTACACCTTATAAAGA 17131

QY      781  ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGAGCTGCACCTGGCCAGGGG 840
DB      17130  GAGAGCGGTATCTGCTGTTTGGGATGTACAGAGTGATATATTGACAGCCCGGGCGGA 17071

QY      841  ATCACCATCGTGGCCGGCGGTGTCAATAATATCACTCTGTATACATCCAAACAGACGA 900
DB      17070  CGGATGGTGATCCCGCTGGCCAGTGCACTGTCTGATAGATAAAGTCTCCCGTGAACCT 17011

QY      901  TAAAGCGCTCTCTTTTATAGTGTAACTTAACTGCACTTTTACG-----AGTCCCT 954
DB      17010  TACCCGGTGGTGATATCGGGGATGAAGCTGGCGCATGATGATACCCAGCATATGGCCAGT 16951

QY      955  GTTCTCGTCAGCAAAAGAGCGCTTCTTCAATTAATTAACCGGGCGACCTCAGCCATCCCTTC 1014
DB      16950  GTGCCGCTCTCGGTATCGGGGAGAGTGGCTGATCTCAGCCACCGCGAAATGACATC 16891

QY      1015  CTGATTTTTCGGTTCACGCTTC---GGCACGACAGACGCGGCTTCATTTTCGATGG- 1070
DB      16890  AAAACGCCATTAACCTGATGTTCTGGGAATATAAATGTACAGCTCCCTTATACACAGC 16831

QY      1071  --TTGGTGTACACAGACCGAGATATTGACATCATATATGCTTTGAGCAACTGATAGCTG 1128
DB      16830  CAGTCTGCAAGTGTGATACAGTAAATACAGAACTTTATCAGTTTATAGTAAATAGATA 16771

QY      1129  TCGCTCTCAACTGTCTCATATATACCTGCTTATAGCACACCTCTTTTGTGACATATCTC 1188
DB      16770  GGCTGAAATCCAGATGAAGCCGACGACTTGTAGAGAAAGATATAAGAGTTGTGAAT 16711

QY      1189  GGTAGTGGCATCAACGCTCTCATTTTTCGCAAAAGTTGGCCAGGGCTTCGCGGTATCA 1248
DB      16710  GGTAGTGGCATCAACGCTCTCATTTTTCGCAAAAGTTGGCCAGGGCTTCGCGGTATCA 16651

QY      1249  ACAGGACACACAGGATTTTATTTCTCGAGAGTGATCTTCCGTACAGGTATTTATTCG 1308
DB      16650  ACAGGACACACAGGATTTTATTTTCTCGAGAGTGATCTTCCGTACAGGTATTTATTCG 16591

QY      1309  GGCAAAGTGCCTGCGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCT 1368
DB      16590  GGCAAAGTGCCTGCGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCT 16531

QY      1369  AAGTAGTGTATTCATAGTACGATATGTTGTTTACAGTATTTATGATGATGCTGTTTT 1428
DB      16530  AAGTAGTGTATTCATAGTACGATATGTTGTTTACAGTATTTATGATGATGCTGTTTT 16471

QY      1429  TTATGCAAAATCTAATTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCT 1488
DB      16470  TTATGCAAAATCTAATTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCT 16411

QY      1489  TTCCTGTAACAAGTTGGCATTAAGAAAGCATTTGCTTATCAATTTTGTTCGAACGACAG 1548
DB      16410  TTCCTGTAACAAGTTGGCATTAAGAAAGCATTTGCTTATCAATTTTGTTCGAACGACAG 16351

QY      1549  GTCACATCAGTCAAAATAAATCAATTTTCCATCCAGCTGCACTC-CTCGAGGAAT 1607
DB      16350  GTCACATCAGTCAAAATAAATCAATTTTCCATCCAGCTGCACTC-CTCGAGGAAT 16291

QY      1608  TCGGTACCCCAATTTGTAAGGAAA-----TAATATTTTCTTTTCTTTTCTTTTCTTTAG 1656
DB      16290  CAAGCTTATCGATTTTGAACCCCAATTTTCCCACTGTAACTCAATCCAAATGTAAATCAAT 16231

QY      1657  TATAAATAGTTAAGTATGTTTAAATAGTATGATTAATAATAATATAGTTTGTATTAATGT 1716
DB      16230  GATAACACAATGACATGATCATGTTTACCTTGTATTATTCATGTTGCTGACTTAATCAAT 16171

QY      1717  GAAAAATAATTTTATAATATATTTTGTACATAAACAACATAGTATGTAAATAAATATG 1776
DB      16170  TAAATTAATAGTCAATCCATTTTGAAGAGTTAATAAATACTACAAGTATTTATTGAAATTAAT 16111

QY      1777  ACAAGTGTGTGTGAAGACGAGAAAGATAAAGTTGAGAG-----TAAGTATATTA 1826
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Db 16110 AAGAAATGTTGATTTGAAATTAATACTATATATAAATGATAGATCTTGGCTTTGTTATATTA 16051
QY 1827 TTTTAAATGAATTTGATCGAACATGTAAGATGATATACCGCGGTGAAGAGTTTCCAAT 1886
Db 16050 GCATTAGATTGTTTGTGTTACATAGATTACTGTTTCTATTATGTTGATATTATTTGTT 15991
QY 1887 TCACCAATATGAATAAGATCACTACCGCGGTATTTTGTGATTTACGAGATTTTCAGG 1946
Db 15990 ACTTTAGCTTGTAT ---TTAATAATTTTGTATTGATAAATTAACAAGCAGATTGGAAT 15935
QY 1947 AGCTAAGGAAGCTAATAATGAGAAATAAATCACTGGATATACACCGTTGATATATCCA 2006
Db 15934 TTCTAACAAATATTTATTAACCTTTTAACTAAATATTTAGTAATGTTAGATATTA 15875
QY 2007 ATGGCATCGTAAAGAACATTTTGGAGCATTTTCACTGATTTGCTCAATGTACCTTATAACCA 2066
Db 15874 ATTATATAATAACTAATTAATCATATAAATAATATTATTAAATTTATTATTTCTATT 15815
QY 2067 GACGGTTCAGCTGGATATTAACGGCTTTTAAAGACGGTAAAGAAATAAGCACAGTT 2126
Db 15814 TACTATAGTATTTTATCATTTGATTTTAAATTTCAATCAAAACAGCTAGAAATTTACTATTATGG 15755
QY 2127 TTATCCGGCTTTATTCACATTTCTTCCCGCTGATGAATGCTCATCCCGAATTCGGTAT 2186
Db 15754 GCCGACATACATATATTTCTTATACCGCAAAATACGCGCGAATACGCACTACTG 15695
QY 2187 GGCATGAAAGACGGTGGTGTGATATGGTAGTTTCAACCTTTGTTA --CACGGTT 2244
Db 15694 TTATCTGGCTTTTGTAGTAAGCGGATCCACGGATTTAGCCCGCCCTGCCACTCATCGCA 15635
QY 2245 TTCCATGAGCAAACTGAAAGTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCGG 2304
Db 15634 GTACTGTTGTAATTCATTAAGCAATTTCCGCAATGGAAGCCATCACAGCGGCATGATG 15575
QY 2305 CAGTTTCTACATATATTTCCGAAGATTTGGCGTGTTCACGGTGAAACCTGGCTATTTC 2364
Db 15574 AACCTGAAATCGCAGCGGATACGACCTTTGTCGCTTGGTATATATTTGGCCATGGT 15515
QY 2365 CCTAAGGGTTTATGAGAAATATGTTTTCGTCTACGCCAATCCCTGGGTGAGTTTCAAC 2424
Db 15514 GAAAAACGGGGGGAAGAAGTTGTCATATTTGGCCAGCTTTAAATCAAACTGGTGAAC 15455
QY 2425 AGTTTTCATTTAACTGGGCAATATGACAACTTTCTTCCCGCCGGTTTTCACCATGGC 2484
Db 15454 CACCGAGGATTTGGCTGAGACGAAACATATTTCTCAATAAACCTTTAGGGAATAGGC 15395
QY 2485 AAATATATACGCAAGCGGACAAAGTGTCTGATGCGCTGGCGATTCAGGTTTCATATGCC 2544
Db 15394 CAGTTTTCACCGTTAACACGCCACATCTTCCGAATATATGTTAGAACTGCCGGAATC 15335
QY 2545 GTCTGTATGCTTCCATGTCGGGAGAAATGTTAATGAATTAACAAGTACTCGGATGAG 2604
Db 15334 GTCTGTATTTCACTCCAGAGCGATGAAACGTTTCAGTTTGTCTCATGGAACG -GTG 15277
QY 2605 TGGCAGGGCGGGGTAATCCGGTGGATCCGGCTTACTAAAAGCCAGATAACAGTATGCG 2664
Db 15276 TAACAAGGGTGAACATATCCATATCACAGCTCACCGTCTTTCATTTGCCATACGGAAT 15217
QY 2665 TATTTGCGCGCTGATTTTTCGGTATGAATATATATCTGATATGTCGGGCCCATATAG 2724
Db 15216 TCCGGATGACATTCATCAGCGGGCAAGATGTAATAAGCGCGGATAAACTTTGTGC 15157
QY 2725 TAATTTCTAGCTGGTTTGTAGTAATTAATATCAATGATAAATACTATAGTAAATAAGA 2784
Db 15156 TTATTTTCTTACCGTCTTTTAAAGGCGGTAATATCCAGCTGAACGGTCTGTTATAG 15097
QY 2785 ATAAATAAATAAATAATTTTTTTTATGATTAATAGTTTATTATATATAATTAATATCT 2844
Db 15096 GTACATTTGAGCACTGCTGAAATGCTCAAAATGTTCTTTTACGATGCCATTTGGATATA 15037
QY 2845 ATACCATTTACTAAATATTTTAGTTTAAAGTTAAATAATTTTTTTAGAAATTTCCAAATC 2904

Db 15036 TCAACGGTGGTATATTCAGTGTATTTTTTCTCCATTTTAGCTTCTCTAGCTCCTGAAAT 14977
QY 2905 TCGTTTGAATTTTCAATAAACAATAATAATA ---ATAACAAGCTAAAGTAAACAAATAA 2960
Db 14976 CTCGATAACTCAAAATAATACGCCCGGTAGTATCTTATTTTCAATTTGGTGAAGTTGGAA 14917
QY 2961 TATCAAACTAATAGAAACAGTAAATCTAATGTAAACAAACATTAATCTAATGCTTAATAAC 3020
Db 14916 CTTCTTACCGCGGTATATCATCTTACATTTTTCATGTTTCGATCAAAATTCATTAATAATATACT 14857
QY 3021 AAAGCGCAAGATCTATCATTTTATATATATTTTCAATCAACATCAATCTTAAATTC 3080
Db 14856 TA -----CTCTCAACTTTTATCTTCTGCTTACATCTCACTGTCATATTTT 14807
QY 3081 TAAATAATATCTTGTAGTTTATTAATCTTCTAATAGATTTGACTATTAATAATAATAATTA 3140
Db 14806 TTACATTACTATGTTTGTATGTAAACAATATATTTATATAATTAATTTTTCACAATATA 14747
QY 3141 GTCGAACATGAATAAACAAGGTAAATGATAGATCATGTCTATGTTTATCATTTGATCTT 3200
Db 14746 ACAACTATATTAATAATATCACTAATTAACATCACTAATCTATTTTATCTAAAGGA 14687
QY 3201 ACATTTGGATTCATTACAGTTTGGGAAATTTGGTTCGAAATCGATAAGCTTTGATCCTCTA 3260
Db 14686 AAAAGAAATAATTT -----ATTCTTACCAATTTGGGTACCGAATTTCTCGA 14638
QY 3261 GAGAGCTCAGCTGGATGCAAAATAATGATTTTATTTTGAATGATGAGTACCTGTTCTGTT 3320
Db 14637 G-GAGCTGAGCTGGATGCAAAATAATGATTTTATTTTGACTGATGATGACCTGTTCTGTT 14579
QY 3321 GCACAAATTTGATAGCAATGCTTTCTTATATGCTTATGATGCACTTTTGTACAAGAAAGCTGAACG 3380
Db 14578 GCAACAAATTTGATAGCAATGCTTTCTTATAATGCCAATTTGTACAAGAAAGCTGAACG 14519
QY 3381 AGAAACGTAAATGATATAAATATCAATATATAATTAATTTAGATTTTGCATAAATAAACAAGAC 3440
Db 14518 AGAACGTAAATGATATAAATATCAATATATAATTAATTTAGATTTTGCATAAATAAACAAGAC 14459
QY 3441 TACATAATCTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGTTAT 3500
Db 14458 TACATAATCTGTAAAAACAACAATATCCAGTCACTATGAATCAACTACTTAGATGTTAT 14399
QY 3501 TAGTACCTGTAGTGCATTAAGTTGGCAGCATCACCGCAGCACTTTTGGCGCGAATAAAT 3560
Db 14398 TAGTACCTGTAGTGCATTAAGTTGGCAGCATCACCGCAGCACTTTTGGCGCGAATAAAT 14339
QY 3561 ACTGTGACGGAAGATCACTTCGCGAATATAATAATCTTGGTGTCCCTGTTTGAATACCGG 3620
Db 14338 ACTGTGACGGAAGATCACTTCGCGAATATAATAATCTTGGTGTCCCTGTTTGAATACCGG 14279
QY 3621 GAAGCCTGGCCAACTTTTGGGAAATGAGACGTTGATGCGCACTACCCATTTTCACAA 3680
Db 14278 GAAGCCTGGCCAACTTTTGGGAAATGAGACGTTGATGCGCACTACCCGAAATGATG 14219
QY 3681 CTCTTATATCTTTCTCTTACAAGTCTTCCGCTTCATCTGGATTTTTCAGCCCTCTATCTT 3740
Db 14218 CAAAAGAGGTGTCTATGAA ---GCAGGTATTACAGTGAAGTGTGACGAGCAGCTA 14162
QY 3741 ACTAAACGTGATAAAGTTTCTGTAAATTTCTATGATATGACCTGACAGCTGCGTGTGAT 3800
Db 14161 TCAGTTGCTCAAGGCATATATGATGTCATATCTCCGGTCTGCTGAAGCAACACCATGCAG 14102
QY 3801 AAGGAGCCTGACATTTATATTTCCCGAATCAAGTAAATGAGGCTTTTTCATGTCATT 3860
Db 14101 AATGAAGCCGCTGCTGCTGCC ---GAACGCTGGAAGCGGAAATCAGGAAGGGATG 14045
QY 3861 TTCCGGCTGGCTGAGATCAGCACTTCTTCCCGATTAACCGGAGACCGGACACTTGGCCAT 3920
Db 14044 GCTGAGCTGCCGGTTTATTGAATGAACGCTCTTTTGTCTGACGAGAACAGGG --- 13990
QY 3921 ATCGGTGTCATATCGCCAGCTTTTCATCCCGATATACACCGGGTAAAGTTACG 3980
Db 13989 -ACTGTGAAATGCAGTTTAAAGTTTACACCTATAAAGAGAGAGCGGTTATCGTCTGTT 13931


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QY 361 ATGCCGTATTAATCATATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGTG 420
Db 381 ATGCCGTATTAATCATATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGTG 440
QY 421 ACAAAATATAAATCATCTACCTATTATATACGCTAGTGTCTGAAATCATCTG 480
Db 441 ACAAAATATAAATCATCTACCTATTATATACGCTAGTGTCTGAAATCATCTG 500
QY 481 CATCAAGAAATTTCAAACTTTTCTTTCTTTCAAGTGTGCGCTTCATCTG 540
Db 501 CATCAAGAAATTTCAAACTTTTCTTTCTTTCAAGTGTGCGCTTCATCTG 560
QY 541 GATTTTCAGCTCTATATCTTACATAAGCTGATAAGTTTCTGTAATTTCTACTGTATCGA 600
Db 561 GATTTTCAGCTCTATATCTTACATAAGCTGATAAGTTTCTGTAATTTCTACTGTATCGA 620
QY 601 CCTGCAGACTGGCTGTGTATAAGGAGCCTGACATTTATATCCCCAGAACATCAGGTTA 660
Db 621 CCTGCAGACTGGCTGTGTATAAGGAGCCTGACATTTATATCCCCAGAACATCAGGTTA 680
QY 661 ATGGCGTTTTGATGTCAATTTTCGCGTGGCTGAGATCAGCACTTCTTCCCGATATGC 720
Db 681 ATGGCGTTTTGATGTCAATTTTCGCGTGGCTGAGATCAGCACTTCTTCCCGATATGC 740
QY 721 GAGACCGGCACATCGGCATATCGTGTCTCATATGCGCGAGCTTTCATCCCGATATGC 780
Db 741 GAGACCGGCACATCGGCATATCGTGTCTCATATGCGCGAGCTTTCATCCCGATATGC 800
QY 781 ACCACCGGGTAAAGTTTACCGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGG 840
Db 801 ACCACCGGGTAAAGTTTACCGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGG 860
QY 841 ATCAACCATCGTCCCGCGGGCTGCAATATATCTGTATCATCCACAAACAGACGA 900
Db 861 ATCAACCATCGTCCCGCGGGCTGCAATATATCTGTATCATCCACAAACAGACGA 920
QY 901 TAAGCGTCTCTCTTTTATAGTGTAAACCTTAACTTCACTTCCAGCAGTCCCTGTCTC 960
Db 921 TAAGCGTCTCTCTTTTATAGTGTAAACCTTAACTTCACTTCCAGCAGTCCCTGTCTC 980
QY 961 GTCAGCAAAAGAGCGGTTCAATTTCAATAAACCGGGGACCTCAGCCATCCCTCTCAT 1020
Db 981 GTCAGCAAAAGAGCGGTTCAATTTCAATAAACCGGGGACCTCAGCCATCCCTCTCAT 1040
QY 1021 TTCGCTTTCAGCGTTTCGCGCAGCAGACGCGGCTTCACTGCGATGGTGGCTTAC 1080
Db 1041 TTCGCTTTCAGCGTTTCGCGCAGCAGACGCGGCTTCACTGCGATGGTGGCTTAC 1100
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGAACCTGATAGCTGCTGCTCAACT 1140
Db 1101 CAGACCGGAGATATTGACATCATATATGCTTGAACCTGATAGCTGCTGCTCAACT 1160
QY 1141 GTCAGTGAATACGCTGCTTCAATGACACACCTCTTTTGGATATCTCGGGTA 1193
Db 1161 GTCAGTGAATACGCTGCTTCAATGACACACCTCTTTTGGATATCTCGGGTA 1213
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RESULT 9

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US-10-357-268-1
; Sequence 1, Application US/10357268
; Publication No. US20030219902A1
; GENERAL INFORMATION:
; APPLICANT: Kahn, Michael L
; APPLICANT: House, Brent L
; APPLICANT: Mortimer, Michael W
; TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
; FILE REFERENCE: WSUR-1-20291
; CURRENT APPLICATION NUMBER: US/10/357,268
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/354,063
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 1
; LENGTH: 4892
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (73)..(100)
; OTHER INFORMATION: T2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (232)..(275)
; OTHER INFORMATION: T1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(563)
; OTHER INFORMATION: attP1 recombination site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (959)..(1264)
; OTHER INFORMATION: ccdB gene
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1606)..(2265)
; OTHER INFORMATION: Cam(r) gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2513)..(2744)
; OTHER INFORMATION: attP2 recombination site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2868)..(3677)
; OTHER INFORMATION: Kan(r) gene
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3794)..(4537)
; OTHER INFORMATION: pUC oriV / RK2 orit
; US-10-357-268-1
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Query Match 24.5%; Score 1193; DB 16; Length 4892;
Best Local Similarity 100.0%; Pred. No. 2.7e-188;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGGCCCCCAATATGATTTTATTTTGAAGTAGTAGTGTGCTGCTGCAACAAATTGA 60
Db 21 CGGGCCCCCAATATGATTTTATTTTGAAGTAGTAGTGTGCTGCTGCAACAAATTGA 80
QY 61 TGAGCAATGCTTTTATATGCACTTTGTACAAAAAGCTGAACGAGAAACGTAAAA 120
Db 81 TGAGCAATGCTTTTATATGCACTTTGTACAAAAAGCTGAACGAGAAACGTAAAA 140
QY 121 TGATATAAATATCAATATATAAATAGATTTTGCATATAAAAAACAGACTACATAACTG 180
Db 141 TGATATAAATATCAATATATAAATAGATTTTGCATATAAAAAACAGACTACATAACTG 200
QY 181 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 240
Db 201 TAAACACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 260
QY 241 GTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAG 300
Db 261 GTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAG 320
QY 301 CTTTCCAAATGTTCTTCTCTAAAACGGAATCGCTGATCCAGCCTACTCGCTATTGTCTCA 360
Db 321 CTTTCCAAATGTTCTTCTCTAAAACGGAATCGCTGATCCAGCCTACTCGCTATTGTCTCA 380
QY 361 ATGCCGTATTAATCATATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGTG 420
Db 381 ATGCCGTATTAATCATATAAAGAAATAGAAAGAGGTGCGAGCCTCTTTTGTGTG 440
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QY 421 ACAAATAAAACATCTACCTATTATATATAGCTAGTGTATAGTCTGAAATATCATCTG 480
Db 441 ACAAATAAAACATCTACCTATTATATATAGCTAGTGTATAGTCTGAAATATCATCTG 500
QY 481 CATCAAGAAACAATTCACAACTCTTATACATTTCTTCAAGTCTGCTGGCTTATCTG 540
Db 501 CATCAAGAAACAATTCACAACTCTTATACATTTCTTCAAGTCTGCTGGCTTATCTG 560
QY 541 GATTTTCAGCTCTATACCTATTAACGCTGATAAAGTTTCTGTAATTTCTTACTGTATCGA 600
Db 561 GATTTTCAGCTCTATACCTATTAACGCTGATAAAGTTTCTGTAATTTCTTACTGTATCGA 620
QY 601 CTGCGAGAGCTGCTGTATAGGAGGCTGATTTATATTTATTTCCCGAGATATATCGA 660
Db 621 CTGCGAGAGCTGCTGTATAGGAGGCTGATTTATATTTATTTCCCGAGATATATCGA 680
QY 661 ATGGCGTTTGTATGTCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCCGGATAACG 720
Db 681 ATGGCGTTTGTATGTCATTTTCGCGGTGCTGAGATCAGCCACTTCTTCCCGGATAACG 740
QY 721 GAGACCGGACATCTGGCCATATCGGTGCTCATATGCGCGAGCTTTTATCCCGGATATGC 780
Db 741 GAGACCGGACATCTGGCCATATCGGTGCTCATATGCGCGAGCTTTTATCCCGGATATGC 800
QY 781 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGAGAGCTGCTGGCCAGGGGG 840
Db 801 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGAGAGCTGCTGGCCAGGGGG 860
QY 841 ATCACCATCGTCCCGGGCGGTGTAATATATCACTCTGTATACATCCCAAAACAGACGA 900
Db 861 ATCACCATCGTCCCGGGCGGTGTAATATATCACTCTGTATACATCCCAAAACAGACGA 920
QY 901 TAACGGCTCTCTTTTATAGGTGTAACCTTAACTGACATTTTCAAGTCTGCTGCTTCTC 960
Db 921 TAACGGCTCTCTTTTATAGGTGTAACCTTAACTGACATTTTCAAGTCTGCTGCTTCTC 980
QY 961 GTCAGCAAAAGAGCCGTTTCAATTAACCGGGGAGCTCTGAGCCATCCCTTCTGATTT 1020
Db 981 GTCAGCAAAAGAGCCGTTTCAATTAACCGGGGAGCTCTGAGCCATCCCTTCTGATTT 1040
QY 1021 TTCCGCTTTCCAGGTTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1041 TTCCGCTTTCCAGGTTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
QY 1081 CAGACCGGAGATATGACATCATATATGCTTACGCACTGATGCTGCTGCTCAACT 1140
Db 1101 CAGACCGGAGATATGACATCATATATGCTTACGCACTGATGCTGCTGCTCAACT 1160
QY 1141 GTCACTGTATACGCTTCTATAGCAGACACCTCTTTTGTACATCTTCCGGGTA 1193
Db 1161 GTCACTGTATACGCTTCTATAGCAGACACCTCTTTTGTACATCTTCCGGGTA 1213
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RESULT 10
US-10-151-690-61/c
; Sequence 61, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942-5120001
; CURRENT APPLICATION NUMBER: US/10151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 5584
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61

Query Match 24.5%; Score 1193; DB 15; Length 5584;
Best Local Similarity 100.0%; Pred. No. 2.8e-188;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGGGCCCCAAAATAATGATTTTATTTGACTGATGAGCCTGTTGTTGCAACAAATTGA 60
Db 5564 CGGGCCCCAAAATAATGATTTTATTTGACTGATGAGCCTGTTGTTGCAACAAATTGA 5505
QY 61 TGAGCAATGCTTTTATATATGCACTTGTACAAAAGCTGAGCAGAAACGTAAAA 120
Db 5504 TGAGCAATGCTTTTATATATGCACTTGTACAAAAGCTGAGCAGAAACGTAAAA 5445
QY 121 TGATATAAATATCAATATATATAATTTAGATTTTGATATAAATAACAGACTACATAACTG 180
Db 5444 TGATATAAATATCAATATATATAATTTAGATTTTGATATAAATAACAGACTACATAACTG 5385
QY 181 TAAACACAACTATCCAGTCACTATGATCAACTCTTAGATGTTAGTGAACCTGTA 240
Db 5384 TAAACACAACTATCCAGTCACTATGATCAACTCTTAGATGTTAGTGAACCTGTA 5325
QY 241 GTCCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTACTGACCGACAG 300
Db 5324 GTCCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTACTGACCGACAG 5265
QY 301 CTTCCAAATGTTCTTCTCAAAACGGAATCGTGTATCCAGCCTTACTGCTATTGTCCTCA 360
Db 5264 CTTCCAAATGTTCTTCTCAAAACGGAATCGTGTATCCAGCCTTACTGCTATTGTCCTCA 5205
QY 361 ATCCGCTATTAATATCAATAAAGAAATAGAAAAGAGTGGAGCTCTTTTGTGTG 420
Db 5204 ATCCGCTATTAATATCAATAAAGAAATAGAAAAGAGTGGAGCTCTTTTGTGTG 5145
QY 421 ACAAATAAAACATCTACCTATTATATACCTAGTGTATAGTCTGAAATATCATCTG 480
Db 5144 ACAAATAAAACATCTACCTATTATATACCTAGTGTATAGTCTGAAATATCATCTG 5085
QY 481 CATCAAGAAACAATTCACAACTCTTATATCTTCTTCAAGTCTGCTGCTTCACTG 540
Db 5084 CATCAAGAAACAATTCACAACTCTTATATCTTCTTCAAGTCTGCTGCTTCACTG 5025
QY 541 GATTTTCAGCTCTATACCTATTAACGCTGATAAAGTTTCTGTAATTTCTTACTGTATCGA 600
Db 5024 GATTTTCAGCTCTATACCTATTAACGCTGATAAAGTTTCTGTAATTTCTTACTGTATCGA 4965
QY 601 CTGCGAGAGCTGCTGTATAGGAGGCTGATTTATTTCCCGAGATATATCGA 660
Db 4964 CTGCGAGAGCTGCTGTATAGGAGGCTGATTTATTTCCCGAGATATATCGA 4905
QY 661 ATGGCGTTTGTATGTCATTTTTCGCGGTGCTGAGATCAGCCACTTCTTCCCGGATAACG 720
Db 4904 ATGGCGTTTGTATGTCATTTTTCGCGGTGCTGAGATCAGCCACTTCTTCCCGGATAACG 4845
QY 721 GAGACCGGACATCTGGCCATATCCGCTGCTATCATGCGCAGCTTTCATCCCGGATATGC 780
Db 4844 GAGACCGGACATCTGGCCATATCCGCTGCTATCATGCGCAGCTTTCATCCCGGATATGC 4785
QY 781 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGAGAGCTGCTGGCCAGGGGG 840
Db 4784 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGAGAGCTGCTGGCCAGGGGG 4725
QY 841 ATCAACATCCGTCGCCCGGGGCTGTCAATAATATCACTCTGTATATCAACAAACAGACGA 900
Db 4724 ATCAACATCCGTCGCCCGGGGCTGTCAATAATATCACTCTGTATATCAACAAACAGACGA 4665
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QY 901 TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTAAACCTGATTTACAGAGTCCCTGTTCTC 960
Db 4664 TAAAGGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTAAACCTGATTTACAGAGTCCCTGTTCTC 4605
QY 961 GTACGCAAAAGAGCGGTTTCATTTCAATAAAGCGGCGACCTCAGCCATCCCTTCTCTGATT 1020
Db 4604 GTACGCAAAAGAGCGGTTTCATTTCAATAAAGCGGCGACCTCAGCCATCCCTTCTCTGATT 4545
QY 1021 TTCCGCTTTCCAGCGTTCCGCGACGCGACGAGCGGGCTTCATTCTGCATGCTTGTGCTTAC 1080
Db 4544 TTCCGCTTTCCAGCGTTCCGCGACGCGACGAGCGGGCTTCATTCTGCATGCTTGTGCTTAC 4485
QY 1081 CAGACCGGAGATTTGACATCATATATGCTTGGAGCAACTGATAGCTGTCGCTGCAACT 1140
Db 4484 CAGACCGGAGATTTGACATCATATATGCTTGGAGCAACTGATAGCTGTCGCTGCAACT 4425
QY 1141 GTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTA 1193
Db 4424 GTCACTGTAATAGCTGCTTCATAGCACACCTCTTTTGGACATACCTTCGGGTA 4372

RESULT 11
US-10-151-690-62
; Sequence 62, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; CURRENT APPLICATION NUMBER: US/10/151,690
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62

Query Match 24.4%; Score 1186.6; DB 15; Length 4428;
Best Local Similarity 99.7%; Pred. No. 3e-187;
Matches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGGCCCCAAATAGATTTATTTGATGATGACCTGTTGCTGCAACAAATGA 60
Db 858 CGGGCCCCAAATAGATTTATTTGATGATGACCTGTTGCTGCAACAAATGA 917
QY 61 TGAGCAATGCTTTTATAAGTCCAACTTTGTACAAAAAGCTGAACGAGAAAGCTAAAA 120
Db 918 TGAGCAATGCTTTTATAAGTCCAACTTTGTACAAAAAGCTGAATCGAAAAAGTAAAA 977
QY 121 TGATATAAATATCAATATATTAATAGATTTTGCATAAAAAAGACATCATATAGT 180
Db 978 TGATATAAATATCAATATATTAATAGATTTTGCATAAAAAAGACATCATATAGT 1037
QY 181 TAAACACAACTATCCAGTCACTATGATCACTACTAGTATGCTATAGTACCTGTA 240
Db 1038 TAAACACAACTATCCAGTCACTATGATCACTACTAGTATGCTATAGTACCTGTA 1097
QY 241 GTCACCGGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCGCAACTTAGTCGACCGACAG 300
Db 1098 GTCACCGGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCGCAACTTAGTCGACCGACAG 1157

QY 301 CCTTCCAAATCTCTCTTCTCAAAAGGAATCGCTGATCTCAGAGCTACTCGCTATTTGCTCTCA 360
Db 1158 CCTTCCAAATGTTCTTCTCAAAAGGAATCGCTGATCTCAGAGCTACTCGCTATTTGCTCTCA 1217
QY 361 ATGCGGTATTTAAATCATATAAAGAAATAAGAAAAAGAGGTGGAGCCTCTTTTGTGTG 420
Db 1218 ATGCGGTATTTAAATCATATAAAGAAATAAGAAAAAGAGGTGGAGCCTCTTTTGTGTG 1277
QY 421 ACAAAATAAAAACATCTACCTATTATCATATAGCTAGTCTCATAGTCTCGTAAATCATCTG 480
Db 1278 ACAAAATAAAAACATCTACCTATTATCATATAGCTAGTCTCATAGTCTCGTAAATCATCTG 1337
QY 481 CATCAAGAACAAATTTCAACAACCTCTTATATCTTTCTTTACAGTCTGTCGGCTTCATCTG 540
Db 1338 CATCAAGAACAAATTTCAACAACCTCTTATATCTTTCTTTACAGTCTGTCGGCTTCATCTG 1397
QY 541 GATTTTCAGCTCTATATCTTACTTAAACGTGATAAGTTTCTGTAAATTTCTACTGCTATCGA 600
Db 1398 GATTTTCAGCTCTATATCTTACTTAAACGTGATAAGTTTCTGTAAATTTCTACTGCTATCGA 1457
QY 601 CCTGCAGAGCTGCTGTGTATTAAGGAGCCTGACATTTATATTTCCCGCAGAACATCAGGTTA 660
Db 1458 CCTGCAGAGCTGCTGTGTATTAAGGAGCCTGACATTTATATTTCCCGCAGAACATCAGGTTA 1517
QY 661 ATGGCGTTTTCATGATGTCATTTTCGGGTGCTGAGATGAGCCACTTCTTCCCGGATAACG 720
Db 1518 ATGGCGTTTTCATGATGTCATTTTCGGGTGCTGAGATGAGCCACTTCTTCCCGGATAACG 1577
QY 721 GAGACCGGCACACTGCGCCATATCGGTGTCATCATGCGCGCAGCTTTCATCCCGGATATGC 780
Db 1578 GAGACCGGCACACTGCGCCATATCGGTGTCATCATGCGCGCAGCTTTCATCCCGGATATGC 1637
QY 781 ACCACCGGCTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGTCATGCGCAGGGGG 840
Db 1638 ACCACCGGCTAAAGTTTCAGGGAGACTTTATCTGACAGCAGACGTGTCATGCGCAGGGGG 1697
QY 841 ATCACCATCCGTCGCGCGGCGGTGTCATTAATATCACTCTGTACATCCACAAACACAGCA 900
Db 1698 ATCACCATCCGTCGCGCGGCGGTGTCATTAATATCACTCTGTACATCCACAAACACAGCA 1757
QY 901 TAACGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTAAACCTTCAACAGTCCCTGTTCTC 960
Db 1758 TAACGCTCTCTCTTTTATAGGTGTAACCTTAAACCTTCAACAGTCCCTGTTCTC 1817
QY 961 GTACGCAAAAGAGCGGTTTCATTTCAATAAAGCGGCGACCTCAGCCATCCCTTCTCTGATT 1020
Db 1818 GTACGCAAAAGAGCGGTTTCATTTCAATAAAGCGGCGACCTCAGCCATCCCTTCTCTGATT 1877
QY 1021 TTCCGCTTTCCAGCGTTCCGCGACGCGAGACGGGCTTCATTCTGCATGCTTGTGCTTAC 1080
Db 1878 TTCCGCTTTCCAGCGTTCCGCGACGCGAGACGGGCTTCATTCTGCATGCTTGTGCTTAC 1937
QY 1081 CAGACCGGAGATTTGACATCATATATGCTTTCAGCAACTGATAGCTGCTGTCCTCAACT 1140
Db 1938 CAGACCGGAGATTTGACATCATATATGCTTTCAGCAACTGATAGCTGCTGTCCTCAACT 1997
QY 1141 GTCACCTGATAGCTGCTTCATAGCACCTCTTTTGGACATACCTTCGGGTA 1193
Db 1998 GTCACCTGATAGCTGCTTCATAGCACCTCTTTTGGACATACCTTCGGGTA 2050

RESULT 12
US-10-151-690-63
; Sequence 63, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120001

[illegible]

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Db 189 TAAACACAAATATCCAGTCATATGAATCAACTCTTAGATGGTATAGTACCTGTA 248
QY 241 GTCGACGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACAG 300
Db 249 GTCGACGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACAG 308
QY 301 CCTTCGAAATGTTCTTCTCAAAAGGAATCTGTGATACGACCTACTGCTATTGCTCTCA 360
Db 309 CCTTCGAAATGTTCTTCTCAAAAGGAATCTGTGATACGACCTACTGCTATTGCTCTCA 368
QY 361 ATGCGGTATTAATATCAATAAAGAAATAAGAAAAGAGGTGCGAGCCTCTTTTTTGTTG 420
Db 369 ATGCGGTATTAATATCAATAAAGAAATAAGAAAAGAGGTGCGAGCCTCTTTTTTGTTG 428
QY 421 ACAAATATAAATACATCTACCTATTATATACGCTAGTGTATATGCTCTGAAATATCTG 480
Db 429 ACAAATATAAATACATCTACCTATTATATACGCTAGTGTATATGCTCTGAAATATCTG 488
QY 481 CATCAAGAACAAATTCACAACTCTTATACCTTTCTTCTTACAAAGTCTGCTTCACTG 540
Db 489 CATCAAGAACAAATTCACAACTCTTATACCTTTCTTCTTACAAAGTCTGCTTCACTG 548
QY 541 GATTTTCAGCCTCTATACCTTACTAAACGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA 600
Db 549 GATTTTCAGCCTCTATACCTTACTAAAGCTGATAAAGTTTCTGTAATTTCTACTGTATCGA 608
QY 601 CTTGACAGACTGGCTGTGTAAGAGGAGCCTGACATTTATATCCCAAGAACATCAGGTTA 660
Db 609 CTTGACAGACTGGCTGTGTAAGAGGAGCCTGACATTTATATCCCAAGAACATCAGGTTA 668
QY 661 ATGCGGTTTTTGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGGATAACG 720
Db 669 ATGCGGTTTTTGATGTCAATTTTCGCGTGGCTGAGATCAGCCACTTCTCCCGGATAACG 728
QY 721 GAGACCGGACACATGGCCATATCGGTGGTCAATGCGCCAGCTTTTATCCCGGATATGC 780
Db 729 GAGACCGGACACATGGCCATATCGGTGGTCAATGCGCCAGCTTTTATCCCGGATATGC 788
QY 781 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGCTGCTGCGCCAGGGG 840
Db 789 ACCACCGGTAAAGTTTACGGGAGACTTTATCTGACAGCAGCTGCTGCGCCAGGGG 848
QY 841 ATCACCATCGCTCGCCCGGCGGTGCTCAATAATATCACTCTGTATCATCCAAACAGACGA 900
Db 849 ATCACCATCGCTCGCCCGGCGGTGCTCAATAATATCACTCTGTATCATCCAAACAGACGA 908
QY 901 TAAAGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGTGATTTCAACAGTCCCTGTCTC 960
Db 909 TAAAGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGTGATTTCAACAGTCCCTGTCTC 968
QY 961 GTCAGCAAAAGAGCCGTTTCAATTAATAACCGGGGACCTCAGCCATCCCTTCTGATT 1020
Db 969 GTCAGCAAAAGAGCCGTTTCAATTAATAACCGGGGACCTCAGCCATCCCTTCTGATT 1028
QY 1021 TTCGGTTTCCAGGTTTCGACGACGACGACGGGTTCAATCTGATGTTGCTGTAC 1080
Db 1029 TTCGGTTTCCAGGTTTCGACGACGACGACGGGTTCAATCTGATGTTGCTGTAC 1088
QY 1081 CAGACCGGAGATATTGACATCATATATGCTTGAAGACATGATGCTGCTGCTCAACT 1140
Db 1089 CAGACCGGAGATATTGACATCATATATGCTTGAAGACATGATGCTGCTGCTCAACT 1148
QY 1141 GTCAGTGAATAGCTGCTTTCATAGCACACCTCTTTTGTGACATCTTCGGGTA 1193
Db 1149 GTCAGTGAATAGCTGCTTTCATAGCACACCTCTTTTGTGACATCTTCGGGTA 1201
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RESULT 14

US-10-270-176-20/c

; Sequence 20, Application US/10270176

; Publication No. US20040033608A1

; GENERAL INFORMATION:

```
; APPLICANT: Wanner, Barry
; APPLICANT: Haldimann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 4782
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-20
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Query Match 18.0%; Score 876.4; DB 13; Length 4782;
Best Local Similarity 71.6%; Pred. No. 1.1e-135;
Matches 1259; Conservative 0; Mismatches 441; Indels 58; Gaps 6;

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QY 1852 TAAGATGATATACGCGCGGTAAAGAGTTTCCAACTTTCACCATAAATGAATAAGATCACTA 1911
Db 4299 TGAGAGCTTGTATCGGCAGCAGTAAGAGGTTCCAACTTTCACCATAAATGAATAAGATCACTA 4240
QY 1912 CCGGGCGTATTTTGGAGTTATCGAGTTTTCAGAGAGCTTAAGGAAGCTAAAAATGGAGAAA 1971
Db 4239 CCGGGCGTATTTTGGAGTTATCGAGTTTTCAGAGAGCTTAAGGAAGCTAAAAATGGAGAAA 4180
QY 1972 AAAATCACTGGATATACCAACCGTTGATATATCCCAATGSCATCGTAAAGAAATTTTGAG 2031
Db 4179 AAAATCACTGGATATACCAACCGTTGATATATCCCAATGSCATCGTAAAGAAATTTTGAG 4120
QY 2032 GCAATTCAGTCACTGCTCAATGTAACCTATACCAAGACCGTTCAGCTGATATAGCGCC 2091
Db 4119 GCAATTCAGTCACTGCTCAATGTAACCTATACCAAGACCGTTCAGCTGATATAGCGCC 4060
QY 2092 TTTTAAAGACCGTAAAGAAAATTAAGCAACAAGTTTATCCGGCCCTTTATTCACATTTCT 2151
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QY 2332 GTGGGCTGTACGTTGAACAACTCGCCCTATTTCCCTAAAGGGTTTATGAGAAATATGTT 2391
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Db 3378 CTGAAGATCAGCAGTCTCAACCTGTTGATAGTACGTACTTAAGCTCTCATGTTTCAGGTACT 3319
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Qy 2992 AACMAACNATACTAATGCTAATATAAACAAGCGCAAGATCTATCAATTTTATATAGTAT 3051
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RESULT 15

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; Sequence 19, Application US/10270176
; Publication No. US20040033608A1
; GENERAL INFORMATION:
; APPLICANT: Wanner, Barry
; APPLICANT: Haldemann, Andreas
; TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
; FILE REFERENCE: 290.00140101
; CURRENT APPLICATION NUMBER: US/10/270,176
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/328,642
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/375,059
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 6742
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: CRIM plasmid
US-10-270-176-19
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Best Local Similarity 71.6%; Pred. No. 1.3e-135;
Matches 1259; Conservative 0; Mismatches 441; Indels 58; Gaps 6;

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Qy 1972 AAATCACTGATATACCACTGATATATCCCAATGCAATCGTAAGAACATTTTGAG 2031
Db 6139 AAATCACTGATATACCACTGATATATCCCAATGCAATCGTAAGAACATTTTGAG 6080
Qy 2032 GCATTTTCAGTCAGTTGCTCAATGATCTATTAACAGACCGTTTCAGCTGGATATTACGGCC 2091
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Qy 2152 GCCGCGCTGATGAATGCTCATCCGGAATTCGATGCAATGAAGACGCTGAGCTGGTG 2211
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Qy 2212 ATATGGATAGTTTTCACCCCTTTTACCGCTTTTCCATGAGCAAACTGAAACGTTTTC 2271
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QY 2632 TCCGGCTTACTAAAGCCAGATAACAGTATGCCGTATTGCGCGCTGATTTTCCGGTATA 2691
Db 5487 TTTTAAAGGCAGTTATTGGTGCCTCACT 5459
QY 2692 AGAATATATCTGATGTCGGGCCCATATAGTAATCTTAGCTGGTTGATCAATTAATA 2751
Db 5458 GATTAAGCATGGTAATCTGTACAGCCAAAGTTTACTCATATATATCTTTAGATTGATTATA 5399
QY 2752 TATCAATGATAAAATACTATAGTAAATAAAGAAATAAATAAATAAATAAATAAATAAATAA 2811
Db 5398 ACTTCATTTTAAATTTTGGCGCGCAAGATCCGGCCACGATCGGTCGGCGTAGAGGAT 5339
QY 2812 ATGATTAATAGTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2871
Db 5338 CTGAAGATCAGCATGTTCAAGCTGTGTAGTAGTACTAAGCTCTCATGTGTTCCAGTACT 5279
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Db 5278 AAGCTCTCATGTTTAAAGTACTAAGCTCTCATGTGTTCCAGTACTAAGCTCTCAT 5159
QY 2932 ATTAAATAACAAGCTAAAGTAACAATAATAATCAAACTAATAGAAACAGTAATCTAATGT 2991
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Db 5158 GTTTGAACAA-----TAAATTAATAATAAATCAGCACTTAAATAGCCTCTAAGGTTTTAA 5103
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Db 5050 ACGGTTGTGACAAACAAGCCAGGAGTGTAAACGCACATGAGAAGCCCTTAGAGCCTCTCAA 4991
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QY 3530 CATCACCGGACGACTTTGGCCGCAATAAATACCTGTGACGGAAGATCACTTCGCAGAA 3589
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:39:35 ; Search time 7540.15 Seconds

(without alignments)

19251.609 Million cell updates/sec

Title: US-10-055-001B-13_COPY_13040_17900

Perfect score: 4861

Sequence: 1 cgggcccacaaataatgattt.....atcattatttggggcccgag 4861

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_esti:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	732	15.1	782	28	BH242215
C 2	712	14.6	939	28	CC219264
C 3	697.4	14.3	783	28	BZ069663
C 4	697.4	14.3	812	28	BZ071317

C	5	697.4	14.3	848	28	BZ067942
C	6	697.4	14.3	903	28	BZ569330
C	7	697.2	14.3	789	28	BZ086476
C	8	696.4	14.3	799	28	BZ070237
C	9	695.4	14.3	794	28	BZ070076
C	10	695.2	14.3	719	28	BZ057486
C	11	695.2	14.3	785	28	BZ077741
C	12	694.8	14.3	792	28	BZ070235
C	13	694.8	14.3	797	28	BZ069987
C	14	693.8	14.3	797	28	BZ070648
C	15	693.6	14.3	725	28	BH960653
C	16	693.4	14.3	762	28	BZ077280
C	17	693	14.3	811	28	BZ070474
C	18	692.8	14.3	799	28	BZ085150
C	19	692.6	14.2	885	28	BZ084529
C	20	691.6	14.2	892	28	BZ083912
C	21	691.2	14.2	746	28	BZ064939
C	22	690	14.2	790	28	BZ070298
C	23	689.6	14.2	751	28	BZ069698
C	24	688.2	14.2	794	28	BH243026
C	25	687.4	14.1	800	28	BZ069387
C	26	687	14.1	930	28	BZ056540
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C	29	683.6	14.1	831	28	BH239118
C	30	682.2	14.0	792	28	BZ069550
C	31	681.2	14.0	780	28	BZ085923
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C	33	681.2	14.0	799	28	BZ069940
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C	35	680.2	14.0	689	28	BH936398
C	36	679.2	14.0	766	28	BZ085715
C	37	679.2	14.0	767	28	BH920449
C	38	678.6	14.0	775	28	BZ063552
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ALIGNMENTS

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LOCUS
DEFINITION
ATZFD43TF ATZF Arabidopsis thaliana genomic clone ATZFD43, genomic survey sequence.
ACCESSION
BH242215
VERSION
BH242215.1
GI:16917233
SOURCE
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ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 782)
Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V., Feldhym, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T20G10
Unpublished (2001)
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1370. Caution: the DNA in this BAC may be from some non-Arabidopsis source
Seq primer: TF

BH242215 782 bp DNA linear GSS 13-NOV-2001
ATZFD43TF ATZF Arabidopsis thaliana genomic clone ATZFD43, genomic survey sequence.

ACCESSION
BH242215
VERSION
BH242215.1
GI:16917233
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 782)
Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V., Feldhym, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T20G10
Unpublished (2001)
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1370. Caution: the DNA in this BAC may be from some non-Arabidopsis source
Seq primer: TF

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Class: sheared ends.
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/db_xref="taxon:3702"
/clone_lib="ATZF"
/notes="Vector: pROS2; Site 1: BstXI; 2-3 Kb sheared BAC
DNA inserted into pROS2 using BstXI linkers"

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Best Local Similarity 98.4%; Pred. No. 8.6e-122;
Matches 760; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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DB 775 TGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCCACCATATGAATAAGATCACTA 716
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DB 655 AAATCACTGATATACACCGTTGATATATCCCAATGGCATCTGAAGACATTTTGAG 596
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DB 595 GCATTTCACTGAGTTGCTCAATGTACCTATATAACAGACCGTTTCAGCTGGATATACCGCC 536
QY 2092 TTTTAAAGCCGTAAGAAAAAATAAGACAAAGTTTATCCGGCTTTATTCACATCTT 2151
DB 535 TTTTAAAGCCGTAAGAAAAAATAAGACAAAGTTTATCCGGCTTTATTCACATCTT 476
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DB 55 AATGCTTAAATGAATPACAACTACTGCGATGAGTGGCAGGCGGGGGGTA 4

RESULT 2
CC219264/c 939 bp DNA linear GSS 12-MAY-2003
LOCUS
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DEFINITION

CH261-114B11_Sp6.1 CH261 Gallus gallus genomic clone CH261-114B11,

genomic survey sequence.

ACCESSION

CC219264

VERSION

CC219264.1 GI:30541330

KEYWORDS

GSS.

SOURCE

Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 939)

AUTHORS

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,

Warren, W., Graves, T., Mardis, E. and Wilson, R.

TITLE

Gallus gallus BAC End Reads

JOURNAL

Unpublished (2003)

COMMENT

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@wustl.edu

Insert Length: 182000 Std Error: 0.00

Seq primer: Sp6 ATTAGGTGACACTATAG

Class: BAC ends

High quality sequence start: 36

High quality sequence stop: 800.

Location/Qualifiers

1. .939

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/mol_type="genomic DNA"

/strain="Red Jungle Fowl"

/db_xref="taxon:9031"

/clone="CH261-114B11"

/sex="female"

/cell_line="UCD001, inbred 256"

/clone_lib="CH261"

/notes="Vector: pARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;

CH261 Female Chicken library - for library and clone

ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 14.6%; Score 712; DB 28; Length 939;

Best Local Similarity 97.7%; Pred. No. 3.2e-118;

Matches 733; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

QY 1876 GGTTCCAACTTTCCACCAATGAATAAA--GATCACTACCGGGGATATTTTTCAGTTAT 1933

DB 918 GTTCCCAATTTTCCCTTATGAATAAAGATCACTTCCCGGGGATATTTTTCAGTTAT 859

QY 1934 CGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCG 1993

DB 858 CGAGATTTTCAGGAGCTAAGGAAGCTAAATGGAGAAAAAATCACTGGATATACCACCG 799

QY 1994 TTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCAGTCTGCTCAAT 2053

DB 798 TTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTTTCAGTCTGCTCAAT 739

QY 2054 GTACCTATAACACGACCGTTTCAGCTGGATATACGCGCTTTTAAAGACCGTAAGAAAA 2113

DB 738 GTACCTATAACACGACCGTTTCAGCTGGATATACGCGCTTTTAAAGACCGTAAGAAAA 679

QY 2114 ATAAGCAAGTTTATCCGCGCTTTATTCACATTTTCCCGCTTCATGATGCTCATC 2173

DB 678 ATAAGCAAGTTTATCCGCGCTTTATTCACATTTTCCCGCTTCATGATGCTCATC 619

QY 2174 CGGAATTCGCTATGGCAATGAAGACGTTGAGTGGTGATATGGGATAGTTCACCGTT 2233

DB 618 CGGAGTTCCGTTATGGCAATGAAGACGTTGAGTGGTGATATGGGATAGTTCACCGTT 559

QY 2234 GTTACACCGTTTTCATGAGCAAACTGAAACGTTTTCATCGCTTCGAGTGAATACACG 2293

DB 558 GTTACACCGTTTTCATGAGCAAACTGAAACGTTTTCATCGCTTCGAGTGAATACACG 499

QY 2294 ACGATTTCCGCGAGTTTTCACATATATTCGCAAGATGTCGCTGTGTACCGTGAACACC 2353

Db 498 ACGATTCCGGCAGTTTCTACACATATATTCGCAAGATGGCGGTGTACGGTGAAACC 439
 QY 2354 TGGCTTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAAATCCCTGGG 2413
 Db 438 TGGCTTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAAATCCCTGGG 379
 QY 2414 TGAAGTTTCACCACTTTTGAATTAAGCGTGGCCAAATATGCACTTCTTCGCCCGCGTTT 2473
 Db 378 TGAAGTTTCACCACTTTTGAATTAAGCGTGGCCAAATATGCACTTCTTCGCCCGCGTTT 319
 QY 2474 TCACCAATGGGCAATATATTACCAAGCGCAAGGTGCTGATGCGCGTGGCGATTTCAGG 2533
 Db 318 TCACCAATGGGCAATATATTACCAAGCGCAAGGTGCTGATGCGCGTGGCGATTTCAGG 259
 QY 2534 TTCAATATGCCGCTCTGATGCGTTTCCATATCGGCAAGATGCTTAATGAATTAACAAGT 2593
 Db 258 TTCAATATGCCGCTCTGATGCGTTTCCATATCGGCAAGATGCTTAATGAATTAACAAGT 199
 QY 2594 ACTGCGATGATGGCAGGGCGGGCGGTAAT 2623
 Db 198 ACTGCGATGATGGCAGGGCGGGCGGTAAT 169

RESULT 3

BZ069663/c 783 bp DNA linear GSS 10-OCT-2002
 LOCUS 1jt36e08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.

ACCESSION BZ069663

VERSION BZ069663.1 GI:23685962

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM

Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 783)

AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

CONTACT: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 1jt36 row: e column: 08

Seq primer: -21UPPOT forward

Class: shotgun

High quality sequence start: 8

High quality sequence stop: 551.

FEATURES Location/Qualifiers

source

1. .783

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/note=Vector: pOTw13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea T01000DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

ORIGIN

Query Match 14.3%; Score 697.4; DB 28; Length 783;

Best Local Similarity 97.8%; Pred.No. 1.5e-115;

Matches 707; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1903 AGATCACTACCGGCGGTTATTTTCAGTATTCGAGATTTTCAGGAGCTAAGGAAGCTAAA 1962

Db 752 AGCTTATCATCGATAAGCTTTTAATGAGTTTCGAGATTTTCAGGAGCTAAGGAAGCTAAA 693

QY 1963 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCATGGCATCGTAAAGAA 2022
 Db 692 ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCATGGCATCGTAAAGAA 633
 QY 2023 CATTTTGAAGGCAATTTTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGCTGGAT 2082
 Db 632 CATTTTGAAGGCAATTTTCAGTCAGTTGCTCAATGTACCTATAACAGACCGTTTCAGCTGGAT 573
 QY 2083 ATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCAAAAGTTTATCCGGCCTTTAT 2142
 Db 572 ATTACGGCCTTTTAAAGACCGTAAAGAAAAATAAGCAAAAGTTTATCCGGCCTTTAT 513
 QY 2143 CACATTTCTTCCCGCTGATGATGCTCATCCGGAATTCGGTATGCAATGAAGACCGT 2202
 Db 512 CACATTTCTTCCCGCTGATGATGCTCATCCGGAATTCGGTATGCAATGAAGACCGT 453
 QY 2203 GAGCTGCTGATATGGGATAGTTTACACCCCTTGTTCACCGCTTTTCCATGAGCAAACTGAA 2262
 Db 452 GAGCTGCTGATATGGGATAGTTTACACCCCTTGTTCACCGCTTTTCCATGAGCAAACTGAA 393
 QY 2263 AGCTTTTCATTCGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACATATAT 2322
 Db 392 AGCTTTTCATTCGCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACATATAT 333
 QY 2323 TCGCAGATGTGGCGTGTACCGTGAAACCTGGCCTATTTCCTAAAGGTTTATTGAG 2382
 Db 332 TCGCAGATGTGGCGTGTACCGTGAAACCTGGCCTATTTCCTAAAGGTTTATTGAG 273
 QY 2383 AATATGTTTTTCTCTCAGCCCAATCCCTGGTGAGTTTCAACAGTTTGTGATTTTAAACGTG 2442
 Db 272 AATATGTTTTTCTCTCAGCCCAATCCCTGGTGAGTTTCAACAGTTTGTGATTTAAACGTG 213
 QY 2443 GCCAATATGGACAACTTCTTCGCCCGCTTTTCCATGGCAAAATATTATAGCAAGGC 2502
 Db 212 GCCAATATGGACAACTTCTTCGCCCGCTTTTCCATGGCAAAATATTATAGCAAGGC 153
 QY 2503 GACAAAGTGTGATGCGCTGGCGATTTCAGTTTCATCATGCCGTCTGTGATGGCTTCCAT 2562
 Db 152 GACAAAGTGTGATGCGCTGGCGATTTCAGTTTCATCATGCCGTCTGTGATGGCTTCCAT 93
 QY 2563 GTCCGCGAAGTGTCTTAATGAATTTACAAAGTACTCGCATGAGTGGCAGGCGGGCGCTAA 2622
 Db 92 GTCCGCGAAGTGTCTTAATGAATTTACAAAGTACTCGCATGAGTGGCAGGCGGGCGCTAA 33
 QY 2623 TCG 2625
 Db 32 TTG 30

RESULT 4

BZ071317/c

LOCUS

DEFINITION

1jul3g05.b1 B.oleracea002 Brassica oleracea genomic, genomic survey

sequence.

ACCESSION BZ071317

VERSION BZ071317.1

KEYWORDS GI:23688254

SOURCE GSS.

ORGANISM

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 812)

AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

CONTACT: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: 1jul3 row: g column: 05

Seq primer: -21UPPOT forward

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Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers
1. 812
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T01000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 14.3%; Score 697.4; DB 28; Length 812;
Best Local Similarity 97.8%; Pred. No. 1.4e-115;
Matches 707; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1903 AGATCACTACCGGCGGTATTTTGGATTATCGAGATTTTCAGGAGCTAAGGAAGCTAAA 1962
DB 774 AGCTTATCATCGATAAGCTTTAAGATTATCGAGATTTTCAGGAGCTAAGGAAGCTAAA 715
QY 1963 ATGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022
DB 714 ATGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA 655
QY 2023 CATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTACTATTAACCAACCGTTTCAGTCGAT 2082
DB 654 CATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTACTATTAACCAACCGTTTCAGTCGAT 595
QY 2083 ATTACGGGCTTTTAAAGACCGTAAAGAAAAAATAAGCAAGTTTATTCGGGCTTTTATT 2142
DB 594 ATTACGGGCTTTTAAAGACCGTAAAGAAAAAATAAGCAAGTTTATTCGGGCTTTTATT 535
QY 2143 CACATTTTCGGGCTCATGAAATGCTCATCGGAATTCGGTATGGCAATGAAGAAGCGT 2202
DB 534 CACATTTTCGGGCTCATGAAATGCTCATCGGAATTCGGTATGGCAATGAAGAAGCGT 475
QY 2203 GAGCTGGTGATGGGATAGTGTTCACCTCTGTACACCGTTTTCATGAGCAAACTGAA 2262
DB 474 GAGCTGGTGATAGGATAGTGTTCACCTCTGTACACCGTTTTCATGAGCAAACTGAA 415
QY 2263 ACGTTTTCATCGCTCTGGAGTGAATACCAACGAGATTTTCGGGAGTTTCTACACATATAT 2322
DB 414 ACGTTTTCATCGCTCTGGAGTGAATACCAACGAGATTTTCGGGAGTTTCTACACATATAT 355
QY 2323 TCGCAAGATGGCGGTGTACGGTGAAACCTGGCTATTTCCCTAAGGGTTTATTGAG 2382
DB 354 TCGCAAGATGGCGGTGTACGGTGAAACCTGGCTATTTCCCTAAGGGTTTATTGAG 295
QY 2383 AATATGTTTTTTCGCTCAGCCAAATCCCTGGGTGAGTTTTCACAGTTTTCATTAACGCTG 2442
DB 294 AATATGTTTTTTCGCTCAGCCAAATCCCTGGGTGAGTTTTCACAGTTTTCATTAACGCTG 235
QY 2443 GCCAATATGGAACAATCTTCGCCCGCGTTTTCACATGGGCAATATATACGAAGGC 2502
DB 234 GCCAATATGGAACAATCTTCGCCCGCGTTTTCACATGGGCAATATATACGAAGGC 175
QY 2503 GACAGGTGCTATGCGGTGCGGATTCAGGTTTCATCGCGTCTGTGATGGCTTCCAT 2562
DB 174 GACAGGTGCTATGCGGTGCGGATTCAGGTTTCATCGCGTCTGTGATGGCTTCCAT 115
QY 2563 GTCCGAGATGCTTAATGAATTACAAAGTACTCGGATGAGTGGCGGGCGGCGTAA 2622
DB 114 GTCCGAGATGCTTAATGAATTACAAAGTACTCGGATGAGTGGCGGGCGGCGTAA 55
QY 2623 TCG 2625
DB 54 TTG 52

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RESULT 5

BZ067942/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 848

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/notes="Vector: pOTw13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea T01000DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

Seq primer: -288PpOT reverse

Class: shotgun

High quality sequence start: 16

High quality sequence stop: 551.

Location/Qualifiers

1. 848

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/notes="Vector: pOTw13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea T01000DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

Query Match 14.3%; Score 697.4; DB 28; Length 848;

Best Local Similarity 97.8%; Pred. No. 1.4e-115;

Matches 707; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 804 AGCTTATCATCGATAAGCTTTAATGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAA 745

QY 1963 ATGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022

DB 744 ATGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA 685

QY 2023 CATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTACTATTAACCAACCGTTTCAGTCGAT 2082

DB 684 CATTTTGGAGCATTTTCAGTCAGTTGCTCAATGTACTATTAACCAACCGTTTCAGTCGAT 625

QY 2083 ATTACGGGCTTTTAAAGACCGTAAAGAAAAAATAAGCAAGTTTATTCGGGCTTTATT 2142

DB 624 ATTACGGGCTTTTAAAGACCGTAAAGAAAAAATAAGCAAGTTTATTCGGGCTTTATT 565

QY 2143 CACATTTTCGGGCTCATGGAATGCTCATCGGAATTCGGTATGGCAATGAAGAAGCGT 2202

DB 564 CACATTTTCGGGCTCATGGAATGCTCATCGGAATTCGGTATGGCAATGAAGAAGCGT 505

QY 2203 GAGCTGGTGATGGGATAGTGTTCACCTCTGTACACCGTTTTCATGAGCAAACTGAA 2262

DB 504 GAGCTGGTGATGGGATAGTGTTCACCTCTGTACACCGTTTTCATGAGCAAACTGAA 445

QY 2263 ACGTTTTCATCGCTCTGGAGTGAATACCAACGAGTTTTCGGGAGTTTCTACACATATAT 2322

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Db      444  AGTTTTCATCGCTCGGAGTGAATACACGACGATTTCCGGAGTTTCTACACATATAT 385
QY      2323  TCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCTAAAGGGTTTATGTAG 2382
Db      384  TCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCTAAAGGGTTTATGTAG 325
QY      2383  ATATATTTTTCGTCCTCAGCAATCCCTGGGTGAGTTTCAACAGTTTGTATTAACGGTG 2442
Db      324  AATATGTTTTCGTCCTCAGCAATCCCTGGGTGAGTTTCAACAGTTTGTATTAACGGTG 265
QY      2443  GCCAATATGCAACACTTCTTCGCCCGCTTTTCACCATGGGCAATATATACGCAAGGC 2502
Db      264  GCCAATATGCAACACTTCTTCGCCCGCTTTTCACCATGGGCAATATATACGCAAGGC 205
QY      2503  GACAAGTGCTGATGCGCTGGCGATTTCAGGTTTCATCATGCCGTCTGTGATGCCCTTCCAT 2562
Db      204  GACAAGTGCTGATGCGCTGGCGATTTCAGGTTTCATCATGCCGTCTGTGATGCCCTTCCAT 145
QY      2563  GTCCGAGAAATGCTTAAATGAATTACACAGTACTGGGATGAGTGGCAGGCGGGCGGTAA 2622
Db      144  GTCCGAGAAATGCTTAAATGAATTACACAGTACTGGGATGAGTGGCAGGCGGGCGGTAA 85
QY      2623  TCG 2625
Db      84  TTG 82

RESULT 6
BZ569330
LOCUS      903 bp      DNA      linear      GSS 17-DEC-2002
DEFINITION pacs2-164_8345.x1 pacs2-164 Pseudomonas aeruginosa genomic clone
ACCESSION BZ569330
VERSION   BZ569330.1 GI:27203786
KEYWORDS  GSS.
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 903)
AUTHORS   Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
          Burns,J.L., Kaul,R. and Olsen,M.V.
          Whole-Genome-Sequence variation among multiple isolates of
          Pseudomonas aeruginosa library
          J. Bacteriol. (2002) In press
          Contact: Chris K. Raymond
          Genome Center
          University of Washington
          Box 352145, Seattle, WA 98105-2145, USA
          Tel: 2062216954
          Fax: 2066857244
          Email: craymond@u.washington.edu
          Class: shotgun.
FEATURES   source
            1. 903
               /organism="Pseudomonas aeruginosa"
               /mol_type="genomic DNA"
               /strain="2-164"
               /db_xref="taxon:287"
               /clone="pacs2-164_8345"
               /clone_lib="pacs2-164"
               /note="clinical isolate 2-164 Whole genomic shotgun
               library."
ORIGIN
Query Match 14.3%; Score 697.4; DB 28; Length 903;
Best Local Similarity 96.6%; Pred. No. 1.4e-115;
Matches 744; Conservative 0; Mismatches 22; Indels 4; Gaps 3;
QY 1854 AGATGATATACGGCGGTGAGAGGTTCCAACTTTCACCAATGAATGAATGAATCACTACC 1913
Db 117 AGACGTTGATCGGCACGTGAAGAGGTTCCAACTTTCACCAATGAATGAATGAATCACTACC 176

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QY      1914  GGGCGTATTTTGTGAGTTATCGAGATTTTTCAGGACGTAAAGAGCTAAATCGAGAAAA 1973
Db      177  GGGCGTATTTTGTGAGTTATCGAGATTTTTCAGGACGTAAAGAGCTAAATCGAGAAAA 236
QY      1974  AATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGC 2033
Db      237  AATCACTGATATACACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGC 296
QY      2034  ATTTCAGTCAGTTGCTCAATGATACCTATTAACAGACCGTTTCAGTGGATATACGCGCTT 2093
Db      297  ATTTCAGTCAGTTGCTCAATGATACCTATTAACAGACCGTTTCAGTGGATATACGCGCTT 356
QY      2094  TTTAAAGCCGTAAAGAAAAATAAGCAAGTTTATCCGGCTTTTATTCACATCTTTCG 2153
Db      357  TTTAAAGCCGTAAAGAAAAATAAGCAAGTTTATCCGGCTTTTATTCACATCTTTCG 416
QY      2154  CCGCCTGATGAATGCTCATCCGGAATTCGATGCAATGCAAGACGGTGAGTGTGAT 2213
Db      417  CCGCCTGATGAATGCTCATCCGGAATTCGATGCAATGCAAGACGGTGAGTGTGAT 476
QY      2214  ATGGGATGATGTTTACCCCTGTTTACACCGTTTTCATGAGCAAACTGAAACGTTTTCATC 2273
Db      477  ATGGGATGATGTTTACCCCTGTTTACACCGTTTTCATGAGCAAACTGAAACGTTTTCATC 536
QY      2274  GCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTTCGCAAGATGT 2333
Db      537  GCTCTGGAGTGAATACACGACGATTTCCGGCAGTTTCTACACATATATTTCGCAAGATGT 596
QY      2334  GGCGTGTACGGTGAACAACTCGCCCTATTTCCTAAAGGGTTTATTCAGAAATATGTTTTT 2393
Db      597  GGCGTGTACGGTGAACAACTCGCCCTATTTCCTAAAGGGTTTATTCAGAAATATGTTTTT 656
QY      2394  CGTCTCAGCCAAATCCCTGGGTGAGTTTTCACAGTTTTCATTTAAACGTGGCCCAATGGA 2453
Db      657  CGTCTCAGCCAAATCCCTGGGTGAGTTTTCACAGTTTTCATTTAAACGTGGCCCAATGGA 716
QY      2454  CAACTTCTTCGCCCGCTTTTTCACCATGGCAATATATACCAAGGCGCAAGGTGCT 2513
Db      717  CAACTTCTTCGCCCGCTTTTTCACCATGGCAATATATATACCAAGGCGCAAGGTGCT 776
QY      2514  GATCCGCTGGCGATTTCAGTTTCATCATGCCGTCTGTGATGGTTCATGTCGGCAGAT 2573
Db      777  GATCCGCTGGCGATTTCAGG-TCATCATGCCGTCTGTGATGGTTCATGTCGGCAGAT 834
QY      2574  GCTTAATGAATTACACAGTACTGCGATGATGCGAGGGCGGGCGGCGCTAAT 2623
Db      835  GCTTA--TGAATTACACAGTACTGCGATGATGCGAGGGCGGGCGGCGCTAAT 882

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RESULT 7

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BZ086476/c
LOCUS      lk194b10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BZ086476
VERSION   BZ086476.1 GI:23718434
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
REFERENCE 1 (bases 1 to 789)
AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
          Nash,W., Rabinowicz,P.D. and Wilson,R.K.
          Whole genome shotgun reads from Brassica oleracea
          Unpublished (2002)
          Contact: Richard K. Wilson
          Genome Sequencing Center
          Washington University School of Medicine
          Email: submissions@watson.wustl.edu
          Plate: lk194 row: b column: 10

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Seq primer: -21UpPOT forward
Class: shotgun
High quality sequence start: 20
High quality sequence stop: 551.
High quality sequence stop: 551.

FEATURES
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        1. .789
            /organism="Brassica oleracea"
            /mol_type="genomic DNA"
            /db_xref="taxon:3712"
            /clone_lib="B.oleracea002"
            /note="Vector: pOTw13; Whole genome shotgun library from
            flowering buds. DNA was purified from a crude nuclear
            prep using Brassica oleracea TO1000DH3 buds provided by
            Thomas Osborn at the University of Wisconsin. Genomic
            DNA was provided by Pablo Rabinowicz (CSHL) and the
            shotgun library prepared at Washington University Genome
            Sequencing Center."

ORIGIN
Query Match      14.3%; Score 697.2; DB 28; Length 789;
Best Local Similarity 97.4%; Pred. No. 1.6e-115;
Matches 708; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1903 AGATCACTACCGGCGGTATTTTGGCTATCGAGATTTTCAGAGCTAAGGAGCTAAA 1962
Db 743 AGCTTATCATCGATAAGCTTTAATGAGTTATCGAGATTTTCAGAGCTAAGGAGCTAAA 684

QY 1963 ATGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022
Db 683 ATGAGAAAAAATCACTGGATATACCACCGTTGATATATCNCATGGCATCGTAAAGAA 624

QY 2023 CATTTGAGGATTTAGTCAGTTGCTCAATGATACCTATTAACGACCGTTCAGCTGGAT 2082
Db 623 CATTTGAGGATTTAGTCAGTTGCTCAATGATACCTATTAACGACCGTTCAGCTGGAT 564

QY 2083 ATTACGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAGATTTTATCCGGCCTTTATT 2142
Db 563 ATTACGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAGATTTTATCCGGCCTTTATT 504

QY 2143 CACATTCGCGCCCTGATGAATGCTCATCCGGAATTCGGATGGCAATGAAGACGGT 2202
Db 503 CACATTCGCGCCCTGATGAATGCTCATCCGGAATTCGGATGGCAATGAAGACGGT 444

QY 2203 GAGCTGGTATGGGATAGTTGTTACCGTTGTTACACCGTTTCCATGACCAACTGAA 2262
Db 443 GAGCTGGTATGGGATAGTTGTTACCGTTGTTACACCGTTTCCATGACCAACTGAA 384

QY 2263 ACCTTTTATCATCGCTCTGAGTGAATACCACGACGATTTTCGGCAGTTTCTACACATAT 2322
Db 383 ACCTTTTATCATCGCTCTGAGTGAATACCACGACGATTTTCGGCAGTTTCTACACATAT 324

QY 2323 TCGAAGATGGGGTGTAGCGTGAATAACCTGGCCTATTTCCCTAAAGGGTTATTGAG 2382
Db 323 TCGAAGATGGGGTGTAGCGTGAATAACCTGGCCTATTTCCCTAAAGGGTTATTGAG 264

QY 2383 AATATGTTTTCGCTCTAGCCCAATCCCTGGGTGAGTTTACACGATTTTGAATTAACGTG 2442
Db 263 AATATGTTTTCGCTCTAGCCCAATCCCTGGGTGAGTTTACACGATTTTGAATTAACGTG 204

QY 2443 GCCAATATGGAACAATCTTCTCGCCCGCGTTTTCACCATGGGCAATATATTACGAAGGC 2502
Db 203 GCCAATATGGAACAATCTTCTCGCCCGCGTTTTCACCATGGGCAATATATTACGAAGGC 144

QY 2503 GACAAAGTCTGATCGCGTGGCGATTGAGTTTCATCATGCGCTCTGTGATGGCTTCCAT 2562
Db 143 GACAAAGTCTGATCGCGTGGCGATTGAGTTTCATCATGCGCTCTGTGATGGCTTCCAT 84

QY 2563 GTCCGAGAGTCTTAATCAATTAACAACAGTACTGCGATGAGTGGCAGGCGGGCGTAA 2622
Db 83 GTCCGAGAGTCTTAATCAATTAACAACAGTACTGCGATGAGTGGCAGGCGGGCGTAA 24

QY 2623 TCGCGTG 2629
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Db 23 TTGGGCG 17

RESULT 8

BZ070237/c

LOCUS

DEFINITION

BZ070237

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 799)

Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Nash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: lkj38 row: a column: 06

Seq primer: -21UpPOT forward

Class: shotgun

High quality sequence start: 8

High quality sequence stop: 551.

Location/Qualifiers

1. .799

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/note="Vector: pOTw13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea TO1000DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

ORIGIN

Query Match

Best Local Similarity

Matches 706; Conservative

14.3%; Score 696.4; DB 28; Length 799;

97.6%; Pred. No. 2.2e-115;

0; Mismatches 17; Indels

0; Gaps

0;

QY 1903 AGATCACTACCGGCGGTATTTTGGATTCAGATTTTCAGAGCTAAGGAGCTAAA 1962

Db 748 AGCTTATCATCGATAAGCTTTAATGAGTTATCGAGATTTTCAGAGCTAAGGAGCTAAA 689

QY 1963 ATGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022

Db 688 ATGAGAAAAAATCACTGGATATACCACCGTTGATATATCNCATGGCATCGTAAAGAA 629

QY 2023 CATTTGAGGATTTAGTCAGTTGCTCAATGATACCTATTAACGACCGTTCAGCTGGAT 2082

Db 628 CATTTGAGGATTTAGTCAGTTGCTCAATGATACCTATTAACGACCGTTCAGCTGGAT 569

QY 2083 ATTACGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAGATTTTATCCGGCCTTTATT 2142

Db 568 ATTACGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAGATTTTATCCGGCCTTTATT 509

QY 2143 CACATTCGCGCCCTGATGAATGCTCATCCGGAATTCGGATGGCAATGAAGACGGT 2202

Db 508 CACATTCGCGCCCTGATGAATGCTCATCCGGAATTCGGATGGCAATGAAGACGGT 449

QY 2203 GAGCTGGTATGGGATAGTTGTTACCGTTGTTACACCGTTTCCATGACCAACTGAA 2262

Db 448 GAGCTGGTATGGGATAGTTGTTACCGTTGTTACACCGTTTCCATGACCAACTGAA 389

QY 2263 ACCTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCGGCAGCTTTCTACACATATAT 2322
 DB |||||
 DB 388 ACCTTTTCATCGCTCTGGAGTGAATACACGACGATTTCCGGCAGCTTTCTACACATATAT 329
 QY 2323 TCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCCTAAAGGGTTTATTGAG 2382
 DB |||||
 DB 328 TCGCAAGATGTGGCGTGTACGGTGAACACCTGGCCCTATTTCCCTAAAGGGTTTATTGAG 269
 QY 2383 AATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTTTCACCAAGTTTGAATTAACAGTG 2442
 DB |||||
 DB 268 AATATGTTTTTCGTCTCAGCCAAATCCCTGGGTGAGTTTCACCAAGTTTGAATTAACAGTG 209
 QY 2443 GCCAATATGCAACACTTCTTCGCCCCCTTTTCCACCATGGCAAAATATTATACGCAAGC 2502
 DB |||||
 DB 208 GCCAATATGCAACACTTCTTCGCCCCCTTTTCCACCATGGCAAAATATTATACGCAAGC 149
 QY 2503 GACAAAGTGTCTGATGCCGTGGCGATTCAGGTTTCATCGCCGTCTGTGATGGCTTCCAT 2562
 DB |||||
 DB 148 GACAAAGTGTCTGATGCCGTGGCGATTCAGGTTTCATCGCCGTCTGTGATGGCTTCCAT 89
 QY 2563 GTCCGAGAGTCTTAAATGAATTAACAACAGTACTGCGATGAGTGGCAGGGCGGGGTAA 2622
 DB |||||
 DB 88 GTCCGAGAGTCTTAAATGAATTAACAACAGTACTGCGATGAGTGGCAGGGCGGGGTAA 29
 QY 2623 TCG 2625
 DB 28 TTG 26

RESULT 9
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 LOCUS 1kf64d08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.
 ACCESSION BZ070076
 VERSION BZ070076.1 GI:23686375
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eutrosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 794)
 AUTHORS Delehaenty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Willson,R.K.
 TITLE Whole genome shotgun reads from Brassica oleracea
 JOURNAL Unpublished (2002)
 COMMENT Contact: Richard K. Willson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Plate: lkf64 row: d column: 08
 Seq primer: -21UPpOT forward
 Class: Shotgun
 High quality sequence start: 24
 High quality sequence stop: 551.
 FEATURES Location/Qualifiers
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 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_lib="B.oleracea002"
 /note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000D3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 14.3%; Score 695.4; DB 28; Length 794;
 Best Local Similarity 99.1%; Pred. No. 3.3e-115;

Matches 699; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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 DB |||||
 DB 787 TTTATGATTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATCGAGAAAAAATCACT 728
 QY 1981 GGATATACACCGTGTATATATCCCAATGGCATCGTAAAGAACATTTTGGAGCATTTTCAG 2040
 DB |||||
 DB 727 GGATATACACCGTGTATATATCCCAATGGCATCGTAAAGAACATTTTGGAGCATTTTCAG 668
 QY 2041 TCAGTTGTCTAATGATACCTATAAACACGACCGTTACGTGGATATTACGCGCTTTTAAAG 2100
 DB |||||
 DB 667 TCAGTTGTCTAATGATACCTATAAACACGACCGTTACGTGGATATTACGCGCTTTTAAAG 608
 QY 2101 ACCGTAAAGAAAAAAGACACAAAGTTTATCCGGCTTTTATTCACATTTCTCCCGCCG 2160
 DB |||||
 DB 607 ACCGTAAAGAAAAAAGACACAAAGTTTATCCGGCTTTTATTCACATTTCTCCCGCCG 548
 QY 2161 ATGAATGCTCATCCGGAATTCGGTATGGCAATGAAAGACGGTGAAGTGGTATGGGAT 2220
 DB |||||
 DB 547 ATGAATGCTCATCCGGAATTCGGTATGGCAATGAAAGACGGTGAAGTGGTATGGGAT 488
 QY 2221 AGTGTTCACCTTTGTACACCGTTTCCATGAGCAACTGAACCGTTTTCATCGCTCTCG 2280
 DB |||||
 DB 487 AGTGTTCACCTTTGTACACCGTTTCCATGAGCAACTGAACCGTTTTCATCGCTCTCG 428
 QY 2281 AGTGAATACACGACGATTTCCGGCAGTTTTCACACATATATTCGCAAGATCTGGCTGT 2340
 DB |||||
 DB 427 AGTGAATACACGACGATTTCCGGCAGTTTTCACACATATATTCGCAAGATCTGGCTGT 368
 QY 2341 TACGGTGAACACCTCGCCTATTTCCTAAAGGGTTTATTGAGAAATATGTTTTTCTCTCA 2400
 DB |||||
 DB 367 TACGGTGAACACCTCGCCTATTTCCTAAAGGGTTTATTGAGAAATATGTTTTTCTCTCA 308
 QY 2401 GCCAATCCCTGGTGAAGTTTACACGATTTTGAATTTAAACGTCGCCAATATGACAACTTC 2460
 DB |||||
 DB 307 GCCAATCCCTGGTGAAGTTTACACGATTTTGAATTTAAACGTCGCCAATATGACAACTTC 248
 QY 2461 TTCGCCCCCGTTTTTACCATGGGCAATATTATACGCAAGGCGACAAAGTGTGTATGCCG 2520
 DB |||||
 DB 247 TTCGCCCCCGTTTTTACCATGGGCAATATTATACGCAAGGCGACAAAGTGTGTATGCCG 188
 QY 2521 CTGGCGAATTCAAGTTTCATCGCGCTGTGATGGCTTCCATGTCGCGAGAAATGCTTAAT 2580
 DB |||||
 DB 187 CTGGCGAATTCAAGTTTCATCGCGCTGTGATGGCTTCCATGTCGCGAGAAATGCTTAAT 128
 QY 2581 GAATTACAACTACTGCGATGAGTGGCAGGGCGGGCGTAAATCG 2625
 DB |||||
 DB 127 GAATTACAACTACTGCGATGAGTGGCAGGGCGGGCGTAAATCG 83

RESULT 10

BZ057486/c
 LOCUS 1kg74c10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.
 ACCESSION BZ057486
 VERSION BZ057486.1 GI:23665427
 KEYWORDS GSS.
 SOURCE Brassica oleracea

ORGANISM

Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eutrosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 719)
 AUTHORS Delehaenty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Willson,R.K.
 TITLE Whole genome shotgun reads from Brassica oleracea
 JOURNAL Unpublished (2002)
 COMMENT Contact: Richard K. Willson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu

RESULT 11
BZ077741/c
LOCUS
DEFINITION
BZ077741
ACCESSION
BZ077741
KEYWORDS
GSS.
SOURCE
ORGANISM
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica
1 (bases 1 to 785)
Delehaunty, K., Fell, G., Fulton, L., McComb, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Plate: 1k18 row: f column: 05
Seq primer: -21UpOT forward
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
1..785
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

Query Match 14.3%; Score 695.2; DB 28; Length 719;
Best Local Similarity 99.6%; Pred. No. 3.7e-115;
Matches 697; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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718 TGAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAATCGAGNAAAAATCACTGATA 659
1986 TACCACCGTTGATATATCCCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAGT 2045
658 TACCACCGTTGATATATCCCAATGGCATCGTAAGAACATTTTGAGGCAATTCAGTCAGT 599
2046 TGCTCAATGTACCTATTAACAGACCGTTAGCTGGATATTAAGCCCTTTTAAAGACCGT 2105
598 TGCTCAATGTACCTATTAACAGACCGTTAGCTGGATATTAAGCCCTTTTAAAGACCGT 539
2106 AAAGAAAAAATAGACAACTTTTCCGGCTTTTATTCACATTTCTCCGCCCTGTAGAA 2165
538 AAAGAAAAAATAGACAACTTTTCCGGCTTTTATTCACATTTCTCCGCCCTGTAGAA 479
2166 TGCTCATCCGGAATTCGGTATGGCAATGAAGACGGTGAGCTGGTATATGGGATAGTGT 2225
478 TGCTCATCCGAGTTCCGTATGGCAATGAAGACGGTGAGCTGGTATATGGGATAGTGT 419
2226 TCACCCCTTTTACACCGTTTTCATGAGCAACTGAAACGTTTTCATCGCTCTCGAGTGA 2285
418 TCACCCCTTTTACACCGTTTTCATGAGCAACTGAAACGTTTTCATCGCTCTCGAGTGA 359
2286 ATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGG 2345
358 ATACACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGG 299
2346 TGAAACCTGGCTATTTCCCTAAAGGTTTATGAGAAATATGTTTTTCGCTCTAGCCAA 2405
298 TGAAACCTGGCTATTTCCCTAAAGGTTTATGAGAAATATGTTTTTCGCTCTAGCCAA 239
2406 TCCCTGGGTGAGTTTACACGTTTGTATTAACCTGGCCATATGAGCAACTCTCTCGC 2465
238 TCCCTGGGTGAGTTTACACGTTTGTATTAACCTGGCCATATGAGCAACTCTCTCGC 179
2466 CCCCGTTTTACATGGGCAATATATACGCAAGCGCAAGGTCGTGATCCGCTGCG 2525
178 CCCCGTTTTACATGGGCAATATATACGCAAGCGCAAGGTCGTGATCCGCTGCG 119
2526 GATTCAGGTTTCATATGCGCTGTGATGGCTTCCATGTCGGAGATGCTTAATGAAT 2585
118 GATTCAGGTTTCATATGCGCTGTGATGGCTTCCATGTCGGAGATGCTTAATGAAT 59
2586 ACAAAGTACTGCGATGAGTGGCAGGCGGGCGGTAAATCG 2625
58 ACAAAGTACTGCGATGAGTGGCAGGCGGGCGGTAAATCG 19

QY	2346	TGAAACCTGGCTATTTCCCTAAAGGTTTATGAGATATGTTTTCGCTCAGCCAA	2405
Db	363	TGAAACCTGGCTATTTCCCTAAAGGTTTATGAGATATGTTTTCGCTCAGCCAA	304
QY	2406	TCCTGGGTGAGTTTACCAAGTTTGAATTTAAAGCTGGCCAAATATGACAACTTCTTCGC	2465
Db	303	TCCTGGGTGAGTTTACCAAGTTTGAATTTAAAGCTGGCCAAATATGACAACTTCTTCGC	244
QY	2466	CCCGTTTTTACCATGGGCAATATATACCAAGGCGACAAAGTGCTGATGCGGTGGC	2525
Db	243	CCCGTTTTTACCATGGGCAATATATACCAAGGCGACAAAGTGCTGATGCGGTGGC	184
QY	2526	GATTGAGTTTCATGCGGTCTGTGATGCTCCATGTCGGCAGATGCTTAATGAAT	2585
Db	183	GATTGAGTTTCATGCGGTCTGTGATGCTCCATGTCGGCAGATGCTTAATGAAT	124
QY	2586	ACACAGTACTGCGATGAGTGGCAGGCGGGCGGCGTAATCG	2625
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LOCUS			
DEFINITION			
BZ070235			
BZ070235.1			
GSS.			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
1 (bases 1 to 792)			
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,			
Nash, W., Rabinowicz, P.D. and Wilson, R.K.			
Whole genome shotgun reads from Brassica oleracea			
Unpublished (2002)			
Contact: Richard K. Wilson			
Genome Sequencing Center			
Washington University School of Medicine			
Email: submissions@watson.wustl.edu			
Plate: lkj38 row: a column: 04			
Seq primer: -2lupPOT forward			
Class: shotgun			
High quality sequence start: 16			
High quality sequence stop: 551.			
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/organism="Brassica oleracea"			
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/note="vector: pOTw13; whole genome shotgun library from			
flowering buds. DNA was purified from a crude nuclear			
prep using Brassica oleracea TO1000DH3 buds provided by			
Thomas Osborn at the University of Wisconsin. Genomic			
DNA was provided by Pablo Rabinowicz (CSHL) and the			
shotgun library prepared at Washington University Genome			
Sequencing Center."			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
14.3%; Score 694.8; Db 28; Length 792;			
97.5%; Pred. No. 4.3e-115;			
0; Mismatches 18; Indels 0; Gaps 0;			
QY	1903	AGATCACTACCGGCGTATTTTGTAGTTATCAGATTTTCAGAGCTAAGGAGCTAAA	1962
Db	748	AGCTTATCATCGATAGCTAAATAGTATTATCAGATTTTCAGAGCTAAGGAGCTAAA	689
QY	1963	ATGAGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA	2022

Db	688	ATGAGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA	629
QY	2023	CATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTAACCTATAACAGACCGTTTCAGCTGGAT	2082
Db	628	CATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTAACCTATAACAGACCGTTTCAGCTGGAT	569
QY	2083	ATTACCGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTATCCGGCTTTATT	2142
Db	568	ATTACCGGCTTTTAAAGACCGTAAAGAAAAAATAGCACAAAGTTTATCCGGCTTTATT	509
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Db	508	CAATTCTTCCCGCTGTGATGTAATGCTCATCCGGAATTCCTGATGGAATGGAAGACGGT	449
QY	2203	GAGCTGTGATATGGGATAGTTTACCCCTTGTACACCGTTTCCATGAGCAAACTGAA	2262
Db	448	GAGCTGTGATATGGGATAGTTTACCCCTTGTACACCGTTTCCATGAGCAAACTGAA	389
QY	2263	ACGTTTTTCATCGCTCTGGAGTGAATACACAGAGATTCGGGCAAGTTTCTACATATAT	2322
Db	388	ACGTTTTTCATCGCTCTGGAGTGAATACACAGAGATTCGGGCAAGTTTCTACATATAT	329
QY	2323	TCGCAAGATGTCGCTGTACGTTGAAACCTGCTTATTTCCCTAAGGGTTTATTGAG	2382
Db	328	TCGCAAGATGTCGCTGTACGTTGAAACCTGCTTATTTCCCTAAGGGTTTATTGAG	269
QY	2383	AATATGTTTTTCGCTCTCAGCAATCCCTGGGTGAGTTTCCACCACTTTTGAATTTAAACGTG	2442
Db	268	AATATGTTTTTCGCTCTCAGCAATCCCTGGGTGAGTTTCCACCACTTTTGAATTTAAACGTG	209
QY	2443	GCCAAATGGAACACTTCTTCCGCCCCCTTTTCCATGAGGCAAAATATATACCAAGGC	2502
Db	208	GCCAAATGGAACACTTCTTCCGCCCCCTTTTCCATGAGGCAAAATATATACCAAGGC	149
QY	2503	GACAAGTGTCTGATGCGCTGCGGCAATTCAGTTTCATCATGCGCTGTGATGGCTTCCAT	2562
Db	148	GACAAGTGTCTGATGCGCTGCGGCAATTCAGTTTCATCATGCGCTGTGATGGCTTCCAT	89
QY	2563	GTCGGCAGATGCTTAATGAATTACACAGTACTGCGATGAGTGGCGGGGCGGTAA	2622
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Db	28	TTG 26	
RESULT 13			
BZ069987/c			
LOCUS			
DEFINITION			
BZ069987			
BZ069987.1			
GSS.			
SOURCE			
ORGANISM			
Brassica oleracea			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
1 (bases 1 to 797)			
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,			
Nash, W., Rabinowicz, P.D. and Wilson, R.K.			
Whole genome shotgun reads from Brassica oleracea			
Unpublished (2002)			
Contact: Richard K. Wilson			
Genome Sequencing Center			
Washington University School of Medicine			
Email: submissions@watson.wustl.edu			
Plate: lkf31 row: c column: 12			
Seq primer: -28RPOT reverse			
Class: shotgun			
797 bp DNA linear GSS 10-OCT-2002			
lkf31c12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey			
sequence.			
BZ069987			
BZ069987.1			
GSS.			
Brassica oleracea			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
1 (bases 1 to 797)			
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,			
Nash, W., Rabinowicz, P.D. and Wilson, R.K.			
Whole genome shotgun reads from Brassica oleracea			
Unpublished (2002)			
Contact: Richard K. Wilson			
Genome Sequencing Center			
Washington University School of Medicine			
Email: submissions@watson.wustl.edu			
Plate: lkf31 row: c column: 12			
Seq primer: -28RPOT reverse			
Class: shotgun			

High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers

1. .797
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T0100DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

FEATURES
source

ORIGIN

Query Match 14.3%; Score 694.8; DB 28; Length 797;
Best Local Similarity 97.5%; Pred. No. 4.3e-115;
Matches 705; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1903 AGATCACTACCGGCGTATTTTGGAGTTATCGAGATTTTCAGGAGCTAAGAGCTAAA 1962
DB 761 AGCTTATCATCGATAAGCTTTAATGAGTTATCGAGATTTTCAGGAGCTAAGAGCTAAA 702

QY 1963 ATGGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA 2022
DB 701 ATGGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAATGGCATCGTAAAGAA 642

QY 2023 CATTTTGAGGCAATTCAGTTCAGTTGCTCAATGTACCTATATACCAACCGTTTCAGCTGGAT 2082
DB 641 CATTTTGAGGCAATTCAGTTCAGTTGCTCAATGTACCTATATACCAACCGTTTCAGCTGGAT 582

QY 2083 ATTACGGCCTTTTAAAGACCGTAAAGAAATTAAGCAAGTTTATCCCGCCTTTATTT 2142
DB 581 ATTACGGCCTTTTAAAGACCGTAAAGAAATTAAGCAAGTTTATTCGCGCCTTTATTT 522

QY 2143 CACATCTTCGCGCCTCATGAATCTCATCCGGAATTCGATGGCAATGAAGAAGCGGT 2202
DB 521 CACATCTTCGCGCCTCATGAATCTCATCCGGAATTCGATGGCAATGAAGAAGCGGT 462

QY 2203 GAGCTGGTGATATGGGATAGTTTCCACCTTTGTTACACCGTTTCCATGAGCAAACTGAA 2262
DB 461 GAGCTGGTGATATGGGATAGTTTCCACCTTTGTTACACCGTTTCCATGAGCAAACTGAA 402

QY 2263 ACGTTTTCATCGCTCTGGAGTGAATACCAACGAGTATTCGCGCAGTTTCTACACATATAT 2322
DB 401 ACGTTTTCATCGCTCTGGAGTGAATACCAACGAGTATTCGCGCAGTTTCTACACATATAT 342

QY 2323 TCGCAAGATGTGGCGTGTACGGTGAAACCTGGCGCTATTTCCCTAAAGGGTTTATTGAG 2382
DB 341 TCGCAAGATGTGGCGTGTACGGTGAAACCTGGCGCTATTTCCCTAAAGGGTTTATTGAG 282

QY 2383 AATATGTTTTTCGTCTACGCCAATCCCTGGGTGAGTTTCCAGATTTTGAATTAACGTTG 2442
DB 281 AATATGTTTTTCGTCTACGCCAATCCCTGGGTGAGTTTCCAGATTTTGAATTAACGTTG 222

QY 2443 GCGATATGGAACAATCTTCTCCGCCCTTTTCCACCATGGGCAAAATATTATACGCAAGGC 2502
DB 221 GCGAATATGGAACAATCTTCTCCGCCCTTTTCCACCATGGGCAAAATATTATACGCAAGGC 162

QY 2503 GACAAGGTGCTATGCGGTGGCGAATTCAGTTTCATCGCGCTCTGTGATGGCTTCCAT 2562
DB 161 GACAAGGTGCTATGCGGTGGCGAATTCAGTTTCATCGCGCTCTGTGATGGCTTCCAT 102

QY 2563 GTCGGCAGATGCTTATGAAATTAACAACAGTACTCGATGAGTGGCAGGCGGGCGGTAA 2622
DB 101 GTCGGCAGATGCTTATGAAATTAACAACAGTACTCGATGAGTGGCAGGCGGGCGGTAA 42

QY 2623 TCG 2625
DB 41 TTG 39

RESULT 14
BZ070648/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BZ070648 797 bp DNA linear GSS 10-OCT-2002
lk33h10.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
BZ070648
BZ070648.1 GI:23687090
GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 797)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: lk33 row: h column: 10
Seq primer: -28RPpOT reverse
Class: shotgun
High quality sequence start: 22
High quality sequence stop: 551.
High quality sequence/Qualifiers
1. .797
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T0100DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN

Query Match 14.3%; Score 693.8; DB 28; Length 797;
Best Local Similarity 99.0%; Pred. No. 6.4e-115;
Matches 698; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1921 TTTTTCGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAATGCGAAAAAATCACT 1980
DB 785 TTTAATGAGTTATCGAGATTTTCAGGAGCTAAGGAAGTAAATAATGCGAAAAAATCACT 726

QY 1981 GGATATACCCCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTCAG 2040
DB 725 GGATATACCCCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCAATTCAG 666

QY 2041 TCAGTTGCTCAATGTACCTATATACCAACCGTTTCAGCTGGATATACCGCCTTTTAAAG 2100
DB 665 TCAGTTGCTCAATGTACCTATATACCAACCGTTTCAGCTGGATATACCGCCTTTTAAAG 606

QY 2101 ACCGTAAAGAAAAATAAGCAAGTTTATCCGCGCTTTATTCACATTTTCGCCGCCCTG 2160
DB 605 ACCGTAAAGAAAAATAAGCAAGTTTATCCGCGCTTTATTCACATTTTCGCCGCCCTG 546

QY 2161 ATGAATGCTATCCGGAATTCGGTATGCAATGAAGACGGTGAGCTGTGATATGGAT 2220
DB 545 ATGAATGCTATCCGGAATTCGGTATGCAATGAAGACGGTGAGCTGTGATATGGAT 486

QY 2221 AGTGTTCACCCCTGTTTACACCGTTTCCATGAGCAAACTGAAACCGTTTTCATCGCTCTGG 2280
DB 485 AGTGTTCACCCCTGTTTACACCGTTTCCATGAGCAAACTGAAACCGTTTTCATCGCTCTGG 426

QY 2281 AGTGAATACCAACGAGATTTTCGGGAGTTTCTACATATATTCGACAGATGCGGCTGT 2340

Db	425	AGTGAATA	CGACGAT	TTCCGCGAG	TTCTCTACA	CATATAT	TCGCAAGAT	TGGCGGT	366				
Qy	2341	TACGGTGA	AAACCTG	GCCTAT	TTCCCTAA	AGGGTT	TATTTG	GAGATAT	GTGTTTCG	CTCA	2400		
Db	365	TACGGTGA	AAACCTG	GCCTAT	TTCCCTAA	AGGGTT	TATTTG	GAGATAT	GTGTTTCG	CTCA	306		
Qy	2401	GCCAA	TCCTGG	TGAGTT	CACAG	TTTTG	ATTAA	CGTGG	CCAA	TATG	GCAACTTC	2460	
Db	305	GCCAA	TCCCTGG	TGAGTT	CACAG	TTTTG	ATTAA	CGTGG	CCAA	TATG	GCAACTTC	246	
Qy	2461	TTGCCCC	CCCGTTT	CACCA	TGGCA	ATAT	TATAC	GCAAG	CGCA	AGGTG	CTGATG	CCG	2520
Db	245	TTGCCCC	CCCGTTT	CACCA	TGGCA	ATAT	TATAC	GCAAG	CGCA	AGGTG	CTGATG	CCG	186
Qy	2521	CTGGCA	TTCAG	GTTCAT	CGCTG	CTGTG	ATGG	CTTCC	ATGTC	GGCA	GAATG	CTTAAT	2580
Db	185	CTGGCA	TTCAG	GTTCAT	CGCTG	CTGTG	ATGG	CTTCC	ATGTC	GGCA	GAATG	CTTAAT	126
Qy	2581	GAATTACA	ACAGT	ACTCG	ATGAG	TGC	AGGCG	GGCG	CGTA	ATG			2625
Db	125	GAATTACA	ACAGT	ACTCG	ATGAG	TGC	AGGCG	GGCG	CGTA	ATG			81

RESULT 15	725 bp	DNA	linear	GSS 01-OCT-2002
BH960653/c	BH960653	odh4a12.b1	Brassica oleracea genomic,	genomic survey
LOCUS				
DEFINITION				sequence.

ACCESSION BH960653
 VERSION BH960653.1 GI:23441879
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 725)
 Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.
 Whole genome shotgun reads from Brassica oleracea
 Unpublished (2002)
 Contact: Richard K. Wilson
 REFERENCE AUTHORS
 TITLE
 JOURNAL
 COMMENT

ORIGIN		Sequencing Center			
Query Match	14.3%	Score 693.6;	DB 28;	Length 725;	
Best Local Similarity	99.4%;	Pred. No. 7.2e-115;			
Matches 696;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0
QY	1927	GAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAAAATCGAGAAAAAAATCTCGATAT	1981		
Db	725	GAGTTATCGAGATTTTCAGGAGCTAAGGAGCTAAAAATCGAGAAAAAAATCTCGATAT	666		

1987	QY	ACCACCGTTGATATATCCCAATGGCACTCTAAAGAACAATTTTGAGCAATTTTCAGTCAGTT	204
665	Db	ACCACCGTTGATATATCCCAATGGCACTCTAAAGAACAATTTTGAGGCAATTTTCAGTCAGTT	606
2047	QY	GCTCAATGTACCTATTAACACAGACCGTTCAGCTGGATATTACGGCCCTTTTAAAGACCGTA	2106
605	Db	GCTCAATGTACCTATTAACACAGACCGTTCAGCTGGATATTACGGCCCTTTTAAAGACCGTA	546
2107	QY	AAGAAAAATAAGCACAAAGTTTATCCGGCCCTTTATTCACATTCCTGCCGCCCTGTATGAAT	2166
545	Db	AAGAAAAATAAGCACAAAGTTTATCCGGCCCTTTATTCACATTCCTGCCGCCCTGTATGAAT	486
2167	QY	GCTCATCCGGAAATCCGTATGGCAANTGAAGACGCTGAGCTGCTGATATCGGATAGTGT	2226
485	Db	GCTCATCCGGAGTTCGTATGGCAANTGAAGACGCTGAGCTGCTGATATCGGATAGTGT	426
2227	QY	CACCTTGTATACACCGGTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTCGAGTGAA	2286
425	Db	CACCTTGTATACACCGGTTTTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTCGAGTGAA	366
2287	QY	TACACAGACGATTCGGCGAGTTCTACACATATATTCGAAGNTGGCGCTGTACGGT	2346
365	Db	TACACAGACGATTCGGCGAGTTCTACACATATATTCGAAGNTGGCGCTGTACGGT	306
2347	QY	GAAACCTGGCCATTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTCGCTCTCAGCCAAT	2406
305	Db	GAAACCTGGCCATTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTCGCTCTCAGCCAAT	246
2407	QY	CCCTGGGTGAGTTTCACAGCTTTTGATTTAAAGTGGCBAATATGGACACTCTTCGCC	2466
245	Db	CCCTGGGTGAGTTTCACAGCTTTTGATTTAAAGTGGCBAATATGGACACTCTTCGCC	186
2467	QY	CCCGTTTTACCATGGGCAAAATATTACGCAAGGGCAAGGTGCTGTATGCCGCTGGCG	2526
185	Db	CCCGTTTTACCATGGGCAAAATATTACGCAAGGGCAAGGTGCTGTATGCCGCTGGCG	126
2527	QY	ATTACAGGTTCAATGCGGCTGTGATGGCTTCCATGTCGCGAGAAGCTTTAATGAATTA	2586
125	Db	ATTACAGGTTCAATGCGGCTGTGATGGCTTCCATGTCGCGAGAAGCTTTAATGAATTA	66
2587	QY	CAACAGTACTCGCATGATGGCAGGGCGGGCGTAATCGC	2626
65	Db	CAACAGTACTCGCATGATGGCAGGGCGGGCGTAATCAC	26

Search completed: May 9, 2004, 21:55:46
Job time : 7545.35 secs